

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 2598.22 Seconds
(without alignments)
5321.503 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatgcgataagtaatgc.....ggaataccgcgtgaactta 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
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11: gb_sbs: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *
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16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
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23: em_pat: *
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27: em_sbs: *
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30: em_hcg_hum: *
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32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rtd: *
36: em_hcg_mam: *
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38: em_gy: *
39: em_hcgo_hum: *
40: em_hcgo_mus: *
41: em_hcgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	6 AR206400	AR206400 Sequence
2	319	100.0	319	6 BD083591	BD083591 Nucleic a
3	319	100.0	319	8 AF117921	AF117921 Nectria h
4	317	99.4	559	8 AY429048	AY429048 Chaetomiu
5	317	99.4	561	8 AY429053	AY429053 Chaetomiu
6	317	99.4	575	8 AY310442	AY310442 Nectria h
7	315.4	98.9	569	8 AY429049	AY429049 Chaetomiu
8	309.2	96.9	501	8 AY273332	AY273332 Unculture
9	308	96.6	509	8 AF165874	AF165874 Nectria h
10	300.2	94.1	582	8 AF455451	AF455451 Nectria h
11	298.6	93.6	550	8 AF178394	AF178394 Nectria h
12	298.6	93.6	550	8 AF178401	AF178401 Nectria h
13	298.6	93.6	569	8 AF129104	AF129104 Nectria h
14	297	92.4	548	8 AF178397	AF178397 Fusaarium
15	294.6	92.1	549	8 AF178398	AF178398 Nectria i
16	292	91.5	298	8 AY226096	AY226096 Nectria h
17	288.6	90.5	546	8 AF178413	AF178413 Neocosmos
18	288.2	90.3	548	8 AF178402	AF178402 Fusaarium
19	287	90.0	547	8 AF178412	AF178412 Neocosmos
20	286	89.7	566	8 NHA317959	AF317959 Nectria h
21	285.6	89.5	544	8 NEXITS	L36627 Neocosmospo
22	280.2	87.8	550	8 AF178406	AF178406 Fusaarium
23	279	87.5	480	8 AF150466	AF150466 Nectria h
24	279	87.5	480	8 AF150467	AF150467 Nectria h
25	279	87.5	480	8 AF40567	AF40567 Nectria h
26	277.2	86.9	550	8 AF178422	AF178422 Fusaarium
27	276.2	86.6	552	8 AF178411	AF178411 Nectria h
28	275.6	86.4	550	8 AF178407	AF178407 Fusaarium
29	275.6	86.4	550	8 AF178408	AF178408 Fusaarium
30	275	86.2	547	8 NECTISA	L36619 Nectria hae
31	270.6	84.8	549	8 AF178409	AF178409 Fusaarium
32	270	84.6	483	8 AY273333	AY273333 Unculture
33	269.2	84.4	548	8 AF178416	AF178416 Nectria h
34	268	84.0	418	8 AY243054	AY243054 Ascomycet
35	268	84.0	548	8 AF178395	AF178395 Nectria h
36	268	84.0	548	8 AF178404	AF178404 Fusaarium
37	268	84.0	566	8 AF130142	AF130142 Nectria h
38	267.4	83.8	518	8 AF437761	AF437761 Fungal is
39	265.8	83.3	547	8 AF178410	AF178410 Nectria h
40	265	83.1	545	8 NECTISB	L36620 Nectria hae
41	265	83.1	552	8 AF178421	AF178421 Nectria h
42	263.6	82.6	540	8 AY332483	AY332483 Stenocarp
43	263.6	82.6	1157	8 AY188918	AY188918 Nectria h
44	263.2	82.5	535	8 AY332486	AY332486 Stenocarp
45	263	82.4	544	8 AF178399	AF178399 Fusaarium

ALIGNMENTS

RESULT 1
AR206400
LOCUS AR206400 319 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6372430.
ACCESSION AR206400
VERSION AR206400.1 GI:21504990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 319)
AUTHORS Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.Soo.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL Patent: US 6372430-A 6 16-APR-2002;

FEATURES
source

ORIGIN

Location/Qualifiers
1..319
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 319; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.4e-79; Mismatches 0; Indels 0; Gaps 0;

Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCA 60
DB 1 GAAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCA 60
QY 61 CATTCGCGCGCGAGTATTCGCGGCGATGCTCTTGTGACGCTTATTAACAACCTTCAAG 120
DB 61 CATTCGCGCGCGAGTATTCGCGGCGATGCTCTTGTGACGCTTATTAACAACCTTCAAG 120
QY 121 CCCCCGCGCTGCGCTTGGGATCGGCGGAGCCCCCTGCGGCGACAACGCGCTCCCCCA 180
DB 121 CCCCCGCGCTGCGCTTGGGATCGGCGGAGCCCCCTGCGGCGACAACGCGCTCCCCCA 180
QY 181 AATACAGTGGCGGTCCCGCGACCTTCATTCGCTAGTACTTAACAACCTTCAAGTGA 240
DB 181 AATACAGTGGCGGTCCCGCGACCTTCATTCGCTAGTACTTAACAACCTTCAAGTGA 240
QY 241 GAGCG 300
DB 241 GAGCG 300
QY 301 GAATACCGCGCTGAACCTTAA 319
DB 301 GAATACCGCGCTGAACCTTAA 319

RESULT 2
BD083591

LOCUS 319 bp DNA linear PAT 27-AUG-2002
DEFINITION Nucleic acids for detecting Aspergillus species and other filamentous fungi.

ACCESSION BD083591.1 GI:22629201
VERSION BD083591.1
KEYWORDS JP 2001525665-A/6.
SOURCE Fusarium solani
ORGANISM Fusarium solani

REFERENCE 1 (bases 1 to 319)
AUTHORS Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.S.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi

JOURNAL Patent: JP 2001525665-A 6 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA HAS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
CENTERS FOR DISEASE PREVENTION AND CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE

COMMENT OS Fusarium solani
PN JP 2001525665-A/6
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PI 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA ALDOREVICH,JONG SOO
PC C1201/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key

FEATURES
source

1..319
Location/Qualifiers
/organism="Fusarium solani"
/mol_type="genomic DNA"
/db_xref="taxon:169388"

ORIGIN

/note="Fusarium solani"

Query Match 100.0%; Score 319; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.4e-79; Mismatches 0; Indels 0; Gaps 0;

Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCA 60
DB 1 GAAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCA 60
QY 61 CATTCGCGCGCGAGTATTCGCGGCGATGCTCTTGTGACGCTTATTAACAACCTTCAAG 120
DB 61 CATTCGCGCGCGAGTATTCGCGGCGATGCTCTTGTGACGCTTATTAACAACCTTCAAG 120
QY 121 CCCCCGCGCTGCGCTTGGGATCGGCGGAGCCCCCTGCGGCGACAACGCGCTCCCCCA 180
DB 121 CCCCCGCGCTGCGCTTGGGATCGGCGGAGCCCCCTGCGGCGACAACGCGCTCCCCCA 180
QY 181 AATACAGTGGCGGTCCCGCGACCTTCATTCGCTAGTACTTAACAACCTTCAAGTGA 240
DB 181 AATACAGTGGCGGTCCCGCGACCTTCATTCGCTAGTACTTAACAACCTTCAAGTGA 240
QY 241 GAGCG 300
DB 241 GAGCG 300
QY 301 GAATACCGCGCTGAACCTTAA 319
DB 301 GAATACCGCGCTGAACCTTAA 319

RESULT 3
AF117921

LOCUS 319 bp DNA linear PIN 17-JUN-2000
DEFINITION Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF117921.1 GI:8570107
VERSION AF117921.1
KEYWORDS
SOURCE Fusarium solani
ORGANISM Fusarium solani

REFERENCE 1 (bases 1 to 319)
AUTHORS Choi,J.S., Westerman,J.M. and Morrison,C.J.
TITLE Rapid differentiation of filamentous fungi using species-specific DNA probes

JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE 2 (bases 1 to 319)
AUTHORS Choi,J.S., Westerman,J.M. and Morrison,C.J.
TITLE Direct Submission

JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA

FEATURES
source

1..319
Location/Qualifiers
/organism="Fusarium solani"
/mol_type="Genomic DNA"
/db_xref="taxon:169388"
<1..159
/product="5.8S ribosomal RNA"
160..272
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/note="ITS2"
273..319
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 319; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.4e-79; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAAATGCGATAAGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 60
 DB 1 GAAAAATGCGATAAGTAATGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 60
 QY 61 CATTGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGG 120
 DB 61 CATTGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGG 120
 QY 121 CCCCCCGGCTTGGCGGATTCGGCGGAGACCCCTTCGCGGACCAACCGCTGCCCCA 180
 DB 121 CCCCCCGGCTTGGCGGATTCGGCGGAGACCCCTTCGCGGACCAACCGCTGCCCCA 180
 QY 181 AATAGAGTGGCGGTCCCGCGAGCTTCGATGCGGAGTGAACCTGCGCACTGGA 240
 DB 181 AATAGAGTGGCGGTCCCGCGAGCTTCGATGCGGAGTGAACCTGCGCACTGGA 240
 QY 241 GAGCGGCGCGGCGACCGCTTAACACCCAACTTGTGAATGTTGAAGCTTGAATCAGGTAG 300
 DB 241 GAGCGGCGCGGCGACCGCTTAACACCCAACTTGTGAATGTTGAAGCTTGAATCAGGTAG 300
 QY 301 GAATACCGCTGAATCTTAA 319
 DB 301 GAATACCGCTGAATCTTAA 319

RESULT 4
 AY429048 559 bp DNA linear PLN 30-NOV-2003

LOCUS
 DEFINITION Chaetomium globosum isolate Cg1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION
 VERSION AY429048.1 GI:38503524

KEYWORDS
 SOURCE Chaetomium globosum

ORGANISM Chaetomium globosum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

REFERENCE
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.
 TITLE Nucleotide sequence of full length ITS region of Cg1 isolate of Chaetomium globosum
 JOURNAL Unpublished

REFERENCE
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India

FEATURES
 SOURCE location/Qualifiers
 1..559
 /organism="Chaetomium globosum"
 /mol_type="genomic DNA"
 /isolate="Cg1"
 /db_xref="taxon:38033"

misc_RNA
 <1..>559
 /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
 Query Match 99.4%; Score 317; DB 8; Length 559;
 Best Local Similarity 100.0%; Pred. No. 5.4e-79; Indels 0; Gaps 0;
 Matches 317; Conservative 0; Mismatches 0;

QY 3 AATGCGATAAGTAATGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 62
 DB 201 AATGCGATAAGTAATGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 62
 QY 63 TTGGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGGCC 122
 DB 261 TTGGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGGCC 320

QY 123 CCGGCGCTGCGGCTTGGGAGATCGGCGAAGCCCTTCGCGGACCAACGCGTCCCCCAA 182
 DB 321 CCGGCGCTGCGGCTTGGGAGATCGGCGAAGCCCTTCGCGGACCAACGCGTCCCCCAA 380
 QY 183 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTGAATGATTAACCTCGCACTGAGAGA 242
 DB 381 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTGAATGATTAACCTCGCACTGAGAGA 440
 QY 243 GCGGCGCGGCGCAACCGCTTAACCAACCACTTGAATGTTGACCTGGAATCAGGTAGA 302
 DB 441 GCGGCGCGGCGCAACCGCTTAACCAACCACTTGAATGTTGACCTGGAATCAGGTAGA 500
 QY 303 ATACCGCTGAATCTTAA 319
 DB 501 ATACCGCTGAATCTTAA 517

RESULT 5
 AY429053 561 bp DNA linear PLN 30-NOV-2003

LOCUS
 DEFINITION Chaetomium globosum isolate Cg6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION
 VERSION AY429053.1 GI:38503529

KEYWORDS
 SOURCE Chaetomium globosum

ORGANISM Chaetomium globosum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

REFERENCE
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.
 TITLE Nucleotide sequence of full length ITS region of Cg6 isolate of Chaetomium globosum
 JOURNAL Unpublished

REFERENCE
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India

FEATURES
 SOURCE location/Qualifiers
 1..561
 /organism="Chaetomium globosum"
 /mol_type="genomic DNA"
 /isolate="Cg6"
 /db_xref="taxon:38033"

misc_RNA
 <1..>561
 /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
 Query Match 99.4%; Score 317; DB 8; Length 561;
 Best Local Similarity 100.0%; Pred. No. 5.4e-79; Indels 0; Gaps 0;
 Matches 317; Conservative 0; Mismatches 0;

QY 3 AATGCGATAAGTAATGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 62
 DB 203 AATGCGATAAGTAATGTAATGTAATGAGAAATTCAGATGATCATGGAATCTTTGAAGCGA 62
 QY 63 TTGGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGGCC 122
 DB 263 TTGGCGCCCGCAGTATTTCTGGCGGAGATGCGCTGTTGAGCGGTATTAACAACCTTCAGGCC 322
 QY 123 CCGGCGCTGCGGCTTGGGAGATCGGCGAAGCCCTTCGCGGACCAACGCGTCCCCCAA 182
 DB 323 CCGGCGCTGCGGCTTGGGAGATCGGCGAAGCCCTTCGCGGACCAACGCGTCCCCCAA 382
 QY 183 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTGAATGATTAACCTCGCACTGAGAGA 242
 DB 383 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTGAATGATTAACCTCGCACTGAGAGA 442

[illegible]

Db	480	GGGCGCGGCCACGCCTTAAACCAACTTCGTGAATGTTGACTCCGAATCAGTAGAGA	539
OY	303	ATAccCGcTAacTTAA 319 	
Db	540	ATAccCGcTAacTTAA 556 	
RESULT 7			
LOCUS	AY429049		
DEFINITION	AY429049	569 bp DNA linear PLN 30-NOV-2003	
	Chaetomium globosum isolate Cg2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AY429049		
VERSION	AY429049.1	GI:38503525	
SOURCE			
ORGANISM	Chaetomium globosum		
	Chaetomium globosum		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.		
REFERENCE	1 (bases 1 to 569)		
AUTHORS	Aggarwal, R., Renu, S. and Singh, D. V.		
TITLE	Nucleotide sequence of full-length ITS region of Cg2 isolate of Chaetomium globosum		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 569)		
AUTHORS	Aggarwal, R., Renu, S. and Singh, D. V.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India		
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misc_RNA			
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Query Match	98.9%; Score 315.4; DB 8; Length 569;		
Best Local Similarity	99.7%; Pred. No. 1.5e-78;		
Matches 316; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
OY	3	AAATGCATAAGTATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	62
Db	212	AAATGCATAAGTATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	271
OY	63	TTTGCCCCCGCAGTATCTTGCGCGGCATGTCCTGTTGAGCGTCATTACAACTCTCAGGCC	122
Db	272	TTTGCCCCCGCAGTATCTTGCGCGGCATGTCCTGTTGAGCGTCATTACAACTCTCAGGCC	331
OY	123	CCCGGAGCTTGCGCGTTGGGGGATTCGGCGGAACCCCCTCGCGGCAACAACGCCGTCGCCCAA	182
Db	332	CCCGGAGCTTGCGCGTTGGGGGATTCGGCGGAACCCCCTCGCGGCAACAACGCCGTCGCCCAA	391
OY	183	TACAGTGGCGGATCCCGCGCAGCTTCATTCGCTAGTAGCTAACACCTCGCACTGGAGA	242
Db	392	TACAGTGGCGGATCCCGCGCAGCTTCATTCGCTAGTAGCTAACACCTCGCACTGGAGA	451
OY	243	GCGGCGGGGCGCACGCCGTAAAACACCACACTTTGTAATGTTGACCTCGAATCAGTAGAGA	302
Db	452	GCGGCGGGGCGCACGCCGTAAAACACCACACTTTGTAATGTTGACCTCGAATCAGTAGAGA	511
OY	303	ATAccCGcTAacTTAA 319 	
Db	512	ATAccCGcTAacTTAA 528 	
RESULT 8			

AY273332 501 bp DNA linear PLN 30-OCT-2003
 LOCUS
 DEFINITION unclutred ascomycete clone T7A6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
 ACCESSION AY273332
 VERSION AY273332.1 GI:34420179
 KEYWORDS
 SOURCE unclutred ascomycete
 ORGANISM Eukaryota; Fungi; Ascomycota; environmental samples.
 REFERENCE 1 (bases 1 to 501)
 AUTHORS Roose-Amaele, C., Brygoo, Y. and Hary, M.
 TITLE Marked discrepancy between fungal diversity in soil-feeding termitaries and tropical soils
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 501)
 AUTHORS Roose-Amaele, C., Brygoo, Y. and Hary, M.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-2003) UFR Sciences Universite Paris 12, UMR137-LBSE, Avenue du General de Gaulle, Creteil cedex 94010, France
 FEATURES
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 1..501
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 /clone="T7A6"
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 /note="<1..141
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 /product="5.8S ribosomal RNA"
 /note="293..>501
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 Best Local Similarity 99.0%; Pred. No. 8.7e-77;
 Matches 311; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 62
 Db 188 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 247
 Oy 63 TTGGCGCCGCGCAGTAATTTCTGGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGCC 122
 Db 248 TTGGCGCCGCGCAGTAATTTCTGGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGCC 307
 Oy 123 CCGGGGCTTGCGCTGGGGGATTCGGGGAAGCCCTTGGGGGACAAAGCCGCTCCGCCAAA 182
 Db 308 CCGGGGCTTGCGCTGGGGGATTCGGGGAAGCCCTTGGGGGACAAAGCCGCTCCGCCAAA 367
 Oy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGTAACTGCACTCGCACTGGAGA 242
 Db 368 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGTAACTGCACTCGCACTGGAGA 427
 Oy 243 GCGGCGGGCCACGCGCTTAACCAACCACTTTGTAATGTTGACCTCGAATCAAGTAGA 302
 Db 428 GCGGCGGGCCACGCGCTTAACCAACCACTTTGTAATGTTGACCTCGAATCAAGTAGA 487
 Oy 303 ATACCCGCTGAAT 316
 Db 488 ATACCCGCTGAAT 501

AF165874 509 bp DNA linear PLN 18-JUL-1999
 LOCUS
 DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
 ACCESSION AF165874
 VERSION AF165874.1 GI:5524731
 KEYWORDS
 SOURCE Fusarium solani
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
 REFERENCE 1 (bases 1 to 509)
 AUTHORS Iwen, P.C., Henry, T. and Hinrichs, S.H.
 TITLE Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive disease
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 509)
 AUTHORS Iwen, P.C., Henry, T. and Hinrichs, S.H.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6495, USA
 FEATURES
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 /organism="Fusarium solani"
 /mol_type="genomic DNA"
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 /db_xref="ATCC:62877"
 /db_xref="taxon:169388"
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 /product="internal transcribed spacer 1"
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 151..307
 /product="5.8S ribosomal RNA"
 308..480
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 481..>509
 /product="28S ribosomal RNA"
 ORIGIN
 Query Match 96.6%; Score 308; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 1.9e-76;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 62
 Db 202 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 261
 Oy 63 TTGGCGCCGCGCAGTAATTTCTGGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGCC 122
 Db 262 TTGGCGCCGCGCAGTAATTTCTGGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGCC 321
 Oy 123 CCGGGGCTTGCGCTGGGGGATTCGGGGAAGCCCTTGGGGGACAAAGCCGCTCCGCCAAA 182
 Db 322 CCGGGGCTTGCGCTGGGGGATTCGGGGAAGCCCTTGGGGGACAAAGCCGCTCCGCCAAA 381
 Oy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGTAACTGCACTCGCACTGGAGA 242
 Db 382 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGTAACTGCACTCGCACTGGAGA 441
 Oy 243 GCGGCGGGCCACGCGCTTAACCAACCACTTTGTAATGTTGACCTCGAATCAAGTAGA 302
 Db 442 GCGGCGGGCCACGCGCTTAACCAACCACTTTGTAATGTTGACCTCGAATCAAGTAGA 501
 Oy 303 ATACCCGC 310
 Db 502 ATACCCGC 509

```

RESULT 10
AF455451      582 bp      DNA      linear      PLN 16-JUN-2003
LOCUS
DEFINITION
Nectria haematococca isolate wb394 small subunit ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene and internal transcribed spacer 2, complete
sequence; and large subunit ribosomal RNA gene, partial sequence.
ACCESSION
AF455451      GI:21666882
VERSION
AF455451.1
KEYWORDS
Nectria haematococca
Nectria haematococca
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE
1 (bases 1 to 582)
Buzina, W., Braun, H., Freudenrichs, K., Lackner, A. and
Stammbeger, H.
Fungal biodiversity as found in nasal mucus
Med. Mycol. 41 (2): 149-161 (2003)
2 (bases 1 to 582)
Buzina, W., Braun, H., Freudenrichs, K., Lackner, A. and
Stammbeger, H.
Direct Submision
Submitted (04-DEC-2001) Laboratory for Mycology and Molecular
Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A
8036, Austria
FEATURES
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1..582
/organism="Nectria haematococca"
/mol_type="genomic DNA"
/isolate="wb394"
/db_xref="taxon:140110"
<1..45
/product="small subunit ribosomal RNA"
46..196
/product="internal transcribed spacer 1"
197..352
/product="5.8S ribosomal RNA"
353..524
/product="internal transcribed spacer 2"
525..582
/product="large subunit ribosomal RNA"
ORIGIN
Query Match      94.1%; Score 300.2; DB 8; Length 582;
Best Local Similarity 98.7%; Pred. No. 3.1e-74;
Matches 313; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 3 AAATGCATAGTATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGACA 62
DB 247 AAATGCATAGTATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGACA 306
QY 63 TTGGCCCGCCAGTATTCGGCGGGCATGCTGTTCGAGCGTCATTACAACTTCAGGCC 122
DB 307 TTGGCCCGCCAGTATTCGGCGGGCATGCTGTTCGAGCGTCATTACAACTTCAGGCC 366
QY 123 CCGGGGCTGGCGGTGGGGATCGCGGGAAGCCCCCTCGCGGACAAAGCGCGTCCCCCAA 182
DB 367 CCGGGGCTGGCGGTGGGGATCGCGGGAAGCCCCCTGTGGGAC-AGCGCGTCCCTCAA 425
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCGATTCGAGTGAAGTAAACACTCGCAACTGGAGA 242
DB 426 TACAGTGGCGGTCCCGCGGAGCTTCGATTCGAGTGAAGTAAACACTCGCAACTGGAGA 485
QY 243 GCGGCGGCGCCACGCGGTAAACACCACTTCTGAATTGTTGAAGTTGAAGTGAAGA 302
DB 486 GCGGCGGCGCCATGCGGTAAACACCACTTCTGAATTGTTGAAGTTGAAGTGAAGA 545
QY 303 ATACCGCGTGAACCTTAA 319
DB 546 ATACCGCGTGAACCTTAA 562

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RESULT 11
AF178394      550 bp      DNA      linear      PLN 20-DEC-2001
LOCUS
DEFINITION
Nectria haematococca mpiv strain NRRL22163 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION
AF178394      GI:10180235
VERSION
AF178394.1
KEYWORDS
Nectria haematococca mpiv (anamorph: Fusarium solani f. sp.
xanthoxyl)
Nectria haematococca mpiv
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE
1 (bases 1 to 550)
O'Donnell, K.
Molecular phylogeny of the Fusarium solani species complex
Unpublished
2 (bases 1 to 550)
O'Donnell, K.
Direct Submision
Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA,
ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES
source
1..550
/organism="Nectria haematococca mpiv"
/mol_type="genomic DNA"
/strain="NRRL22163"
/db_xref="taxon:135211"
/notes="forma specialis: xanthoxyl; anamorph: Fusarium
solani f. sp. xanthoxyl;"
<1..350
/notes="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"
ORIGIN
Query Match      93.6%; Score 298.6; DB 8; Length 550;
Best Local Similarity 98.4%; Pred. No. 8.8e-74;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 3 AAATGCATAGTATGTAATGCAATTCGAGTGAATCATCGAATCTTTGAACGACA 62
DB 235 AAATGCATAGTATGTAATGCAATTCGAGTGAATCATCGAATCTTTGAACGACA 294
QY 63 TTGGCCCGCCAGTATTCGGCGGGCATGCTGTTCGAGCGTCATTACAACTTCAGGCC 122
DB 295 TTGGCCCGCCAGTATTCGGCGGGCATGCTGTTCGAGCGTCATTACAACTTCAGGCC 354
QY 123 CCGGGGCTGGCGGTGGGGATCGCGGGAAGCCCCCTCGCGGACAAAGCGCGTCCCCCAA 182
DB 355 CCGGGGCTGGCGGTGGGGATCGCGGGAAGCCCCCTCGCGGAC-AGCGCGTCCCTCAA 413
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCGATTCGAGTGAAGTAAACACTCGCAACTGGAGA 242
DB 414 TACAGTGGCGGTCCCGCGGAGCTTCGATTCGAGTGAAGTAAACACTCGCAACTGGAGA 473
QY 243 GCGGCGGCGCCACGCGGTAAACACCCAACTTCTGAATGTTGAAGTTGAAGTGAAGA 302
DB 474 GCGGCGGCGCCACGCGGTAAACACCCAACTTCTGAATGTTGAAGTTGAAGTGAAGA 533
QY 303 ATACCGCGTGAACCTTAA 319
DB 534 ATACCGCGTGAACCTTAA 550

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RESULT 12
AF178401      550 bp      DNA      linear      PLN 20-DEC-2001
LOCUS
DEFINITION
Nectria haematococca mpiv strain NRRL22277 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S

```

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Min,B.R.	Direct Submision	Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji Dong, Chong Ro-cu, Seoul 110-743, Korea
FEATURES	source	Location/Qualifiers	
	organism="Fusarium solani"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:169388"		
	/note="submitted as Fusarium solani"		
	<1..30	/product="18S ribosomal RNA"	
	31..182	/product="internal transcribed spacer 1"	
	/note="ITS-1"		
	183..340	/product="5.8S ribosomal RNA"	
	341..511	/product="internal transcribed spacer 2"	
	/note="ITS-2"		
	512..>569	/product="28S ribosomal RNA"	
ORIGIN	Query Match	Best Local Similarity	Matches
	93.6%; Score 298.6; DB 8; Length 569;	98.4%; Pred. No. 8,9e-74;	Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Oy	3 AAATGCATTAAGTATGTGAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCACA	62	
Db	234 AAATGCATTAAGTATGTGAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCACA	293	
Oy	63 TTGGCCCCCGCAGATTCTGGCCGGGCAATGCCTGTTGAGAGTCAATTCAACCTTCAGGCC	122	
Db	294 TTGGCCCCCGCAGATTCTGGCCGGGCAATGCCTGTTGAGAGTCAATTCAACCTTCAGGCC	353	
Oy	123 CCGCGGCGCTGGCGTTGGGGGATTCGGCGGAGGCCCTCGGGCACAAGCGCCGTCCCAAA	182	
Db	354 CCGCGGCGCTGGCGTTGGGGGATTCGGCGGAGGCCCTCGGGCACAAGCGCCGTCCCAAA	412	
Oy	183 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTAGTGTACACCTTCGCACTGAGGA	242	
Db	413 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTAGTGTACACCTTCGCACTGAGGA	472	
Oy	243 GCGGCGGGGCGCAGCGCGTAAACCCCACTTCTGAATGTTGACCTGGAATCAGATGGA	302	
Db	473 GCGGCGGGGCGCAGCGCGTAAACCCCACTTCTGAATGTTGACCTGGAATCAGATGGA	532	
Oy	303 ATACCGCGTGAACCTTA 319		
Db	533 ATACCGCGTGAACCTTA 549		
RESULT 14	AF178397	548 bp	DNA
LOCUS	AF178397	548 bp	linear
DEFINITION	Fusarium ambrosium strain NRRL20438 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF178397		
VERSION	AF178397.1		
KEYWORDS			
SOURCE	Fusarium ambrosium		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; microsporitic Hypocreales; Fusarium.		
REFERENCE	1 (bases 1 to 548)		
AUTHORS	O'Donnell,K.		
TITLE	Molecular phylogeny of the Fusarium solani species complex		

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 548)
ATMOSPHERIC O'Donnell &	

Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA,
ARS, 1815 N. University St., Peoria, IL 61604, USA

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misc_RNA
<1..>548
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"
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ORIGIN

Query Match	93.1%	Score 297	DB 8	Length 548
Best Local Similarity	98.1%	Pred. No. 2.5e-73		
Matches 311; Conservative	0	Mismatches 5	Indels 1	Gaps 1

[illegible]

RESULT 15

LOCUS	AF178398	549 bp	DNA	linear	PLN 20-DEC-2001
DEFINITION	Nectria ipomoeae strain NRRL2101 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.				

REFERENCE 1 (bases 1 to 549)

TITLE	JOURNAL	REFERENCE
Molecular phylogeny of the <i>Fusarium solani</i> species complex	Unpublished	2 (bases 1 to 549)

TITLE	Direct Submission
JOURNAL	Submitted (18-AUG-1999)
ARS	Microbial Properties Research, NCAR, USA
FEATURES	1815 N. University St., Peoria, IL 61604, USA
	Location/Qualifiers

misc_RNA

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/mol_type="genomic DNA"
/strain="NRR122101"
/db_xref="taxon:57162"
<!-->549
/notes="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA".

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ORIGIN

Query Match	92.4%;	Score 294.6;	DB 8;	Length 549;
Best Local Similarity	95.6%;	Pred. No. 1.2e-72;		
Matches 303;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;

Qy	3	AAATGGGATGAGAAATGTGAATTGAGAAATTCAGTGAATCATCCAAATCTTTGAACGCACA	62
Db	233	AAATGGGATGAGTAATGTGAATTGAGAAATTCAGTGAATCATCCAAATCTTTGAACGCACA	232
Qy	63	TTGCGCCCGCAGATATTCGCGGGCAGTCCCTGTTGCAGCGGTCAATTACAAACCCCAAGGCC	122
Db	293	TTTCGCGCCCGCAGATATTCGCGGGCAGTCCCTGTTGCAGCTCATACAAACCCCAAGGCC	352
Qy	123	CCCGGGCCTTGCGTTGGAGGATCGGGGGAAGCCCCCTCGGGCAGACAAGCGTCGCCCAAA	182
Db	353	CCCGGGCCTTGCGTTGGAGGATCGGGGGAAGCCCCCTGTGGGAAGCGCGTCGCCCAAAA	412
Qy	183	TACAGTGGCGGTCTCCCGCCGACGCTTCGATGTGGTATGTGCTAAACAACCTCGCAATGTGAGA	242
Db	413	TACAGTGGCGGTCTCCCGCCGACGCTTCGATGTGGTATGTGCTAAACAACCTCGCAATGTGAGA	472
Qy	243	GGCGCGGAGCAGCGCGTAAAAACCCCACTTCTGAATGTTGACCTCGATCAGGTAGGA	302
Db	473	GGCGCGGAGCAGCGCGTAAAAACCCCAACTTCTGAATGTTGACCTCGAATCAGGTAGGA	532
Qy	303	ATAACCGCTGAACCTTAA	319
Db	533	ATAACCGCTGAACCTTAA	549

Search completed: October 1, 2004, 05:16:56
Job time : 2606.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57; Search time 565.953 seconds
(without alignments)
2394.501 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319
Sequence: 1 gaaatgcatgaatgaatgc.....ggaataccgcctgaacttaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N Geneseq_29Jan04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002s:*\n7: geneseqn2003as:*\n8: geneseqn2003bs:*\n9: geneseqn2003cs:*\n10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	2	AAV70850 Internal
2	244.4	76.6	2293	4	AA616211 Fungus ge
3	241.8	75.8	502	3	AAA61893 Fungarium
4	240.8	75.5	659	6	ABV78724 C. sinens
5	240.4	75.4	534	7	ACC50001 Internal
6	240.2	75.3	310	2	AAV70851 Internal
7	240	75.2	561	2	AAV59009 F. avenac
8	213.2	66.8	647	6	ABV78700 C. crassi
9	195.2	61.2	582	2	AAV65100 T. harzia
10	190	59.6	661	6	ABV78721 C. sinens
11	184.8	57.9	569	2	AAV65101 T. harzia
12	183.8	57.6	504	2	AAV65400 Fungarium
13	183.8	57.6	504	2	AAV62591 Fungarium
14	183.8	57.6	504	2	AAV59028 F. culmor
15	183.2	57.4	522	7	ACC49999 Internal
16	183.2	57.4	522	7	ACC50002 Internal
17	180.4	56.6	545	2	AAV62593 Fungarium
18	180.4	56.6	545	2	AAV59030 F. monili
19	180	56.4	546	2	AAV62596 Fungarium
20	180	56.4	546	2	AAV59007 F. poae i
21	179.6	56.3	546	2	AAV65099 T. harzia
22	176.4	55.3	521	7	ACC50000 Internal
23	174.8	54.8	503	2	AAV65401 Fungarium

24	174.8	54.8	503	2	AAV62592 Fungarium
25	174.8	54.8	503	2	AAV59029 F. gramin
26	171.4	53.7	504	4	AAV608426 Internal
27	166.8	52.3	659	6	ABV78715 C. sinens
28	165.2	51.8	625	6	ABV78718 C. sinens
29	165.2	51.8	632	6	ABV78709 C. sinens
30	165.2	51.8	632	6	ABV78706 C. sinens
31	165.2	51.8	664	6	ABV78703 C. sinens
32	165.2	51.8	667	6	ABV78712 C. sinens
33	163.6	51.3	615	5	AAV76260 Cortycaps
34	156.8	49.2	610	2	AAV90111 Phomopsis
35	155	48.6	537	3	AAZ91725 Rosellini
36	154.8	48.5	545	2	AAV05403 Microdoch
37	145.6	45.6	608	2	AAV90110 Phomopsis
38	138.8	43.5	549	3	AAZ91723 Rosellini
39	138.8	43.5	549	3	AAZ91724 Rosellini
40	134.2	42.1	382	3	AAA72783 5.8s rRNA
41	133.4	41.8	686	6	ABV78727 C. sinens
42	131.8	41.3	652	7	ABZ20765 Mucor
43	128.4	40.3	605	2	AAV90108 Euryptella
44	127.8	40.1	553	3	AAZ91726 Rosellini
45	127.4	39.9	537	6	ABA01153 Deuteromy

ALIGNMENTS

RESULT 1
AAV70850 standard; DNA; 319 BP.
ID AAV70850; 26-FEB-1999 (first entry)
Internal transcribed spacer 2 (ITS2) and adjacent regions.
Internal transcribed spacer 2: ITS2; probe: Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinellioideus f. circinellioideus; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
Fusarium solani.
MO9850584-A2.
12-NOV-1998.
01-MAY-1998; 98WO-US008926.
02-MAY-1997; 97US-0045400P.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Morrison CJ, Reiss E, Aldorevich L, Choi JS;
WPI; 1999-034737/03.
New nucleic acid probes for filamentous fungi - for detecting e.g. Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia, Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix species.
Claim 1; Page 12; 45pp; English.
The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,

DT 14-NOV-2000 (first entry)
 XX Fuvarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
 DE Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
 XX HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
 KW acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
 KW symptomatic infection; asymptomatic infection; potential HIV exposure;
 KW combination therapy; ds.
 XX Fuvarium sp. MF6381.
 OS WO200036132-A1.
 XX 22-JUN-2000.
 XX 09-DEC-1999; 99WO-US029356.
 XX 14-DEC-1998; 98US-0112168P.
 XX (MERI) MERCK & CO INC.
 XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
 PI Dombrowski AW;
 DR MPI; 2000-431606/37.
 XX New steroid compounds are HIV integrase inhibitors used for treating HIV
 PT infection and AIDS.
 XX Disclosure; Page 14; 113pp; English.
 XX The invention relates to novel steroid compounds derived from the African
 CC soil fungus Fuvarium sp. MF6381 (ATCC 74469) which act as inhibitors of
 CC HIV integrase. The invention encompasses cultures of Fuvarium sp. MF6381.
 CC The invention also relates to a composition comprising a compound of the
 CC invention in combination with an AIDS antiviral agent, an immunomodulator
 CC and an antileptic agent. The compounds of the invention may be used in
 CC the inhibition of HIV integrase and in the prevention and treatment of
 CC HIV infection. A wide range of state of HIV infection may be treated;
 CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
 CC both symptomatic and asymptomatic HIV infection; and actual or potential
 CC exposure to HIV. The compounds may be used to isolate HIV integrase
 CC mutants which are potentially useful as screening tools for antiviral
 CC compounds. The compounds may also be used to establish or determine the
 CC site at which other antivirals bind to HIV integrase (e.g., by
 CC competitive inhibition). The present sequence represents the ribosomal
 CC DNA (rDNA) internal transcribed spacer (ITS) region of Fuvarium sp.
 CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
 CC to standardise OS field)
 XX
 SQ Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
 Query Match 75.8%; Score 241.8; DB 3; Length 502;
 Best Local Similarity 88.2%; Pred. No. 1.6e-70;
 Matches 276; Conservative 0; Mismatches 32; Indels 5; Gaps 1;
 QY 2 AAAATGCGATGAATGTAATGCAATTCAGATTCATCGAATCTTTGAACGCAC 61
 DB 195 AAAATGCGATGAATGTAATGCAATTCAGATTCATCGAATCTTTGAACGCAC 254
 QY 62 ATTGCGCGCCGACGATTTCTGCGCGGCGATGCTGTTGACGCGTATTACAACCTTCAGGC 121
 DB 255 ATTGCGCGCCGACGATTTCTGCGCGGCGATGCTGTTGACGCGTATTACAACCTTCAGGC 314
 QY 122 CCGCGGCGCTGCGGATGCGGATCGGCGGAGCCCGCTGCGGCGACAACGCGTCCCGCAA 181
 DB 315 CCGCGGCGCTGCGGATGCGGATCGGCGGAGCCCGCTGCGGCGACAACGCGTCCCGCAA 369
 QY 182 ATACAGTGGCGGTCCTCCGCGGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAG 241
 DB 370 ATACAGTGGCGGTCCTCCGCGGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAA 429

QY 242 AGCGCGCGGCGACCGCTTAACACCACTTCTGATGTTGACCTCGAATCAGTAGG 301
 DB 430 CGCGCGCGGCGACCGCTTAACACCACTTCTGATGTTGACCTCGAATCAGTAGG 489
 QY 302 AATACCGGCTGAA 314
 DB 490 AATACCGGCTGAA 502
 RESULT 4
 ABV78724
 ID ABV78724 standard; rRNA; 659 BP.
 XX
 AC ABV78724;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE C. sinensis rRNA sequence #23.
 XX
 KW Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
 KW Cordyceps sinensis; ss.
 XX
 OS Cordyceps sinensis.
 XX
 XX JP2002204696-A.
 XX 23-JUN-2002.
 XX 12-JAN-2001; 2001JP-00004805.
 XX 12-JAN-2001; 2001JP-00004805.
 XX
 PA (HEAL-) HEALTHWAY KK.
 PA (KANE/) KANESHIRO N.
 XX
 DR MPI; 2002-639075/69.
 XX
 PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
 PT of seeds of Cordyceps sinensis.
 XX
 XX 26; Page 25; 33pp; Japanese.
 CC The invention relates to a novel base sequence which is part of a fully
 CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
 CC The base sequences can be used for the classification of Cordyceps
 CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
 CC invention.
 XX
 SQ Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;
 Query Match 75.5%; Score 240.8; DB 6; Length 659;
 Best Local Similarity 89.3%; Pred. No. 3.9e-70;
 Matches 284; Conservative 0; Mismatches 27; Indels 7; Gaps 2;
 QY 2 AAAATGCGATGAATGTAATGCAATTCAGATTCATCGAATCTTTGAACGCAC 61
 DB 259 AAAATGCGATGAATGTAATGCAATTCAGATTCATCGAATCTTTGAACGCAC 318
 QY 62 ATTGCGCGCCGACGATTTCTGCGCGGCGATGCTGTTGACGCGTATTACAACCTTCAGGC 121
 DB 319 ATTGCGCGCCGACGATTTCTGCGCGGCGATGCTGTTGACGCGTATTACAACCTTCAGGC 378
 QY 122 CCGCGGCGCTGCGGATGCGGATCGGCGGAGCCCGCTGCGGCGACAACGCGTCCCGCAA 181
 DB 379 CCGCGGCGCTGCGGATGCGGATCGGCGGAGCCCGCTGCGGCGACAACGCGTCCCGCAA 432
 QY 182 ATACAGTGGCGGTCCTCCGCGGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAG 241
 DB 433 ATACAGTGGCGGTCCTCCGCGGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAA 492
 QY 242 AGCGCGCGGCGACCGCTTAACACCACTTCTGATGTTGACCTCGAATCAGTAGG 301
 DB 493 CGCGCGCGGCGACCGCTTAACACCACTTCTGATGTTGACCTCGAATCAGTAGG 551

Accession	Species	Gene	Location/Qualifiers
Db	1T9GCGCCGCAAGATTC	GS	61
Qy	123	CCCGGAGCTCTGGG	123
Db	121	CCCGGAGCTCTGGG	121
Qy	183	TACAGTGGAGCTCCG	183
Db	174	TCNAGTGGAGCTCTC	174
Qy	243	GCAGCGGAGCTCCG	243
Db	234	GCAGCGGAGCTCCG	234
Qy	303	ATACCGCTGAACCTT	303
Db	294	ATACCGCTGAACCTT	294
AAVS9009	standard	DNA	561 BP
AAVS9009			
17-OCT-2003	(revised)		
25-MAR-2003	(revised)		
06-JAN-1999	(first entry)		
F. avenaceum	internal transcribed spacer		
Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;			
Fungal pathogen identification; infection identification; ss.			
Gibberella avenacea.			
Key	Location/Qualifiers		
misc_feature	31..181		
misc_feature	/*tag= a		
misc_feature	/note= "ITS1"		
misc_feature	339..504		
misc_feature	/*tag= b		
misc_feature	/note= "ITS2"		
US5827695-A.			
27-OCT-1998.			
04-AUG-1997;	97US-00905314.		
04-AUG-1997;	97US-00905314.		
(NOVS) NOVARTIS FINANCE CORP.			
Beck JI;			
WPI; 1998-593995/50.			
Wheat pathogen internal transcribed spacer sequences - used as a basis			
for primers for the species-specific polymerase chain reaction detection			
of the pathogens.			
Claim 1; Col 29-30; 20pp; English.			

CC	correct PR field. (updated on 17-Oct-2003 to standardise OS field)
xx	
50	Sequence 561 BP, 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;
	Query Match 75.2%; Score 240; DB 2; Length 561;
	Best Local Similarity 88.7%; Pred. No. 6.8e-70;
	Matches 282; Conservative 2; Mismatches 27; Indels 7; Gaps 2
Qy	2 AAATGCGATAGTAAATGTAATTCGACAAATTCAGTGAATATCGAATCTTTGAAAGCGAC 61
Db	231 AAAATGCGATAGTAAATGTAATTCGACAAATTCAGTGAATATCGAATCTTTGAAAGCGAC 290
Qy	62 ATTGCGCGCGCGCAGTAATTCGCGCGGCATGCTGTTCCAGCGTCATTCAACCCCTCAGGC 121
Db	291 ATTGCGCGCGCGTGGTAATTCGCGCGGCATGCTGTTCCAGCGTCATTCAACCCCTCAGC 350
Qy	122 CCCCgggCCTTGCGTTGGGGGATTCGGCGGAAGCCCCCTTGGCGGCACAAAGCGCTCCCCCA 181
Db	351 CCCCgggTGTGTGTGTGGGGATTCGCTTGTGCGCGG-----TGCCTCCCCCGAA 404
Qy	182 ATACAGTGGCGGTCGCCGCGAGCTTCATTGTGCGTAGTACCACTTCGCACTGGAG 241
Db	405 ATACATTGGCGGTCTCGCTGCAGCTCCATTGCGTAGTACCACTTCGCACTGGAA 464
Qy	242 AGCGGCGCGGCACAGCGCGTAATAAACCCCACTTCTGAA TGTTCAGCTCGAATCAGTAGG 301
Db	465 CGCGGCGCGGCATAGCGGTAAAC-CCCACTTCTGAA TGTTCAGCTCGAATCAGTAGG 523
Qy	302 AATACCGCGTAGACTTAA 319
Db	524 AATACCGCGTAGACTTAA 541

XX	RESULT 8
XX	ABV78700
ID	ABV78700 standard; rRNA; 647 BP.
XX	
AC	ABV78700;
XX	
DT	14-JAN-2003 (first entry)
XX	
DE	C. crassispora rRNA sequence #2.
XX	
KM	Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
KM	Cordyceps sinensis; ss.
XX	
OS	Cordyceps crassispora.
XX	
PN	JP2002204696-A.
XX	
PD	23-JUL-2002.
XX	
PF	12-JAN-2001; 2001JP-00004805.
XX	
PR	12-JAN-2001; 2001JP-00004805.
XX	
PA	(HEAL-) HEALTHWAY KK.
XX	(KANE/) KANESHIRO N.
DR	WPI; 2002-639075/69.
XX	
PT	Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT	of seeds of Cordyceps sinensis.
XX	
PS	2; Page 12; 33pp; Japanese.
XX	
CC	The invention relates to a novel base sequence which is part of a fully
CC	defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
CC	The base sequences can be used for the classification of Cordyceps
CC	sinensis. The sequence represents a C. crassispora rRNA sequence of the
XX	invention
XX	
XX	Sequence 647 BP; 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;

Query	Subject	Score	Length	Identical	Mismatches	Gaps	Indels	Score	Length	Identical	Mismatches	Gaps	Indels
Q1	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	62	122	100	0	0	0	62	122	100	0	0	0
D1	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	328	122	100	0	0	0	328	122	100	0	0	0
Q2	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	122	122	100	0	0	0	122	122	100	0	0	0
D2	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	388	122	100	0	0	0	388	122	100	0	0	0
Q3	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	181	122	100	0	0	0	181	122	100	0	0	0
D3	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	430	122	100	0	0	0	430	122	100	0	0	0
Q4	ATACAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	241	122	100	0	0	0	241	122	100	0	0	0
D4	ATACAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	488	122	100	0	0	0	488	122	100	0	0	0
Q5	ATGCAAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	301	122	100	0	0	0	301	122	100	0	0	0
D5	ATGCAAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	548	122	100	0	0	0	548	122	100	0	0	0
Q6	AGCGGCGCGGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	319	122	100	0	0	0	319	122	100	0	0	0
D6	AGCGGCGCGGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	566	122	100	0	0	0	566	122	100	0	0	0
Q7	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	62	122	100	0	0	0	62	122	100	0	0	0
D7	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	328	122	100	0	0	0	328	122	100	0	0	0
Q8	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	122	122	100	0	0	0	122	122	100	0	0	0
D8	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	388	122	100	0	0	0	388	122	100	0	0	0
Q9	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	181	122	100	0	0	0	181	122	100	0	0	0
D9	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	430	122	100	0	0	0	430	122	100	0	0	0
Q10	ATACAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	241	122	100	0	0	0	241	122	100	0	0	0
D10	ATACAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	488	122	100	0	0	0	488	122	100	0	0	0
Q11	ATGCAAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	301	122	100	0	0	0	301	122	100	0	0	0
D11	ATGCAAGTGCAGCGATCCCGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	548	122	100	0	0	0	548	122	100	0	0	0
Q12	AGCGGCGCGGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	319	122	100	0	0	0	319	122	100	0	0	0
D12	AGCGGCGCGGCGCGAGCTTCGATTCGTAAGTAAACACCTCGCACTGGAG	566	122	100	0	0	0	566	122	100	0	0	0
Q13	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	62	122	100	0	0	0	62	122	100	0	0	0
D13	AAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTAAGCACA	328	122	100	0	0	0	328	122	100	0	0	0
Q14	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	122	122	100	0	0	0	122	122	100	0	0	0
D14	TTGGCCGCCGCGAGTATTCCTGGCGGCGATGCTTTCGAGCGTCATTACAACCTCAGGCC	388	122	100	0	0	0	388	122	100	0	0	0
Q15	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	181	122	100	0	0	0	181	122	100	0	0	0
D15	CCCC-GGGCTGCGCTTGGGGGATCGCGGGAAGCCCCCTCGGGGACAAAGCGCGTCCCCCA	430	122	100	0	0	0	430	122	100	0	0	0
Q16	ATACAGTGCAGCGAT												

(UTSA - UNIV SALAMANCA.
(CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
Monte Vazquez E, Grondona Espana I, Garcia Ancha I;
WPI, 1997-280728/25.

Liquid formulation of *Trichoderma harzianum* and *Trichoderma viride* strains - are used as biological control agents against diseases of plants and plant material and as bioinhibition agents.

Disclosure: Page 27, 37pp; Spanish.

The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA gene from the filamentous fungi *Trichoderma harzianum* strain IMI 352941. A novel liquid formulation based on strains of *T. harzianum* and *T. viride*, has the following composition (w/v%): 0.1-6 sorbitol; 0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)2PO4; 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2 manganese; and a biological component comprising at least one of: *T. harzianum* IMI 352939 (3 x 105 to 10 x 107 conidia/ml), *T. harzianum* IMI 352940 (3 x 105 to 10 x 107 conidia/ml), *T. harzianum* IMI 352941 (3 x 105 to 10 x 107 conidia/ml), *T. harzianum* CECT 20119 and/or *T. viride* CECT 20178. The *Trichoderma* fungi, alone or in combination, are used as gene recipients to increase activity of the formulation as a biological control agent against diseases of plants and plant material and biological entities causing biodeterioration, and as a bioinhibition (leaching) agent. It is particularly used e.g. in agriculture, forestry and gardening; for controlling microorganisms which damage food and its packaging; construction materials, raw materials and manufactured products. The antagonistic capacity of the four types of *T. harzianum* and one type of *T. viride* over other soil fungi makes them useful for control of plant diseases. Use of this formulation allows reduced application of polluting chemical pesticides and is thus more eco-friendly. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 569 BP, 139 A; 171 C; 143 G; 116 T; 0 U; 0 Other;

Query Match 57.9%; Score 184.8; DB 2; Length 569;
Best Local Similarity 83.4%; Pred. No. 2,1e-51;
Matches 272; Conservative 0; Mismatches 42; Indels 12; Gaps 5;

Y 3 AATGCGATAGTAATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGACA 62
Db 247 AATGCGATAGTAATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGACA 306

Y 63 TTGGGCCCCGCAAGTTCTGGCCGGGCAATGCTTTTCAGAGCTCATTTACACCCCTCAGGCC 122
Db 307 TTGGGCCCCGCAAGTTCTGGCCGGGCAATGCTTTTCAGAGCTCATTTACACCCCTCAGACC 366

Y 123 CC----CGGGCCTGCGGCTTGGGGAATCGGGCGGAGACCCCTCGCGGACCAACGCCGTCGCC 178
Db 367 CCTCGGGGGGGTCCGGCGTTGGGGACCTTCGGAGGCCCTTAAGACGG--GATCCCGGGCCC 423

Y 179 CAAATPACAGTGGCGGTCCCGCCGAGCTTCCATTGCGTAGTAGTAAACACTC--GCAG 235
Db 424 GAAATPACAGTGGCGGTCTTCGCCGAGCCTTCCTCGGAGTAGTAGTTGACAACTCGACAC 483

Y 236 CTGAGAGCGCGCGGGGCGACG--CCGTAAACACCCCACTTTCG--AATGTTGACCTCGAAT 293
Db 484 CGGAGCGCGCGGGCGGTCCACCTCGTAAACACCCCACTTCTGAAATGTTGACCTCGAAT 543

Y 294 CAGGTAGGAATPACCGCGTGAACCTTAA 319
Db 544 CAGGTAGGAATPACCGCGTGAACCTTAA 569

RESULT 12
AAT05400
ID AAT05400 standard; DNA; 504 BP.
AC
XX AAT05400;
XX

Sequence 1, Application US/09645073
Patent No. 6287800
GENERAL INFORMATION:
APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
PRIORITY FILING DATE: 2000-08-25
PRIORITY FILING DATE: 2000-08-25
PRIORITY FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent version 3.0
SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match 76.6%; Score 244.4; DB 3; Length 2293;
Best Local Similarity 88.1%; Pred. No. 1.1e-69;
Matches 280; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AAAATGCGATAGTAATGTGATGAGAAATTCAGTAATCATGAACTTTTGAACGAC 61
DB 1971 AAAATGCGATAGTAATGTGATGAGAAATTCAGTAATCATGAACTTTTGAACGAC 2030
QY 62 ATTGCGCGCGCGAGTATTCGCGCGGCAATGCTTTGAGCGCTATTACAACCTTCAGGC 121
DB 2031 ATTGCGCGCGCGAGTATTCGCGCGGCAATGCTTTGAGCGCTATTACAACCTTCAGGC 2090
QY 122 CCGCGGCGCTGCGCTTGGGAGATGCGCGGAAGCCCTTGGCGGCAACAAGCGCTCCCGCA 181
DB 2091 CCGCGGCGCTTGGGAGATGCGCGGCAAGCCCTTGGCGGCAACAAGCGCTCCCGCA 2143
QY 182 ATACAGTGGCGGCTCCCGCGAGCTTCATTCGTAAGTAACTTGAACCTTCAGGAG 241
DB 2144 ATACAGTGGCGGCTCCCGCGAGCTTCATTCGTAAGTAACTTGAACCTTCAGGAG 2203
QY 242 AGCG 301
DB 2204 CG 2263
QY 302 AATACCGCGTGAACCTTAA 319
DB 2264 AATACCGCGTGAACCTTAA 2281

RESULT 3
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
PRIORITY FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent version 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match 75.3%; Score 240.2; DB 4; Length 310;
Best Local Similarity 87.4%; Pred. No. 1.1e-68;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 3 AAATGCGATAGTAATGTGATGAGAAATTCAGTAATCATGAACTTTTGAACGAC 62
|||||

DB 1 AAATGCGATAGTAATGTGATGAGAAATTCAGTAATCATGAACTTTTGAACGAC 60
QY 63 TTGCGCGCGCGAGTATTCGCGCGGCAATGCTTTGAGCGCTATTACAACCTTCAGGC 122
DB 61 TTGCGCGCGCGAGTATTCGCGCGGCAATGCTTTGAGCGCTATTACAACCTTCAGGC 120
QY 123 CCGCGGCGCTGCGCTTGGGAGATGCGCGGAAGCCCTTGGCGGCAACAAGCGCTCCCGCA 182
DB 121 CCGCGGCGCTTGGGAGATGCGCGGAAGCCCTTGGCGGCAACAAGCGCTCCCGCA 173
QY 183 TACAGTGGCGGCTCCCGCGAGCTTCATTCGTAAGTAACTTGAACCTTCAGGAG 242
DB 174 TACAGTGGCGGCTCCCGCGAGCTTCATTCGTAAGTAACTTGAACCTTCAGGAG 233
QY 243 GCG 302
DB 234 GCG 293
QY 303 AATACCGCGTGAACCTTAA 319
DB 294 AATACCGCGTGAACCTTAA 310

RESULT 4
US-08-905-314A-24
Sequence 24, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8589
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..181

OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 75.2%; Score 240; DB 1; Length 561;
Best Local Similarity 88.7%; Pred. No. 1.6e-68;
Matches 282; Conservative 2; Mismatches 27; Indels 7; Gaps 2;

QY 2 AAATGCATAGTAATGTGAATTCAGAAATTCAGTAATTCAGAACTTTGAAGCAGC 61
DB 231 AAATGCATAGTAATGTGAATTCAGAAATTCAGTAATTCAGAACTTTGAAGCAGC 290
QY 62 ATGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGCGCTATTAACAACCTTCAGGC 121
DB 291 ATGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGCGCTATTAACAACCTTCAGGC 350
QY 122 CCGCGGCGCTGGCGGTGGGGAATCGCGGAGCCCGCTGCGGCAACGCGCTCCCGCA 181
DB 351 CCGCGGCGCTGGCGGTGGGGAATCGCGGAGCCCGCTGCGGCAACGCGCTCCCGCA 404
QY 182 ATACAGTGGCGGTCCCGCGCAGCTTCATTCGTAAGTGAAGTGAAGTGAAGTGAAG 241
DB 405 ATACAGTGGCGGTCCCGCGCAGCTTCATTCGTAAGTGAAGTGAAGTGAAGTGAAG 464
QY 242 AGCGCGCGGCGCAGCGCTTAACCAACCACTTCGTAAGTGAAGTGAAGTGAAGTGAAG 301
DB 465 AGCGCGCGGCGCAGCGCTTAACCAACCACTTCGTAAGTGAAGTGAAGTGAAGTGAAG 523
QY 302 AATACCGCGCTGAACCTTAA 319
DB 524 AATACCGCGCTGAACCTTAA 541

RESULT 5
US-08-652-127C-6
Sequence 6, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6

Query Match 66.1%; Score 211; DB 1; Length 581;
Best Local Similarity 85.5%; Pred. No. 4.5e-55;
Matches 272; Conservative 0; Mismatches 36; Indels 10; Gaps 3;

QY 3 AAATGCATAGTAATGTGAATTCAGAAATTCAGTAATTCAGAACTTTGAAGCAGCA 62
DB 253 AAATGCATAGTAATGTGAATTCAGAAATTCAGTAATTCAGAACTTTGAAGCAGCA 312
QY 63 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGCGCTATTAACAACCTTCAGGC 122
DB 313 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGCGCTATTAACAACCTTCAGGC 372
QY 123 CCGCGGCGCTGGCGGTGGGGAATCGCGGAGCCCGCTGCGGCAACGCGCTCCCGCA 182
DB 373 CCGCGGCGCTGGCGGTGGGGAATCGCGGAGCCCGCTGCGGCAACGCGCTCCCGCA 426
QY 183 TACAGTGGCGGTCCCGCGCAGCTTCATTCGTAAGTGAAGTGAAGTGAAGTGAAG 242
DB 427 TACAGTGGCGGTCCCGCGCAGCTTCATTCGTAAGTGAAGTGAAGTGAAGTGAAG 483
QY 243 GCGCGCGGCGCAGCGCTTAACCAACCACTTCGTAAGTGAAGTGAAGTGAAGTGAAG 301
DB 484 ACACGCGGCGCAGCGCTTAACCAACCACTTCGTAAGTGAAGTGAAGTGAAGTGAAG 543
QY 302 AATACCGCGCTGAACCTTAA 319
DB 544 AATACCGCGCTGAACCTTAA 561

RESULT 6
US-08-652-127C-7
Sequence 7, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831


```

1      RESULT 9
2      US-08-887-480-82
3      : Sequence 82, Application US/08887480
4      : Patent No.5814453
5      : GENERAL INFORMATION:
6      : APPLICANT: Beck, James J
7      : TITLE OF INVENTION: Detection of Fungal Pathogens Using the
8      : TITLE OF INVENTION: Polymerase Chain Reaction
9      : NUMBER OF SEQUENCES: 96
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: No. 581445Jartis Corporation
12     : STREET: 520 White Plains Road
13     : CITY: Tarrytown
14     : STATE: NY
15     : COUNTRY: USA
16     : ZIP: 10591
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: Patentln Release #1.0, Version #1.25
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: US/08/887,480
24     : FILING DATE:
25     : CLASSIFICATION: 435
26     : PRIOR APPLICATION DATA:
27     : APPLICATION NUMBER: US 08/722,187
28     : FILING DATE: 15-OCT-1996
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: Meigs, J. Timothy
31     : REGISTRATION NUMBER: 38,241
32     : REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: 919-541-8587
35     : TELEFAX: 919-541-8689
36     : INFORMATION FOR SEQ ID NO: 82:
37     : SEQUENCE CHARACTERISTICS:
38     : LENGTH: 504 base pairs
39     : TYPE: nucleic acid
40     : STRANDEDNESS: single
41     : TOPOLOGY: linear
42     : MOLECULE TYPE: DNA (genomic)
43     : ORIGINAL SOURCE:
44     : ORGANISM: Fusarium culmorum
45     :
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92     :
93     :
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100    :

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Query Match          57.6%; Score 183.8; DB 1; Length 504;
Best Local Similarity 81.5%; Pred. No. 2,9e-50;
Matches 255; Conservative 1; Mismatches 36; Indels 19; Gaps 3;

QY      2  AAAATGCCATAGTAATGTGAATTGCAGAAATTCAGTAATCATGCAATCTTTGAACGCAC 61
DB      211 AAAATGCGAATAGTAATGTAATGCAGAAATTCAGTAATCATGCAATCTTTGAACGCAC 270
QY      62  ATTCGCGCCGCGCAGATATTCTGGCGGGGAGATGCGCTGTTGAGCGGTATACAAACCTCAAGC 121
DB      271 ATTCGCGCCGCGCAGATATTCTGGCGGGGAGATGCGCTGTTGAGCGGTATATTCACCTCAAGC 330
QY      122 CCCCAGGACCTTGCGCGTTGGGGGATCGGCGGAAACCCCTGCGGGACAAACGCCGTCCTCCCAA 181
DB      331 CC--ACGTTGGTGTGGAGCTG-----CAGTCCTGTGCATCTCCCAA 372
QY      182 ATACAGTGGGGGATCCCGCGCAGCTTCATTTGCTAGTACTACACTCGGCACCTGGAG 241
DB      373 ATACATTTGGGGGTACCTCGTAGCTTCCATAGGCGTAGTAATTTACATATCGTTACGGTA 432
QY      242 AGCGGCGCGGCGCAGCCGCTGAAAAACCCCAACTTCTGAATCTTGACCTCGAATCAGTAGG 301
DB      433 ATGCTGCGGGCGAAGCCGCTTAAC-CCCACTTCTGAATTTGACCTCGAATCAGTAGG 491
QY      302 AATACCCGCTGAA 314
DB      492 AATACCCGCTGAA 504

RESULT 10
US-08-905-314A-19
; Sequence 19, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 319..472
OTHER INFORMATION: /note= "ITS 2"
NAME/KEY: misc feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19
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Query Match 57.6%; Score 183.8; DB 1; Length 504;
Best Local Similarity 81.5%; Pred. No. 2.9e-50;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

QY 2 AAAATGCGATGAATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGAC 61
DB 211 AAAATGCGATGAATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGAC 270
QY 62 ATTGCGCCCGCAGTATTCGCGGGGATGCTGTCGAGCGCATTAACCCCTGAGGC 121
DB 271 ATTGCGCCCGCAGTATTCGCGGGGATGCTGTCGAGCGCATTAACCCCTGAGGC 330
QY 122 CCCCAGGCTGCGGTGGGATCGGCGGAAGCCCTCGCGGCAACGCGTCCCCCA 181
DB 331 CC---AGCTTGTTGGTGGAGCTG-----CAGTCTGCTGCACTCCCA 372
QY 182 ATTCAGTGGGGTCCCGCCGACCTTCATGCGTAGTACTTAACCTTCGCACTGAG 241
DB 373 ATTCAGTGGGGTCCCGCCGACCTTCATGCGTAGTACTTAACCTTCGCACTGAG 432
QY 242 AGCGGCGCGGCAAGCGCGTAACCACTTGAATGTTGACCTCGAATCAGGTAG 301
DB 433 ATGCTGGCGGCAAGCGCGTAAAC-CCCACTTGAATGTTGACCTCGAATCAGGTAG 491
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QY 302 AATACCCGCTGAA 314
DB 492 AATACCCGCTGAA 504
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RESULT 11
US-08-722-187-82
Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligdon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum"
OTHER INFORMATION: (fcuim.con)"
US-08-722-187-82
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Query Match 57.6%; Score 183.8; DB 2; Length 504;
Best Local Similarity 81.5%; Pred. No. 2.9e-50;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

QY 2 AAAATGCGATGAATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGAC 61
DB 211 AAAATGCGATGAATGTAATGCAATTCAGTGAATCATCGAATCTTTGAACGAC 270
QY 62 ATTGCGCCCGCAGTATTCGCGGGGATGCTGTCGAGCGCATTAACCCCTGAGGC 121
DB 271 ATTGCGCCCGCAGTATTCGCGGGGATGCTGTCGAGCGCATTAACCCCTGAGGC 330
QY 122 CCCCAGGCTGCGGTGGGATCGGCGGAAGCCCTCGCGGCAACGCGTCCCCCA 181
DB 331 CC---AGCTTGTTGGTGGAGCTG-----CAGTCTGCTGCACTCCCA 372
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QY 182 ATACAGTGGCGGTCCTCCGCGCAGCTTCATTCGTAAGTACAGCACTCGCACTGGAG 241
DB 373 ATACATTTGGCGGTCAGCTGCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA 432
QY 242 AGCGCGCGGCGCCAGCCGCTAAACACCACTTGTGAATGTTGACCTCGAATCAGGTAGG 301
DB 433 ATCGTCGGCGGTCACCGCGTTAAAC-CCCAACTTGTGAATGTTGACCTCGAATCAGGTAGG 491
QY 302 AATACCGGCTGAA 314
DB 492 AATACCGGCTGAA 504

RESULT 12

PCT-US95-04712-82
Sequence 82, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fcuilm.con)"
PCT-US95-04712-82

Query Match 57.6%; Score 183.8; DB 5; Length 504;
Best Local Similarity 81.5%; Pred. No. 2.9e-50;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

QY 2 AATATGCAATAGTAATGTAATTCAGATTCAGTAATCATGATCTTTGACGAC 61
DB 211 AATATGCAATAGTAATGTAATTCAGATTCAGTAATCATGATCTTTGACGAC 270
QY 62 ATTGCGCGCGCAGATTCCTGGCGGCAATGCTGTGTGAGGCTATTACACCTCGAGC 121

DB 271 ATTTGGCGCGCAGATTCCTGGCGGCGATGCTGTGTGAGGCTATTACACCTCGAGC 330
QY 122 CCGCGGCGCTGGCGCTGGGGATGCGCGAGACCCCTCGCGGCAACGCCCTCCCAA 181
DB 331 CC---AGCTTGCTGTGGGAGCTG-----CAGTCTGTGTGACATCCCA 372
QY 182 ATACAGTGGCGGTCCTCCGCGCAGCTTCATTCGTAAGTACAGCACTCGCACTGGAG 241
DB 373 ATACATTTGGCGGTCAGCTGCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTA 432
QY 242 AGCGCGCGGCGCCAGCCGCTAAACACCACTTGTGAATGTTGACCTCGAATCAGGTAGG 301
DB 433 ATCGTCGGCGGTCACCGCGTTAAAC-CCCAACTTGTGAATGTTGACCTCGAATCAGGTAGG 491
QY 302 AATACCGGCTGAA 314
DB 492 AATACCGGCTGAA 504

RESULT 13

US-08-887-480-84
Sequence 84, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: pCRFMON1
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"

NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-887-480-84

Query Match 56.6%; Score 180.4; DB 1; Length 545;
Best Local Similarity 82.4%; Pred. No. 3.8e-49;
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

QY 2 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAAGCGAC 61
DB 228 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAAGCGAC 287
QY 62 ATTGGCGCGCGCAATATTGCGCGGCGATGCTGTGAGCGTCAATTAACCTTCAGGC 121
DB 288 ATTGGCGCGCGCAATATTGCGCGGCGATGCTGTGAGCGTCAATTAACCTTCAGGC 347
QY 122 CCCCGGCGCTGCGCTTGGGGATCGCGGAAAGCCCTCGCGGCGCAACGCCGTCCCCCA 181
DB 348 CC---AGCTTGCTGTGGAGCTG-----CAGTCTGCTGACTCCGCCAA 389
QY 182 ATACAGTGGCGGCTCCCGCGAGCTTCATGCGTAGTACCTTAACCTTCGCACTGGAG 241
DB 390 ATACATGGCGGCTCAGCTCG-AGCTTCATAGCGTAGTAATTACATCATGTTACTGTGA 448
QY 242 AGCGGCGCGCGCGCGCGCTTAACACCCCACTTCTGAATTTGACCTCGCAATGAGTAGG 301
DB 449 ATGCTCGCGCGCGCGCGCTTAAC-CCCAACTTCTGAATTTGACCTCGGATGAGTAGG 507
QY 302 AATACCGCTGAACCTTAA 319
DB 508 AATACCGCTGAACCTTAA 525

RESULT 14
US-08-905-314A-21
Sequence 21, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwells Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ. ID NO. 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: pCRFMON1
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-21

Query Match 56.6%; Score 180.4; DB 1; Length 545;
Best Local Similarity 82.4%; Pred. No. 3.8e-49;
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

QY 2 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAAGCGAC 61
DB 228 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAAGCGAC 287
QY 62 ATTGGCGCGCGCAATATTGCGCGGCGATGCTGTGAGCGTCAATTAACCTTCAGGC 121
DB 288 ATTGGCGCGCGCAATATTGCGCGGCGATGCTGTGAGCGTCAATTAACCTTCAGGC 347
QY 122 CCCCGGCGCTGCGCTTGGGGATCGCGGAAAGCCCTCGCGGCGCAACGCCGTCCCCCA 181
DB 348 CC---AGCTTGCTGTGGAGCTG-----CAGTCTGCTGACTCCGCCAA 389
QY 182 ATACAGTGGCGGCTCCCGCGAGCTTCATGCGTAGTACCTTAACCTTCGCACTGGAG 241
DB 390 ATACATGGCGGCTCAGCTCG-AGCTTCATAGCGTAGTAATTACATCATGTTACTGTGA 448
QY 242 AGCGGCGCGCGCGCGCGCTTAACACCCCACTTCTGAATTTGACCTCGCAATGAGTAGG 301
DB 449 ATGCTCGCGCGCGCGCGCTTAAC-CCCAACTTCTGAATTTGACCTCGGATGAGTAGG 507
QY 302 AATACCGCTGAACCTTAA 319
DB 508 AATACCGCTGAACCTTAA 525

RESULT 15
US-08-887-480-96

Sequence 96, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigse, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
FAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
IMMEDIATE SOURCE: sequence
CLONE: PCRpoaeT427(1-2), PCRpoaeT534(2-2), and
PCRpoaeT756(3-1)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..310
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-887-480-96
Query Match 56.4%; Score 180; DB 1; Length 546;
Best Local Similarity 82.4%; Pred. No. 5.2e-49;

Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4;
QY 2 AAAATGCGATAGTAATGTGAATTCAGATTCAGTGAATCATGATCTTTGAACGAC 61
DB 230 AAAATGCGATAGTAATGTGAATTCAGATTCAGTGAATCATGATCTTTGAACGAC 289
QY 62 ATTGGGCGCGCGAGTATTCGTGGCGGCAATGCTGTGAGGCGTATTAACCCCTCAGC 121
DB 290 ATTGGGCGCGCGAGTATTCGTGGCGGCAATGCTGTGAGGCGTATTAACCCCTCAGC 349
QY 122 CCGCGGCGCGCGCGTGGGCGATCGCGGAGCCCTCGCGGCAACAACGCGTCCCAA 181
DB 350 CC---AGCTTGCTGTGGG-----ATCTGTGCGAACAACAGTCCCAA 390
QY 182 ATAGAGTGGCGGTCCCGCGAGCTTCATTCGTAGTGAACCTCGCAACTGGAG 241
DB 391 ATTGATTGGCGGTCACTCG-AGCTTCATAGCTAGTATTAACATCGTTACTGGTA 449
QY 242 AGCGGCGCGCGCGAGCGGTAAACACCACTTGTGAATGTGACCTCGAATCAGTAGG 301
DB 450 ATCGTGGCGCGCGCGGTAAAC-CCCACTTGTGAATGTGACCTCGAATCAGTAGG 508
QY 302 AATACCGCGTGAAGCTTAA 319
DB 509 AATACCGCGTGAAGCTTAA 526

Search completed: October 1, 2004, 08:05:39
Job time : 110.125 secs

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2	240.4	75.4	534	10	US-09-961-755A-7	Sequence 7, Appl1
3	240.2	75.3	310	15	US-10-046-955-7	Sequence 7, Appl1
4	183.2	57.4	522	10	US-09-961-755A-5	Sequence 5, Appl1
5	183.2	57.4	522	10	US-09-961-755A-8	Sequence 8, Appl1
6	176.4	55.3	521	10	US-09-961-755A-6	Sequence 6, Appl1
7	131.8	41.3	652	15	US-10-121-740-2	Sequence 2, Appl1
8	131.8	41.3	652	17	US-10-623-432-2	Sequence 2, Appl1
9	126.6	39.7	365	15	US-10-046-955-3	Sequence 3, Appl1
10	123.2	38.6	365	15	US-10-046-955-5	Sequence 5, Appl1
11	121.2	38.0	364	15	US-10-046-955-2	Sequence 2, Appl1
12	119.8	37.6	650	15	US-10-623-740-4	Sequence 4, Appl1
13	119.8	37.6	650	17	US-10-623-432-4	Sequence 4, Appl1
14	114.2	35.8	641	9	US-09-766-173C-4	Sequence 4, Appl1

15	111.2	34.9	346	15	US-10-046-955-24	Sequence 24, Appl
16	110.6	34.7	618	9	US-09-766-173-C-5	Sequence 5, Appl1
17	110.2	34.5	343	15	US-10-046-955-27	Sequence 27, Appl
18	110.2	34.5	344	15	US-10-046-955-26	Sequence 26, Appl
19	109.2	34.2	346	15	US-10-046-955-25	Sequence 25, Appl
20	108	33.9	309	15	US-10-046-955-28	Sequence 28, Appl
21	107.2	33.6	466	16	US-10-356-120-1	Sequence 1, Appl1
22	106.4	33.4	336	15	US-10-046-955-29	Sequence 29, Appl
23	105.6	33.1	377	9	US-09-961-663-14	Sequence 14, Appl
24	105.6	33.1	377	9	US-09-961-663-15	Sequence 15, Appl
25	105.6	33.1	377	9	US-09-961-663-16	Sequence 16, Appl
26	105.6	33.1	377	9	US-09-961-663-19	Sequence 19, Appl
27	102.4	32.1	534	9	US-09-961-663-17	Sequence 17, Appl
28	101.8	31.9	540	9	US-09-961-663-18	Sequence 18, Appl
29	101.2	31.7	356	15	US-10-024-657-1	Sequence 1, Appl1
30	96.4	30.2	355	15	US-10-046-955-4	Sequence 4, Appl1
31	90.4	28.3	219	15	US-10-083-357-72	Sequence 72, Appl
32	90.4	28.3	228	15	US-10-083-357-71	Sequence 71, Appl
33	90.4	28.3	754	17	US-10-358-929A-4	Sequence 4, Appl1
34	90.4	28.3	754	17	US-10-358-929A-5	Sequence 5, Appl1
35	90.4	28.3	3480	15	US-10-297-621-2	Sequence 2, Appl1
36	82.4	25.8	377	17	US-10-358-929A-3	Sequence 3, Appl1
37	77	24.1	117	15	US-10-083-357-73	Sequence 372, Appl
38	62	19.4	327	15	US-10-046-955-10	Sequence 10, Appl
39	62	19.4	328	15	US-10-046-955-9	Sequence 9, Appl1
40	62	19.4	330	15	US-10-046-955-8	Sequence 8, Appl1
41	62	19.4	330	15	US-10-046-955-12	Sequence 12, Appl
42	60	18.8	1235	17	US-10-047-963-59964	Sequence 59964, A
43	57.4	18.0	876	9	US-09-897-231-6	Sequence 6, Appl1
44	56.6	17.7	102	9	US-10-083-357-360	Sequence 360, Appl
45	56	17.6	1516	13	US-10-424-599-82575	Sequence 82575, A

ALIGNMENTS

RESULT 1

```

? Sequence 6, Application US/10046955
? Publication No. US20030129600A1
? GENERAL INFORMATION:
? APPLICANT: The Government of the United States of America, as Represented by the
? APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
? APPLICANT: Control and Prevention
? APPLICANT: Morrison, Christine J.
? APPLICANT: Reis, Errol
? APPLICANT: Aldorevich, Liliana
? APPLICANT: Choi, Jong Soo
? TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
? TITLE OF INVENTION: Other Filamentous Fungi
? FILE REFERENCE: 6395-62064
? CURRENT APPLICATION NUMBER: US/10/046,955
? CURRENT FILING DATE: 2002-06-04
? PRIOR APPLICATION NUMBER: US 09/423,233
? PRIOR FILING DATE: 2000-06-27
? PRIOR APPLICATION NUMBER: PCT/US98/08926
? PRIOR FILING DATE: 1998-05-01
? PRIOR APPLICATION NUMBER: US 60/045,400
? PRIOR FILING DATE: 1997-05-02
? NUMBER OF SEQ ID NOS: 61
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 6
? LENGTH: 319
? TYPE: DNA
? ORGANISM: Fusarium solani
? US-10-046-955-6

```

```

Query Match 100.0%; Score 319; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 1e-104;
Matches 319; Conservative 0; Mismatches 0; Gaps 0

1 GAAATGCCATAGTATGTCGATTCAGTATCATCGAATCTTTGAACCA 60
|||||

```

```

Db      1  GAAATGGGATAGTAATGTAATTCAGAAATTCATGATCATGAAATCTTTGAAGCA 60
Qy      61  CATTGCGCGCCGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 120
Db      61  CATTGCGCGCCGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 120
Qy      121  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 180
Db      121  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 180
Qy      181  AATACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 240
Db      181  AATACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 240
Qy      241  GAGCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 300
Db      241  GAGCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 300
Qy      301  GAATACCGGCTGAACCTTAA 319
Db      301  GAATACCGGCTGAACCTTAA 319

```

```

RESULT 2
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

```

```

Query Match      75.4%; Score 240.4; DB 10; Length 534;
Best Local Similarity 87.9%; Pred. No. 3.6e-76;
Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

Qy      2  AAAATGCGATTAATGTAATTCAGAAATTCATGATCATGAAATCTTTGAAGCA 61
Db      228  AAAATGCGATTAATGTAATTCAGAAATTCATGATCATGAAATCTTTGAAGCA 287
Qy      62  ATTGCGCGCGGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 121
Db      288  ATTGCGCGCGGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 347
Qy      122  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 181
Db      348  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 400
Qy      182  AATACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 241
Db      401  AATACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 460
Qy      242  AGCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 301
Db      461  AGCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 520
Qy      302  AATACCGGCTGAAC 315
Db      521  AATACCGGCTGAAC 534

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RESULT 3

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US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrisson, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilianna
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCES: Other Filamentous Fungi
; FILE REFERENCES: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

```

```

Query Match      75.3%; Score 240.2; DB 15; Length 310;
Best Local Similarity 87.4%; Pred. No. 3.3e-76;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

Qy      3  AATGCGATTAATGTAATTCAGAAATTCATGATCATGAAATCTTTGAAGCA 62
Db      1  AATGCGATTAATGTAATTCAGAAATTCATGATCATGAAATCTTTGAAGCA 60
Qy      63  TTGCGCGCGCGGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 122
Db      61  TTGCGCGCGCGGACGATATTCGGCGGCGATGCTGTTGACGCTGATTAACAACCTTCAGG 120
Qy      123  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 182
Db      121  CCCCCGCGGCTGGGCTGGGAGTGGGAGAGCCCGCTGGGGGACAACCGCGTCCCGCA 173
Qy      183  TACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 242
Db      174  TACAGTGGCGGTCCTCCGCGACGCTTCATTTGGGTAGTACTTAACAACCTTCGAACTGGA 233
Qy      243  GCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 302
Db      234  GCGGCGCGGCGACGCGCTTAACACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 293
Qy      303  AATACCGGCTGAAC 319
Db      294  AATACCGGCTGAAC 310

```

```

RESULT 4
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0

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; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/363,072
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 652
 ; TYPE: DNA
 ; ORGANISM: Muscodor albus
 US-10-121-740-2

Query Match 41.3%; Score 131.8; DB 15; Length 652;
 Best Local Similarity 72.6%; Pred. No. 7.9e-37;
 Matches 230; Conservative 0; Mismatches 72; Indels 15; Gaps 4;

QY 3 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 62
 DB 329 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 388
 QY 63 TTGCGCCCGCAGTATTCGTGGGGGCGATGCTGTTGCGAGCTTCAACCCCTCAGGCC 122
 DB 389 TTGCGCCCATTAAGTATTCATGAGGGGCGATGCTGTTGCGAGCTTCAACCCATTAAGCC 448
 QY 123 CCGGGGCTGGGCTTGGGGATGCGGGAAGCCCTGCGGGGACAGCCGCTCCCAAA 182
 DB 449 CTGTGCTTAAGCTGGGAGGCTACGGGCACTGCC-----CGTAGCTCCCTAAA 496
 QY 183 TACAGTGGCGGCTCCCGCGCAGCTTCCATTCGCTAGTAAGCTAACCTCCGCACTGACGA 242
 DB 497 GTGATGGCGGAGTTGTTCTCACTCTA-GGCGTAGTAAT-CTATCTCGCTCTGTAGT 554
 QY 243 GCGGGCGGCGCAGCCGCTAAACCCCACTTGTGAATGTGACCTCGAATCAGGTAGA 302
 DB 555 GGTTCGGGCGCCCTGCGTAACCCCTATATC-AAAGTTGACTCGATCAGTAGGA 613
 QY 303 ATACCCGCTGAACCTTA 319
 DB 614 ATACCCGCTGAACCTTA 630

RESULT 8
 US-10-623-432-2
 ; Sequence 2, Application US/10623432
 ; Publication No. US20040141955A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Manke, Gary
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
 ; FILE REFERENCE: AQ 2019, 40
 ; CURRENT APPLICATION NUMBER: US/10/623,432
 ; PRIOR FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: US/10/121,740
 ; PRIOR FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/283,902
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/363,072
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 652
 ; TYPE: DNA
 ; ORGANISM: Muscodor albus
 US-10-623-432-2

Query Match 41.3%; Score 131.8; DB 17; Length 652;
 Best Local Similarity 72.6%; Pred. No. 7.9e-37;
 Matches 230; Conservative 0; Mismatches 72; Indels 15; Gaps 4;

QY 3 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 62
 DB 329 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 388

QY 63 TTGCGCCCGCAGTATTCGTGGGGGCGATGCTGTTGCGAGCTTCAACACCTCCAGGCC 122
 DB 389 TTGCGCCCATTAAGTATTCATGAGGGGCGATGCTGTTGCGAGCTTCAACACCTTAAGCC 448
 QY 123 CCGGGGCTGGGCTTGGGGATGCGGGAAGCCCTGCGGGGACAGCCGCTCCCAAA 182
 DB 449 CTGTGCTTAAGCTGGGAGGCTACGGGCACTGCC-----CGTAGCTCCCTAAA 496
 QY 183 TACAGTGGCGGCTCCCGCGCAGCTTCCATTCGCTAGTAAGCTAACCTCCGCACTGACGA 242
 DB 497 GTGATGGCGGAGTTGTTCTCACTCTA-GGCGTAGTAAT-CTATCTCGCTCTGTAGT 554
 QY 243 GCGGGCGGCGCAGCCGCTAAACCCCACTTGTGAATGTGACCTCGAATCAGGTAGA 302
 DB 555 GGTTCGGGCGCCCTGCGTAACCCCTATATC-AAAGTTGACTCGATCAGTAGGA 613
 QY 303 ATACCCGCTGAACCTTA 319
 DB 614 ATACCCGCTGAACCTTA 630

RESULT 9
 US-10-046-955-3
 ; Sequence 3, Application US/10046955
 ; Publication No. US20030129600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America, as Represented by the
 ; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
 ; APPLICANT: Control and Prevention
 ; APPLICANT: Morison, Christine J.
 ; APPLICANT: Reiss, Errol
 ; APPLICANT: Ahdorovich, Lilliana
 ; APPLICANT: Choi, Jong Soo
 ; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
 ; FILE REFERENCE: 6395-62064
 ; CURRENT APPLICATION NUMBER: US/10/046,955
 ; PRIOR FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 09/423,233
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: PCT/US98/08926
 ; PRIOR FILING DATE: 1998-05-01
 ; PRIOR APPLICATION NUMBER: US 60/045,400
 ; PRIOR FILING DATE: 1997-05-02
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 365
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 US-10-046-955-3

Query Match 39.7%; Score 126.6; DB 15; Length 365;
 Best Local Similarity 64.7%; Pred. No. 4.7e-35;
 Matches 205; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

QY 3 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 62
 DB 52 AAATGCGATTAAGTATGTAATGGAATTCAGATTCATCGATTCGATTTGGAACGACA 111
 QY 63 TTGCGCCCGCAGTATTCGTGGGGGCGATGCTGTTGCGAGGCTATTAACCCCTCAGGCC 122
 DB 112 TTGCGCCCGCTGATTCGCGGGGCGATGCTGTTGCGAGGCTATTCAGGCTCCTCAAGCA 171
 QY 123 CCGGGGCTGGGCTTGGGGATGCGGGAAGCCCTGCGGGGACAGCCGCTCCCAAA 182
 DB 172 C---GGCTTGTGTGTGGTGCCTGCTCCCGGGGAGCGGGCCGGAAGGACAG 228
 QY 183 TACAGTGGCGGCTCCCGGCGAGCTTCATTCGATGCTAGTACCTGCAACTGGAAGA 242
 DB 229 GCGGGCAGCGGCTCGATCTCAAGCGTATGGGGCTTTGTCACTGCTGTAGGCCGG 288

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 650
 TYPE: DNA
 ORGANISM: Muscodor roseus
 US-10-121-740-4

Query Match 37.6%; Score 119.8; DB 15; Length 650;
 Best Local Similarity 72.2%; Pred. No. 1.7e-32;
 Matches 229; Conservative 0; Mismatches 72; Indels 16; Gaps 5;

QY 3 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62
 Db 329 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 388
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 122
 Db 389 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 447
 QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGCGCGGACAAAGCCGCTCCCAAA 182
 Db 448 CTGTGCTTAGCGTTGGAGCGCTACGCGCACTGCC-----CGTAGCTCCCTTAA 495
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCTACACCTCGAAGTGAAGA 242
 Db 496 GTGATTGGCGAGTTGGTCTCACTCTA-GGCGTAGTAAT-CTATCTGGCTCTGTAAGT 553
 QY 243 GCGGCGCGCGACGCGTAAACACCCAACTTGAATTTGACCTCGAATCAGGTGAAGA 302
 Db 554 GGTTCGCGCGCTCGCGCTAAACCCCTATATC-AAAGTTGACCTCGAATCAGGTGAAGA 612
 QY 303 ATACCGCGTGAACCTTAA 319
 Db 613 ATACCGCGTGAACCTTAA 629

RESULT 13

US-10-623-432-4
 Sequence 4, Application US/10623432
 Publication No. US20040141955A1
 GENERAL INFORMATION:

APPLICANT: Strobel, Gary
 APPLICANT: Manker, Denise
 TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
 FILE REFERENCE: USE

CURRENT APPLICATION NUMBER: US/10/623,432
 CURRENT FILING DATE: 2003-07-17
 PRIOR APPLICATION NUMBER: US/10/121,740
 PRIOR FILING DATE: 2002-04-11
 PRIOR APPLICATION NUMBER: 60/283,902
 PRIOR FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: 60/363,072
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 650
 TYPE: DNA
 ORGANISM: Muscodor roseus
 US-10-623-432-4

Query Match 37.6%; Score 119.8; DB 17; Length 650;
 Best Local Similarity 72.2%; Pred. No. 1.7e-32;
 Matches 229; Conservative 0; Mismatches 72; Indels 16; Gaps 5;

QY 3 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62
 Db 329 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 388
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 122
 Db 389 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 447

QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGTGGCGGACAAAGCCGCTCCCAAA 182
 Db 448 CTGTGCTTAGCGTTGGAGCGCTACGCGCACTGCC-----CGTAGCTCCCTTAA 495
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCTACACCTTCGAACTGAGGA 242
 Db 496 GTGATTGGCGAGTTGGTCTCACTCTA-GGCGTAGTAAT-CTATCTGGCTCTGTAAGT 553
 QY 243 GCGGCGCGCGACGCGTAAACACCCAACTTGAATTTGACCTCGAATCAGGTGAAGA 302
 Db 554 GGTTCGCGCGCTCGCGCTAAACCCCTATATC-AAAGTTGACCTCGAATCAGGTGAAGA 612
 QY 303 ATACCGCGTGAACCTTAA 319
 Db 613 ATACCGCGTGAACCTTAA 629

RESULT 14

US-09-766-173C-4
 Sequence 4, Application US/09766173C
 Patent No. US20020172945A1
 GENERAL INFORMATION:

APPLICANT: Cartroll, George C.
 TITLE OF INVENTION: Materials and Methods For Detection of
 FILE REFERENCE: Oregon 99-09
 CURRENT APPLICATION NUMBER: US/09/766,173C
 CURRENT FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: PCT/US01/01735

PRIOR FILING DATE: 2001-01-19
 PRIOR APPLICATION NUMBER: 60/177,013
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 641
 TYPE: DNA
 ORGANISM: Guignardia Citricarpa
 US-09-766-173C-4

Query Match 35.8%; Score 114.2; DB 9; Length 641;
 Best Local Similarity 62.5%; Pred. No. 1.8e-30;
 Matches 198; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 3 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62
 Db 318 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 377
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 122
 Db 378 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTTCATTACAACTTCAGGCC 437
 QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGTGGCGGACAAAGCGTCCCAAA 182
 Db 438 CTGTGCTTAGCGTTGGAGCGCTCGCGGAGCGCGCTGGAAGACTCGG-----CGA 491
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCTACACCTTCGAACTGAGGA 242
 Db 492 CCGGCTTACGCTTCAGCGCTAGTAAATAATTCGCTTGGAGAGGGGGCGCTGG 551
 QY 243 GCGGCGCGCGACGCGTAAACACCCAACTTGAATTTGACCTCGAATCAGGTGAAGA 302
 Db 552 CCGCGGACAAATGACCTTCGCACTATTTTCCAAAGTTGACCTCGAATCAGGTGAAGA 611
 QY 303 ATACCGCGTGAACCTTAA 319
 Db 612 ATACCGCGTGAACCTTAA 628

RESULT 15

US-10-046-955-24
 Sequence 24, Application US/10046955

Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldrevich, Lilliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 346
TYPE: DNA
ORGANISM: Pseudallescheria boydii
US-10-046-955-24

Query Match 34.9%; Score 111.2; DB 15; Length 346;
Best Local Similarity 70.5%; Pred. No. 1.7e-29;
Matches 244; Conservative 0; Mismatches 73; Indels 29; Gaps 6;

QY 3 AAATCCGATAGTATGATGATGCAATTCAGTAATCATCGAATCTTTG-AAGCAG 61
DB 1 AAATCCGATAGTATGATGCAATTCAGTAATCATCGAATCTTTGAAACGAC 60
QY 62 ATTGGCCCGGCGAGATTCGCGGGGCAATGCTGTCAGGCTTACAAACCTCAGGC 121
DB 61 ATTGGCCCGGCGAGATTCGCGGGGCAATGCTGTCAGGCTTACAAACCTCAGAC 120
QY 122 CCCC-----GCGCTGCGGTTGGGATCGCGGAAGCCCTGCGGCGACAAC 169
DB 121 CTCGGTTCTTAGGGAAGCCTAGGCTGCTGTTGGGCGGTAAGGCAAGTCCTCGAAC 180
QY 170 GCC-----GTCCCAATAACAGTGGGCTCCGCGCGACGCTTCAT-TGCGTAGACTA 224
DB 181 CCGCGTAGGCGCTGAATAACAGTGGGCTCCGCGCGGCTTCTGCGTAGACTA 240
QY 225 AC-----ACCTGCACTGAGAGCGCGCGCGACGCGGTAAACACCACTTCTG 277
DB 241 TCTTTTGCAGCTGCGATTTGGTCCCGCGAGGCTGCGTCAACCACTTAACACTC 300
QY 278 AA-----TGTGACCTCGATCAGTAGAATACCGCTGAACCTTA 319
DB 301 CAGATGTTTGAACCTCGATCAGTAGAATACCGCTGAACCTTA 346

Search completed: October 1, 2004, 08:53:42
Job time : 1304.11 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 : Search time 4466 Seconds
(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-6
Perfect score: 319
Sequence: 1 gaaatgcgataagtaagtgt.....ggatacccgctgacttaaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_earth:.*
2: em_earth:.*
3: em_earth:.*
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6: em_earth:.*
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9: gb_earth:.*
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25: em_earth:.*
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27: em_earth:.*
28: gb_earth:.*
29: gb_earth:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	57.4	739	14	CF870552 trico24xb
2	183	57.4	739	14	CF870552 trico24xb
3	183	57.4	739	14	CF870552 trico24xb
4	183	57.4	739	14	CF870552 trico24xb

Result No.	Score	Query Match	Length	ID	Description
5	139.4	43.7	735	14	CF880267 trico24xb
6	139.4	43.7	735	14	CF880267 trico24xb
7	117.2	36.7	704	13	BQ751285
8	117.2	36.7	725	13	BQ751285
9	117.2	36.7	806	13	BQ751015
10	117.2	36.7	806	13	BQ751015
11	115.6	36.2	745	13	BQ751971
12	115.6	36.2	758	13	BQ751971
13	114.4	35.9	169	12	BM870292
14	110.6	34.7	774	13	BQ751216
15	109	34.2	743	13	BQ751027
16	105	32.9	225	28	BZ424439
17	102.8	32.2	214	10	BF251183
18	101.8	31.9	195	28	BZ425056
19	101.8	31.9	389	28	BZ424690
20	100.2	31.4	213	9	A1209736
21	100.2	31.4	318	9	A1213025
22	93.6	29.3	570	28	BZ293287
23	93.6	29.3	597	28	BZ293462
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27	92	28.8	141	9	A1327879
28	92	28.8	384	28	BZ304161
29	92	28.8	458	28	BZ304060
30	92	28.8	497	28	BZ302024
31	92	28.8	498	28	BZ304069
32	92	28.8	549	28	BZ303682
33	92	28.8	556	28	BZ304433
34	92	28.8	870	29	CNS06K29
35	92	28.8	1004	29	CNS06K29
36	92	28.8	1043	29	CNS06K29
37	92	28.8	846	29	CNS07820
38	91.2	28.6	893	29	CNS0795G
39	91.2	28.6	939	29	CNS06K16
40	91.2	28.6	995	29	CNS07A08
41	91.2	28.6	999	29	CNS07730
42	91.2	28.6	1034	29	CNS07922
43	91.2	28.6	1094	29	CNS076RE
44	91.2	28.6	1098	29	CNS07812
45	90.8	28.5	981	29	CNS0769H

ALIGNMENTS

RESULT 1
LOCUS CF870552
DEFINITION trico24xb14.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION CF870552
VERSION CF870552.1 GI:38125234
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
AUTHORS Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.

TITLE Analysis of the protein processing and secretion pathways in a
JOURNAL Trichoderma reesei EST dataset
COMMENT Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: UT-F1 primer.

FEATURES
source

Location/Qualifiers
1. 739
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="Qm6a"
/db_xref="taxon:51453"
/clone="tric024xb14"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: PREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 57.4%; Score 183; DB 14; Length 739;
Best Local Similarity 83.8%; Pred. No. 8.5e-39;
Matches 269; Conservative 0; Mismatches 40; Indels 12; Gaps 5;

Qy 3 AATGCGATTAAGTAATGTAATTCGAGAAATTCAGTATCATCATCTTTGAACGACA 62
Db 43 AATGCGATTAAGTAATGTAATTCGAGAAATTCAGTATCATCATCTTTGAACGACA 102
Qy 63 TTGCGCCCGCAATATTCGCGGGGATGCTGTTGAGCGCTCATTAACCCCTCAGACC 122
Db 103 TTGCGCCCGCAATATTCGCGGGGATGCTGTTGAGCGCTCATTAACCCCTCAGACC 162
Qy 123 CCGGGGCTGCGGTGGGGATCGCGAAGCCCTCGGGGCAACAGCCGTCCTCCCAAA 182
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Qy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTCGAGTGAAGTAAAC-CTCGCACTGGAG 241
Db 215 TACAGTGGCGGTCTCGCGGAGCTCTCTCGGAGTGTGACACACTCGCACCGGAG 274
Qy 242 AGCGGGCGGGCAC-GCCGTAAACACCC--AACTTGAATGTTGACTCGAATCAGT 298
Db 275 CGCGGGCGGGCAGCGGTAAACACCCCAACTGGAATGTGACTCGAATCAGT 334
Qy 299 AGGAATACCCGCTGAATTA 319
Db 335 AGGAATACCCGCTGAATTA 355

RESULT 2
CF870665 755 bp mRNA linear EST 31-OCT-2003
LOCUS tric024xb104.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone tric024xb104, mRNA sequence.
ACCESSION CF870665.1 GI:38125347
VERSION CF870665.1
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
AUTHORS 1 (bases 1 to 755)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.

TITLE Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL Unpublished (2003)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu

FEATURES
source
Seq primer: LR-F1 primer.
Location/Qualifiers
1. 755

/organism="Hypocrea jecorina"
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/strain="Qm6a"
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/clone="tric024xb14"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: PREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 57.4%; Score 183; DB 14; Length 755;
Best Local Similarity 83.8%; Pred. No. 8.6e-39;
Matches 269; Conservative 0; Mismatches 40; Indels 12; Gaps 5;

Qy 3 AATGCGATTAAGTAATGTAATTCGAGAAATTCAGTATCATCATCTTTGAACGACA 62
Db 43 AATGCGATTAAGTAATGTAATTCGAGAAATTCAGTATCATCATCTTTGAACGACA 102
Qy 63 TTGCGCCCGCAATATTCGCGGGGATGCTGTTGAGCGCTCATTAACCCCTCAGACC 122
Db 103 TTGCGCCCGCAATATTCGCGGGGATGCTGTTGAGCGCTCATTAACCCCTCAGACC 162
Qy 123 CCGGGGCTGCGGTGGGGATCGCGAAGCCCTCGGGGCAACAGCCGTCCTCCCAAA 182
Db 163 CC---TCCGGGGGCTGCGGTGGGGATCGCGAAGCCCTCGGGGCAACAGCCGTCCTCCCAAA 214
Qy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTCGAGTGAAGTAAAC-CTCGCACTGGAG 241
Db 215 TACAGTGGCGGTCTCGCGGAGCTCTCTCGGAGTGTGACACACTCGCACCGGAG 274
Qy 242 AGCGGGCGGGCAC-GCCGTAAACACCC--AACTTGAATGTTGACTCGAATCAGT 298
Db 275 CGCGGGCGGGCAGCGGTAAACACCCCAACTGGAATGTGACTCGAATCAGT 334
Qy 299 AGGAATACCCGCTGAATTA 319
Db 335 AGGAATACCCGCTGAATTA 355

RESULT 3
CB900742 796 bp mRNA linear EST 02-JUL-2003
LOCUS tric024xb14.T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone tric024xb14, mRNA sequence.
ACCESSION CB900742
VERSION CB900742.1 GI:30115400
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
AUTHORS 1 (bases 1 to 796)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.T., Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.

TITLE Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei
JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)
MEDLINE 22803314
PUBMED 12788920

COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genencor.com

FEATURES
source
Seq primer: LR-F1 primer.
Location/Qualifiers
1. 796

Query Match	43.7%	Score 139.4	DB 14	Length 735
Best Local Similarity	79.9%	Pred. No. 5.5e-27		
Matches 203, Conservative		0, Mismatches 42	Indels 9	Gaps 3

RESULT 6	CB907036	840 bp	mRNA	linear	EST 02-UTL-2003
LOCUS	CB907036				
DEFINITION	tricc081xc18 T. reesei mycelial culture, Version 3				april Hypocrea
ACCESSION	tricc081xc18				mRNA sequence.
	CB907036				

REFERENCE
AUTHORS
1 (bases 1 to 840)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

TITLE	JOURNAL	DATE
Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus <i>Trichoderma reesei</i>	J. Biol. Chem.	278 (34), 31988-31997 (2003)
3200314	MEDLINE	

PUBMED 12788920
COMMENT Contact: Pamela K. Foreman

FEATURES	Location/Qualifiers
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"note="Vector: pRESEI; Site_: Not I/Sal I; Mycelial

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Query Match	43.7%	Score 139.4;	DB 14;	Length 840;
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Matches 203; Conservative	0;	Mismatches 42;	Indels 9;	Gaps 3;

QY	3	AAATGGATAAATAATGGAATTGAGAAATTCAGTGAATCATCGAATCTTTGAAAGCAC	62
Db	155	AAATGGATAAATAATGGAATTGAGAAATTCAGTGAATCATCGAATCTTTGAAAGCAC	214
QY	63	TTGCGCGCCGCAATTTCTGGCGGAGCATGCTGTTCAGAGCTCATTAACAACCTCAGGCC	122
Db	215	TTGCGCGCCGCAATTTCTGGCGGAGCATGCTGTTCAGAGCTCATTAACAACCTCAGAAC	274
QY	123	CCGGGAGCTGGAGTGGGGAGTCGGGAGAGCCCCCTGCGGAGCAACAAGCCGTCGCCCA	182
Db	275	CC----TCCGGGGGGGTCGGTTTTGGGGAGTCGGCCCCT-----CACCGGGCGGCCCCGAAA	326
QY	183	TACAGTGGCGGATCCCGCGGACGCTTCATTGCGTAGTACGTAACAC-CTCGCAATCGAG	241
Db	327	TACAGTGGGGGCTCGCGGACCTTTTTCGCGAGCTACTTCGACACTGTCAACCCGAG	386
QY	242	AGCGGCGCGGCAC	255
Db	387	CGCGGCGGCGCAC	400

RESULT	7
B0751285	
LOCUS	B0751285
DEFINITION	704 bp mRNA linear EST 18-JUL-2002
ACCESSION	B0751285 DSCOT Colletotrichum trifolii cDNA clone pdSCT4-17, mRNA
VERSION	B0751285
KEYWORDS	B0751285.1 GI:21906630
SOURCE	EST
ORGANISM	Colletotrichum trifolii Colletotrichum trifolii Colletotrichum trifolii

REFERENCE
AUTHORS
1 (bases 1 to 704)
Samad D A Dickman M Town C D Voss Amon C
17444621

INDEX	ESTS FROM MYCELS OF COLLECTOTRICHUM ERITROLI PAGE 1
JOURNAL	Unpublished (2002)
COMMENT	Other ESTS: EST631847

Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 191 Upper Buford Circle, St. Paul, MN 55108, USA
Tel.: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAD17V More information is available at:
www.medicago.org
Seq primer: (gcta ata cga ctc act ata ggg c).

FEATURES	Location/Qualifiers
source	1. .704

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/clone="pDSCt4-17"
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/dev_stages="young, actively growing mycelia (3 days after
inoculation), grown in liquid culture (cutin minimal medium
containing 2glucose)."
/lab_host="DHSalpha"
/clone_lib="DSCt"
/notes="Vector: Bluescript SK+, Site_1: EcoRI, Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
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enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 704;
Best Local Similarity 77.6%; Pred. No. 5.5e-21;
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTCTTTGAACGACATTTGCGCCGACATTTCTGGCGGCGATGCTT 94
DB 1 AGTGAATCATGAACTCTTTGAACGACATTTGCGCCGACATTTCTGGCGGCGATGCTT 60
QY 95 GTTGGAGGCTATTCACACCTCGAGCCCGGCGCTGGCTGGGGGATCGGCGGAAGCC 154
DB 61 GTTGGAGGCTATTCACACCTCGAGCCCGGCGCTGGCTGGGGGATCGGCGGAAGCC 104
QY 155 CCTGCGGGGACAAACGCGCTCCGCCAAATACAGTGGCGGTCGCCG-CGACGCTTCATTTG 213
DB 105 -CTTCCAGCGGCTGAGCGTGGGCTCAAGAGAGAGTGGCGGACCTTCGCGGAGCTCTTTG 163
QY 214 CGTAGTAGC-TAACACCTTCGCACTGGA-GAGCGCGCGGCCACCGCTTAACACCCAA 271
DB 164 CGTAGTAGCATACCACTCGACCGCGGACCCGACAGGCGACCTCTCTTAACACCCCA 223
QY 272 CTCTT-GAATGTTGACCTCGAATGAGTAGGTAATACCGCTGAACTTAA 319
DB 224 ATTTTACAGGTTGACCTCGAATGAGTAGGTAATACCGCTGAACTTAA 273

RESULT 8
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LOCUS EST1632564 DSCOT Colletotrichum trifolii cDNA clone pDSC79-22, mRNA
DEFINITION
ACCESSION B0752001
VERSION B0752001
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 725)
REFERENCE Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
AUTHORS Cheung,F., and Fraser,C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST632563
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTS4122TV More information is available at:
www.medicago.org
Seq primer: (gca ACA CGA CTC Act ACA 999 C) .
Location/Qualifiers

FEATURES

source
1..725
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/db_xref="taxon:5466"
/clone="pDSC79-22"
/issue_type="mycelia"

/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/clone_id="DSC7"
/note="Vector: pBluescript SK+, Site 1: EcoRI, Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 725;
Best Local Similarity 77.6%; Pred. No. 5.6e-21;
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTCTTTGAACGACATTTGCGCCGACATTTCTGGCGGCGATGCTT 94
DB 1 AGTGAATCATGAACTCTTTGAACGACATTTGCGCCGACATTTCTGGCGGCGATGCTT 60
QY 95 GTTGGAGGCTATTCACACCTCGAGCCCGGCGCTGGCTGGGGGATCGGCGGAAGCC 154
DB 61 GTTGGAGGCTATTCACACCTCGAGCCCGGCGCTGGCTGGGGGATCGGCGGAAGCC 104
QY 155 CCTGCGGGGACAAACGCGCTCCGCCAAATACAGTGGCGGTCGCCG-CGACGCTTCATTTG 213
DB 105 -CTTCCAGCGGCTGAGCGTGGGCTCAAGAGAGAGTGGCGGACCTTCGCGGAGCTCTTTG 163
QY 214 CGTAGTAGC-TAACACCTTCGCACTGGA-GAGCGCGCGGCCACCGCTTAACACCCAA 271
DB 164 CGTAGTAGCATACCACTCGACCGGAGACCGGACAGGCGACCTCTCTTAACACCCCA 223
QY 272 CTCTT-GAATGTTGACCTCGAATGAGTAGGTAATACCGCTGAACTTAA 319
DB 224 ATTTTACAGGTTGACCTCGAATGAGTAGGTAATACCGCTGAACTTAA 273

RESULT 9
B0751015 806 bp mRNA linear EST 18-JUL-2002
LOCUS EST1631578 DSCOT Colletotrichum trifolii cDNA clone pDSC72-7, mRNA
DEFINITION
ACCESSION B0751015
VERSION B0751015
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 806)
REFERENCE Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
AUTHORS Cheung,F., and Fraser,C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST631577
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTS4077TV More information is available at:
www.medicago.org
Seq primer: (gca ACA CGA CTC Act ACA 999 C) .
Location/Qualifiers

FEATURES

source

1. 806
/organism="Colletoctrichum trifolii"
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/lab_host="DH5alpha"
/clone_1ib="DSC2"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 806;
Best Local Similarity 77.6%; Pred. No. 5.9e-21;
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTTTTGAACGACATTGCGCCGCAATTTCTGGCGGATGCT 94
DB 1 AGTGAATCATGAACTTTTGAACGACATTGCGCCGCAATTTCTGGCGGATGCT 60

QY 95 GTTCGAGCGTCATTAAACCTCTCAGGCCCGCGGCTGGCGGATGCGCGAAGCC 154
DB 61 GTTCGAGCGTCATTAAACCTCTCAGGACC--GCTTGGCGTTGGGG----- 104

QY 155 CCTCGGGGACAAAGCCGCTCCCAATACAGTGGCGTCCGCG--CGACGTTCCATTG 213
DB 105 -CTTCCAGCGCTGACGCGGCGCTCAAGACAGTGGGAGACCTCGGGAGCTCTTTG 163

QY 214 CGTAGTAGC-TAAACCTCGCACTGGA-GAGCGCGCGGCGACGCCGTAAACACCCAA 271
DB 164 CGTAGTAGCATACCACTCGACCGGAGCCGCGGCGACCTCTGCGGTAAACCCCA 223

QY 272 CTCTCT--GAATGTGACCTCGAATCAGTAGAATATACCGCTGAATCTAA 319
DB 224 ATTTTACAGGTTGACCTCGAATCAGTAGAATATACCGCTGAATCTAA 273

RESULT 10 806 bp mRNA linear EST 18-JUL-2002
LOCUS B0751484
DEFINITION EST632047 DSC2 Colletoctrichum trifolii cDNA clone pDSC2-48, mRNA
ACCESSION B0751484
VERSION B0751484.1 GI:21906889
SOURCE EST.
ORGANISM Colletoctrichum trifolii
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;
mitosporic Phyllochoraceae; Colletoctrichum.
1 (bases 1 to 806)
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
Cheung,F., and Fraser,C.M.
ESTs from mycelia of Colletoctrichum trifolii race 1
Unpublished (2002)
Other_ESTs: EST632046
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

FEATURES

source

1. 806
/organism="Colletoctrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC2-48"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_1ib="DSC2"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 806;
Best Local Similarity 77.6%; Pred. No. 5.9e-21;
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTTTTGAACGACATTGCGCCGCAATTTCTGGCGGATGCT 94
DB 1 AGTGAATCATGAACTTTTGAACGACATTGCGCCGCAATTTCTGGCGGATGCT 60

QY 95 GTTCGAGCGTCATTAAACCTCTCAGGCCCGCGGCTGGCGGATGCGCGAAGCC 154
DB 61 GTTCGAGCGTCATTAAACCTCTCAGGACC--GCTTGGCGTTGGGG----- 104

QY 155 CCTCGGGGACAAAGCCGCTCCCAATACAGTGGCGTCCGCG--CGACGTTCCATTG 213
DB 105 -CTTCCAGCGCTGACGCGGCGCTCAAGACAGTGGGAGACCTCGGGAGCTCTTTG 163

QY 214 CGTAGTAGC-TAAACCTCGCACTGGA-GAGCGCGCGGCGACGCCGTAAACACCCAA 271
DB 164 CGTAGTAGCATACCACTCGACCGGAGCCGCGGCGACCTCTGCGGTAAACCCCA 223

QY 272 CTCTCT--GAATGTGACCTCGAATCAGTAGAATATACCGCTGAATCTAA 319
DB 224 ATTTTACAGGTTGACCTCGAATCAGTAGAATATACCGCTGAATCTAA 273

RESULT 11 745 bp mRNA linear EST 18-JUL-2002
LOCUS B0751971
DEFINITION EST632534 DSC2 Colletoctrichum trifolii cDNA clone pDSC2-3, mRNA
ACCESSION B0751971
VERSION B0751971.1 GI:21907376
SOURCE EST.
ORGANISM Colletoctrichum trifolii
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;
mitosporic Phyllochoraceae; Colletoctrichum.
1 (bases 1 to 745)
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
Cheung,F., and Fraser,C.M.

TITLE
JOURNAL
COMMENT

ESTs from mycelia of *Colletotrichum trifolii* race 1
Unpublished (2002)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAD103TV More information is available at:
www.medicago.org
Seq primer: (gta Aca CGA CTC Act Aca 999 C) .
Location/Qualifiers
1. 745
/organism="Colletotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC79-3"
/issue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC7"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

FEATURES

SOURCE

ORIGIN

Query Match 36.2%; Score 115.6; DB 13; Length 745;
Best Local Similarity 77.2%; Pred. No. 1.5e-20;
Matches 224; Conservative 0; Mismatches 44; Indels 22; Gaps 6;

35 AGTGAATCATGCAATCTTTGAAGCAATGCGCCGCGAGTATTCGGGGGATGCT 94
1 AGTGAATCATGCAATCTTTGAAGCAATGCGCCGCGAGTATTCGGGGGATGCT 60
95 GTTGAAGCGTATTAACAACCTCAGAGCCCGCGGCTGGCTGGAGATCCGCGAAGCC 154
61 GTTGAAGCGTATTAACAACCTCAGAGCCCGCGGCTGGCTGGAGATCCGCGAAGCC 104
155 CCTGCGGGGCAACGCGCTGCCCAATAAGTGGCGGTCCGC-CGACCTTCATTG 213
105 -CTTCCACGCGTGAAGTGGGCTCAAGAGACAGTGGCGAGCCTCGCGAGACCTCTTTG 163
214 CGTAGTAGC-TAACAACCTCGCACTGA-GAGCGCGCGGCGAGCGCTAAACACCA 271
164 CGTAGTAGC-TAACAACCTCGCACTGA-GAGCGCGCGGCGAGCGCTAAACACCA 223
272 CTCTT--GAATGTGACCTCGAATCAGTAGAATACCGCTGAACCTTA 319
224 ATTTTTCAAGGTGACCTCGAATCAGTAGAATACCGCTGAACCTTA 273

RESULT 12
BQ751399 758 bp mRNA linear EST 18-JUL-2002
LOCUS EST613962 DSC7 Colletotrichum trifolii cDNA clone pDSC74-95, mRNA
DEFINITION
ACCESSION BQ751399
VERSION BQ751399.1 GI:21906804
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 758)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uteback, T.,
Cheung, F., and Fraser, C.M.
ESTs from mycelia of *Colletotrichum trifolii* race 1
Unpublished (2002)
Other ESTs: EST613961
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAD95TV More information is available at:
www.medicago.org
Seq primer: (gta Aca CGA CTC Act Aca 999 C) .
Location/Qualifiers
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/db_xref="taxon:5466"
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/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC7"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

FEATURES

SOURCE

ORIGIN

Query Match 36.2%; Score 115.6; DB 13; Length 758;
Best Local Similarity 77.2%; Pred. No. 1.6e-20;
Matches 224; Conservative 0; Mismatches 44; Indels 22; Gaps 6;

35 AGTGAATCATGCAATCTTTGAAGCAATGCGCCGCGAGTATTCGGGGGATGCT 94
1 AGTGAATCATGCAATCTTTGAAGCAATGCGCCGCGAGTATTCGGGGGATGCT 60
95 GTTGAAGCGTATTAACAACCTCAGAGCCCGCGGCTGGCTGGAGATCCGCGAAGCC 154
61 GTTGAAGCGTATTAACAACCTCAGAGCCCGCGGCTGGCTGGAGATCCGCGAAGCC 104
155 CCTGCGGGGCAACGCGCTGCCCAATAAGTGGCGGTCCGC-CGACCTTCATTG 213
105 -CTTCCACGCGTGAAGTGGGCTCAAGAGACAGTGGCGAGCCTCGCGAGACCTCTTTG 163
214 CGTAGTAGC-TAACAACCTCGCACTGA-GAGCGCGCGGCGAGCGCTAAACACCA 271
164 CGTAGTAGC-TAACAACCTCGCACTGA-GAGCGCGCGGCGAGCGCTAAACACCA 223
272 CTCTT--GAATGTGACCTCGAATCAGTAGAATACCGCTGAACCTTA 319
224 ATTTTTCAAGGTGACCTCGAATCAGTAGAATACCGCTGAACCTTA 273

RESULT 13
BM870292 169 bp mRNA linear EST 06-MAY-2003
LOCUS BM870292

DEFINITION mgns009xj23f.b Magnaporthe grisea NS uni-Zap XR library Magnaporthe grisea cDNA clone mgns009xj23 5', mRNA sequence.

ACCESSION BM670292

VERSION BM670292.2 GI:30404719

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.

AUTHORS Expressed sequence tags from the rice blast fungus, Magnaporthe grisea

TITLE Unpublished (2002)

JOURNAL On Mar 7, 2002 this sequence version replaced gi:19237974.

COMMENT Contact: Ebbole, DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) gb|AL179278.1| unknown [Saccharomyces cerevisiae] 79 1e-14

PCR Primers
FORWARD: T3 primer
E-mail: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) gb|AL179278.1| unknown [Saccharomyces cerevisiae] 79 1e-14

BACKWARD: T7 primer
Plate: mgns009 row: J column: 23
Seq primer: T3.

FEATURES
source location/Qualifiers
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/db_xref="taxon:148305"
/clone="mgns009xj23"
/sex="Male-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea NS uni-Zap XR library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI, Site_2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN
Query Match 35.9%; Score 114.4; DB 12; Length 169;
Best Local Similarity 95.2%; Pred. No. 1.6e-20;
Matches 118; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

3 AATGCGATTAAGTATGATGATGAGAAATTCAGTAATCATGATCTTTGAAGCACA 62
DB AATGCGATTAAGTATGATGATGAGAAATTCAGTAATCATGATCTTTGAAGCACA 98
63 TTGCGCGCCGAGATTTTGGCGCGGCGATGCTTTTGAAGGTCATTACAACCCCTGAGGC 122
DB TTGCGCGCCGAGATTTTGGCGCGGCGATGCTTTTGAAGGTCATTACAACCCCTGAGGC 158
99 TTGCGCGCCGAGATTTTGGCGCGGCGATGCTTTTGAAGGTCATTACAACCCCTGAGGC 158
QY 123 CCGG 126
DB 159 TCGG 162

RESULT 14

LOCUS BQ752136

DEFINITION EST632699 DSCOT Colletotrichum trifolii cDNA clone pDSCOT10-23, mRNA

ACCESSION BQ752136

VERSION BQ752136.1 GI:21907541

KEYWORDS EST.

SOURCE Colletotrichum trifolii

ORGANISM Colletotrichum trifolii

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Mitoportic Phyllachoraceae; Colletotrichum.

AUTHORS Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T., Cheung,F. and Frazer,C.M.

TITLE ESTs from mycelia of Colletotrichum trifolii race 1

JOURNAL Unpublished (2002)

COMMENT Other_ESTs: EST632698
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSMJ23TV More information is available at: www.medicago.org
Seq primer: (gta ata cga ctc act ata ggg c).

FEATURES
source location/Qualifiers
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/mol_type="mRNA"
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/clone="pDSCOT10-23"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (curin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSCOT"
/note="Vector: pBluescript SK+; Site_1: EcoRI, Site_2: EcoRI; isolate: 2SP2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN
Query Match 34.7%; Score 110.6; DB 13; Length 774;
Best Local Similarity 76.8%; Pred. No. 3.6e-19;
Matches 219; Conservative 0; Mismatches 44; Indels 22; Gaps 6;

40 ATCATCGAATCTTTGAACGCGCATTTGGCGCGGCGAGATTCGCGGCGGAGTCTGTTGC 99
DB ATTATCGAATCTTTGAACGCGCATTTGGCGCGGCGAGATTCGCGGCGGAGTCTGTTGC 64
100 AGCGTCAATTACAACCTTCAGGCCCCCGCGCTGCGGATTCGCGGAGTTCGCGGAGCCCCCTG 159
DB AGCGTCAATTACAACCTTCAGGCCCCCGCGCTGCGGATTCGCGGAGTTCGCGGAGCCCCCTG 107
160 CGGCGACAAGCGCGCTCCCGCAATACGTCGCGGCTCCCG-CCGAGCTTCATTGCGTAG 218
DB CACGCGTGAAGTGGCGCCTCAAGACAGTGGCGGAGCCCTCGCGAGAGCTCTTGGCGTAG 167

OY	219	TAGC-TAACACCTGCAACTGGA-GAGGGGGCGGCACGGCGTAAACACCAACTTCT	276
Dd	168	TAACTATCACACTCCACCGGAGCCGACGGGCACTCTTCGCCGTAAAAACCCCCCAATTTT	227
OY	277	--GAATGTGACCTCGAATCAGTAGTAATACCCGCTGAACTTAA	319
Dd	228	TACAAGTTGACCTCGATCAGTAGTGAAATACCGCTGAACTTAA	272
RESULT 15			
LOCUS	B0751027	743 bp	mRNA linear EST 18-JUL-2002
DEFINITION	EST631590 DSCT Colletotrichum trifolii cDNA clone pDSCT2-20,		mRNA sequence.
ACCESSION	B0751027		
VERSION	B0751027.1	GI:21906432	
KEYWORDS	EST.		
SOURCE	Colletotrichum trifolii		
ORGANISM	Colletotrichum trifolii		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
	Mitosporiumces incertae sedis; Phyllachorales; Phyllachoraceae;		
	mitosporic Phyllachoraceae; Colletotrichum.		
REFERENCE	1 (bases 1 to 743)		
AUTHORS	Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,		
TITLE	Cheung,F. and Fraser,C.M.		
JOURNAL	Ests from mycelia of Colletotrichum trifolii race 1		
COMMENT	Unpublished (2002)		
	Other_Ests: EST631589		

FEATURES
 Email: debbys@puccini.crl.umn.edu
 TIGR sequence name: MTSAB2TV More information is available at:
 www.medicago.org
 Seq primer: (gta AtA CGA Ctc Act AtA ggg C) .
 location/Qualifiers
 1..743

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/organism="Colleotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
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/clone="pDSC1-20"
/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC1"
/notes="Vector: Bluescript SK+; Site_1: EcoRI; Site_2: EcoRI; isolate: 2ap2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gell from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

```

ORIGIN

Query Match	34.2%	Score 109;	DB 13;	Length 743;
Best Local Similarity	76.5%;	Pred. No. 9.5e-19;		
Matches 218; Conservative	0;	Mismatches 45;	Indels 22;	Gaps 6;

QY 40 ATCATCGAATTTTGAAGCAGCATTTGCGCCCGCAGATTTCTGGCGGGCATTGCCGTTTG 99
Db 5 ATTTTCGAATCTTTGAGCGCACAATTGCGCCCGCCAGCAATTTCTGGCGGGCATTGCCGTTTG 64
QY 100 AGCGTCATTACACCTTCAGGCCCCCGGGCTCGGGGTTGGGGAAATCGCGGAAGCCCCCTG 159

Db	65	AGCGTATTTCAACCTCAAGCAC--GCTTGGGTTGGGG-----CTTC	107
Qy	160	CGGGCAACAGCGCGTCCCCCAATACAGTGGCGGGTCCGC--CGAGCTTCATTTGCGTAG	218
Db	108	CACGGCTACGTGGGGCCCTCAAGACAGTGGGGAGCCTTCGGGAGGCTCTCTTTGGGTAG	167
Qy	219	TAGC-TAAGACCTCGCAACTGGA--GAGCGCGCGGGCCACGCGTAATAACACCCAACTTCT	276
Db	168	TAACTATACACTCTCGCACCGGAGCCCGAGGGCACTCTTGGCGTAATAACCCCAATTTT	227
Qy	277	--GATGTTGACCTCGAATCAGTAGGATACCCGCTGAATCTAA	319
Db	228	TACAGGTTGACCTCGATCAGTGGGAATACCGGTAACCTTAA	272

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Job time : 4475.33 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 05:20:41 ; Search time 1621.37 Seconds

(without alignments)
8527.610 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaataatgcataagtaagtcgt.....ggataaccgcctgaactraa 319

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1166728

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
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6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
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11: gb_scs:*
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15: em_ba:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
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26: em_ro:*
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36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_ay:*
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40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	6 AR206400	AR206400 Sequence
2	319	100.0	319	6 BD083591	BD083591 Nucleic a
3	319	100.0	319	6 AF117921	AF117921 Nectria h
4	317	99.4	559	8 AY429048	AY429048 Chaetomiu
5	317	99.4	561	8 AY429053	AY429053 Chaetomiu
6	317	99.4	576	8 AY310442	AY310442 Nectria h
7	308	96.6	509	8 AF165874	AF165874 Nectria h
8	292	91.5	298	8 AY226096	AY226096 Nectria h
9	279	87.5	480	8 AF150466	AF150466 Nectria h
10	279	87.5	480	8 AF150467	AF150467 Nectria h
11	279	87.5	480	8 AF440567	AF440567 Nectria h
12	266	83.4	569	8 AY429049	AY429049 Chaetomiu
13	181	56.7	501	8 AY273332	AY273332 Unculture
14	157	49.2	478	8 AF132801	AF132801 Nectria h
15	157	49.2	478	8 AF150459	AF150459 Nectria h
16	157	49.2	478	8 AF150460	AF150460 Nectria h
17	157	49.2	478	8 AF150461	AF150461 Nectria h
18	157	49.2	478	8 AF150462	AF150462 Nectria h
19	157	49.2	478	8 AF150463	AF150463 Nectria h
20	157	49.2	478	8 AF150464	AF150464 Nectria h
21	157	49.2	582	8 AF455451	AF455451 Nectria h
22	152	47.6	546	8 AF178413	AF178413 Neocosmos
23	152	47.6	548	8 AF178397	AF178397 Fusarium
24	149	46.7	544	8 NEXIRS	L36627 Neocosmospo
25	148	46.4	411	8 AF111061	AF111061 Fusarium
26	148	46.4	418	8 AY243054	AY243054 Ascomycet
27	148	46.4	471	8 AF150476	AF150476 Nectria h
28	148	46.4	478	8 AF150449	AF150449 Nectria h
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34	148	46.4	478	8 AF150456	AF150456 Nectria h
35	148	46.4	478	8 AF150457	AF150457 Nectria h
36	148	46.4	479	8 AF058207	AF058207 Nectria h
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45	148	46.4	480	8 AF150480	AF150480 Nectria h

ALIGNMENTS

RESULT 1
LOCUS AR206400
DEFINITION Sequence 6 from patent US 6372430.
ACCESSION AR206400
VERSION AR206400.1 GI:21504990
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 319)
Morrison,C.U., Reiss,E., Aldorevich,L. and Choi,J.Soo.
Nucleic acids for detecting Aspergillus species and other
filamentous fungi
TITLE JOURNAL Patent: US 6372430-A 6 16-APR-2002;

FEATURES	Location/Qualifiers
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Matches 319; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	61 CATTGCGCGCCGCGAGTATCTGGCGGGGATGCTCTTGGAGCGTCAATTAACAACCTCAG 120
Db	61 CATTGCGCGCGCGAGTATCTGGCGGGGATGCTCTTGGAGCGTCAATTAACAACCTCAG 120
QY	121 CCCCCGGGCGCTTGGCGTTGGGAGATCGGCGGAAGCCCCCTGCGGGCAACAGCGCTCCCCA 180
Db	121 CCCCCGGGCGCTTGGCGTTGGGAGATCGGCGGAAGCCCCCTGCGGGCAACAGCGCTCCCCA 180
QY	181 AATAAGTGGCGGTCCCGCCGAGCTTCCATTGGCGTAGCTAACACTTGGCAACTGGA 240
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QY	241 GAGCGGCGCGCGCCAGCGCGTAAACCAACCACTTGTGAATGTGACCTCGAATAGGATG 300
Db	241 GAGCGGCGCGCGCCAGCGCGTAAACCAACCACTTGTGAATGTGACCTCGAATAGGATG 300
QY	301 GAATACCCGCTGAATCTTAA 319
Db	301 GAATACCCGCTGAATCTTAA 319
RESULT 2	
BD083591	
LOCUS	BD083591 319 bp DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi.
ACCESSION	BD083591
VERSION	BD083591.1 GI:22629201
KEYWORDS	JP 2001525665-A/6.
SOURCE	<i>Fusarium solani</i>
ORGANISM	<i>Fusarium solani</i> Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria. 1 (bases 1 to 319) Morrison,C.U., Reiss,E., Aldorevich,L. and Choi,J.S. Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi
REFERENCE	Patent: JP 2001525665-A 6 11-DEC-2001;
AUTHORS	THE SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
TITLE	<i>Fusarium solani</i>
JOURNAL	OS <i>Fusarium solani</i> PN JP 2001525665-A/6 PD 11-DEC-2001 PF 01-MAY-1998 JP 1998548275 PR 02-MAY-1997 US 60/045400 PI CHRISTINE J MORRISON,ERROL REISS,LILIANA ALDOREVICH,JONG SOO PI CHOI PC C1201/68 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers. 1..319 Location/Qualifiers
COMMENT	
FEATURES	
source	1..319 /organism="Fusarium solani" /mol_type="genomic DNA" /db_xref="taxon:163988"

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QY	1	GAAATGGCAATGATGATGATTTGCAGATTCAGTGAATCATCGAATCTTTGAACCA	60	
Db	1	GAAAAATGGCAATGATGATGATTTGCAGATTCAGTGAATCATCGAATCTTTGAACCA	60	
QY	61	CATTGCGCGCCCGCAGATTTCTGGCGGGGATCCGTTGGAGCGTCATTACAACCTCAGG	120	
Db	61	CATTGCGCGCCCGCAGATTTCTGGCGGGGATCCGTTGGAGCGTCATTACAACCTCAGG	120	
QY	121	CCCCCGGGGCTGGCGTTGGGGATCGGGGGAAGCCCTCGCGGGACAAACGCGCTCCCA	180	
Db	121	CCCCCGGGGCTGGCGTTGGGGATCGGGGGAAGCCCTCGCGGGACAAACGCGCTCCCA	180	
QY	181	AATACAGTGGCGGTGCCGCGCAGCTTCATTTGGTGTAGTACCACTTGCAATCGGA	240	
Db	181	AATACAGTGGCGGTGCCGCGCAGCTTCATTTGGTGTAGTACCACTTGCAATCGGA	240	
QY	241	GAGGGGGCGGGCCACGGCCGTAAACACCCCACTTCTGAATTTACCTCGAATCAGTAG	300	
Db	241	GAGGGGGCGGGCCACGGCCGTAAACACCCCACTTCTGAATTTACCTCGAATCAGTAG	300	
QY	301	GAATACCGCTGAACCTTAA 319		
Db	301	GAATACCGCTGAACCTTAA 319		

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RESULT 3
AF117921
LOCUS          319 bp      DNA      linear      PLN 17-JUN-2000
DEFINITION    Nectria haematococca 5.8S ribosomal RNA gene, partial sequence;
               internal transcribed spacer 2, complete sequence; and 28S ribosomal
               RNA gene, partial sequence.
ACCESSION     AF117921
KEYWORDS
SOURCE
ORGANISM      Fusarium solani
               Fusarium solani
               Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
               Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE     Choi,J.S., Westernman,J.M. and Morrison,C.J.
               1 (bases 1 to 319)
               Rapid differentiation of filamentous fungi using species-specific
               DNA probes
AUTHORS       Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
TITLE         2 (bases 1 to 319)
               Choi,J.S., Westernman,J.M. and Morrison,C.J.
               Direct Submission
               Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
               30333, USA
FEATURES
             source
             location/Qualifiers
               1..319
               /organism="Fusarium solani"
               /mol_type="genomic DNA"
               /db_xref="taxon:169388"
               <1..159
               /product="5.8S ribosomal RNA"
               160..272
               /product="internal transcribed spacer 2"
               /note="ITS2"
               273..>319
               /product="28S ribosomal RNA"
ORIGIN
Query Match          100.0%; Score 319; DB 8; Length 319;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAAATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 60
DB 1 GAAATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 60
QY 61 CATTGCGCCCGCAGTATTTCTGCGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 120
DB 61 CATTGCGCCCGCAGTATTTCTGCGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 120
QY 121 CCCCCGGGCTTGGCTTGGGGGATTCGGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCA 180
DB 121 CCCCCGGGCTTGGCTTGGGGGATTCGGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCA 180
QY 181 AATACAGTGGCGGTCCCGCGGAGCTTCATTCAGTACGTAACACCTCGCAACTGGA 240
DB 181 AATACAGTGGCGGTCCCGCGGAGCTTCATTCAGTACGTAACACCTCGCAACTGGA 240
QY 241 GAGCGCGCGGCGCAACCGGCTTAACACCCAACTTGTGAATGTGAATCTCGAATCAGGTAG 300
DB 241 GAGCGCGCGGCGCAACCGGCTTAACACCCAACTTGTGAATGTGAATCTCGAATCAGGTAG 300
QY 301 GAATACCCGCTGCACTTAA 319
DB 301 GAATACCCGCTGCACTTAA 319

RESULT 4

AY429048

LOCUS AY429048 559 bp DNA linear PLN 30-NOV-2003
DEFINITION Chaetomium globosum isolate Cgl 185 ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.

ACCESSION AY429048.1 GI:38503524
VERSION AY429048.1
KEYWORDS
SOURCE Chaetomium globosum
ORGANISM Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

REFERENCE 1 (bases 1 to 559)
Aggarwal, R., Renu, S. and Singh, D. V.
Nucleotide sequence of full length ITS region of Cgl isolate of
Chaetomium globosum
Unpublished
2 (bases 1 to 559)
Aggarwal, R., Renu, S. and Singh, D. V.
Direct Submission
Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa
Road, New Delhi, Delhi 110012, India
Location/Qualifiers

FEATURES
source
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/db_xref="taxon:38033"
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/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"

ORIGIN

Query Match 99.4%; Score 317; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.5e-164;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 62
DB 201 AATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 62
QY 63 TTGCGCCCGCAGTATTTCTGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 122
DB 261 TTGCGCCCGCAGTATTTCTGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 122

QY 123 CCGGCGCTGCGCTTGGGGATTCGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCAA 182
DB 321 CCGGCGCTGCGCTTGGGGATTCGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCAA 180
QY 183 TACAGTGGCGGTCCCGCGGAGCTTTCAGTACGTAACACCTCGCAACTGGA 242
DB 381 TACAGTGGCGGTCCCGCGGAGCTTTCAGTACGTAACACCTCGCAACTGGA 240
QY 243 GCGGCGGCGCAACCGGCTTAACACCCAACTTGTGAATGTGAATCTCGAATCAGGTAG 302
DB 441 GCGGCGGCGCAACCGGCTTAACACCCAACTTGTGAATGTGAATCTCGAATCAGGTAG 300
QY 303 ATACCGCTGCACTTAA 319
DB 501 ATACCGCTGCACTTAA 317

RESULT 5

AY429053

LOCUS AY429053 561 bp DNA linear PLN 30-NOV-2003
DEFINITION Chaetomium globosum isolate Cg6 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.

ACCESSION AY429053.1 GI:38503529
VERSION AY429053
KEYWORDS
SOURCE Chaetomium globosum
ORGANISM Chaetomium globosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

REFERENCE 1 (bases 1 to 561)
Aggarwal, R., Renu, S. and Singh, D. V.
Nucleotide sequence of full length ITS region of Cg6 isolate of
Chaetomium globosum
Unpublished
2 (bases 1 to 561)
Aggarwal, R., Renu, S. and Singh, D. V.
Direct Submission
Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa
Road, New Delhi, Delhi 110012, India
Location/Qualifiers

FEATURES

source
1..561
/organism="Chaetomium globosum"
/mol_type="genomic DNA"
/isolate="Cg6"
/db_xref="taxon:38033"
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/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"

ORIGIN

Query Match 99.4%; Score 317; DB 8; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.5e-164;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 62
DB 203 AATGCGATTAAGTATGATGATGCAAAATTCAGTATCATCGAAATCTTTGAACGA 62
QY 63 TTGCGCCCGCAGTATTTCTGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 122
DB 263 TTGCGCCCGCAGTATTTCTGCGGAGATGCTTTGAGAGCTTATTAACAACCTCAGG 122
QY 123 CCGGCGCTGCGCTTGGGGATTCGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCAA 182
DB 323 CCGGCGCTGCGCTTGGGGATTCGCGGAGACCCCTTCGCGGACAAACGCGTCCCCCAA 180
QY 183 TACAGTGGCGGTCCCGCGGAGCTTTCAGTACGTAACACCTCGCAACTGGA 242
DB 383 TACAGTGGCGGTCCCGCGGAGCTTTCAGTACGTAACACCTCGCAACTGGA 240

QY	243	GGGCGCGGCACGCCCTGAACAACCCCACTTCTGAATGTGAAGCTCGAATAGGTAGA	302
Db	443	GCGCGCGGCACGCCCTGAACAACCCCACTTCTGAATGTGAAGCTCGAATAGGTAGA	502
QY	303	ATAACCGCTGAACCTTA	319
Db	503	ATAACCGCTGAACCTTA	519
RESULT 6			
LOCUS	AYJ10442		
DEFINITION	AYJ10442	576 bp DNA linear	PLN 01-JUL-2003
ACCESSION	Nectria haematococca 18S ribosomal RNA gene, partial sequence;		
VERSION	internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal		
KEYWORDS	transcribed spacer 2, complete sequence; and 28S ribosomal RNA		
SOURCE	AYJ10442.1 GI:32264972		
ORGANISM	Nectria haematococca		
REFERENCE	Nectria haematococca		
AUTHORS	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
TITLE	Hypocistromycetidae; Hypocreales; Nectriaceae; Nectria.		
JOURNAL	1 (bases 1 to 576)		
REFERENCE	Scott,P.T., Martin,H.L., Boreel,S.M., Wearing,A.H. and Maclean,D.J.		
AUTHORS	Isolation and characterization of Nectria haematococca from table		
TITLE	beet grown in the Lockyer Valley, Queensland, Australia		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 576)		
AUTHORS	Scott,P.T.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUN-2003) Agronomy and Horticulture, The University		
FEATURES	of Queensland, Warrego Highway, Gatton, QLD 4343, Australia		
SOURCE	Location/Qualifiers		
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misc_RNA	39..188		
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rRNA	189..345		
	/product="5.8S ribosomal RNA"		
misc_RNA	346..518		
	/product="Internal transcribed spacer 2"		
rRNA	519..>576		
	/product="28S ribosomal RNA"		
ORIGIN			
Query Match	99.4%; Score 317; DB 8; Length 576;		
Best Local Similarity	100.0%; Pred. No.2.5e-164;		
Matches	317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	3	AAATGCGATTAAGTAATGTGAATTGCAAGATTTCAGTAGATCATGAACTTTGAACGACA	62
Db	240	AAATGCGATTAAGTAATGTGAATTGCAAGATTTCAGTAGATCATGAACTTTGAACGACA	299
QY	63	TTGCGCCCCGACATATTTCTGCGCGGCAGATGCTTTTGAGCGTATTACAACCTCAGGCT	122
Db	300	TTGCGCCCCGACATATTTCTGCGCGGCAGATGCTTTTGAGCGTATTACAACCTCAGGCT	359
QY	123	CCCGGAGCTTGCGTTGGGAGTCGCGAGGAAGCCCCTGCGGGGACAAAGCGCGTCCGCCCAA	182
Db	360	CCCGGAGCTTGCGTTGGGAGTCGCGAGGAAGCCCCTGCGGGGACAAAGCGCGTCCGCCCAA	419
QY	183	TACAGTGGGGGTCCCGCCGAGCTTCATCTGGTGAAGTACTTAACACTTGCAACTGGAGA	242
Db	420	TACAGTGGGGGTCCCGCCGAGCTTCATCTGGTGAAGTACTTAACACTTGCAACTGGAGA	479
QY	243	GCGCGCGGCACGCCCTGAACAACCCCACTTCTGAATGTGAAGCTCGAATAGGTAGA	302
Db			

Db	480	GGGGGGGGGCAAGCCGGTAAAAACACCCAACTTCTGAATGTTGACCTCGAATCAGTGAAGA	539
Qy	303	ATACCCGCTGAATTAA 319	
Db	540	ATACCCGCTGAATTAA 556	
RESULT 7			
LOCUS	AF165874	509 bp	linear
DEFINITION	Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF165874		
VERSION	AF165874.1	GI:5524731	
KEYWORDS			
SOURCE	Fusarium solani		
ORGANISM	Fusarium solani		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.		
AUTHORS	Iwen, P.C., Henry, T. and Hinrichs, S.H.		
TITLE	Sequence analysis of the internal transcribed spacer regions of <i>Fusarium</i> species most commonly associated with human invasive disease		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 509)		
AUTHORS	Iwen, P.C., Henry, T. and Hinrichs, S.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6493, USA		
FEATURES	Location/Qualifiers		
source	1..509		
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misc_RNA	1..150		
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rRNA	151..307		
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misc_RNA	308..480		
	/product="internal transcribed spacer 2"		
	/note="ITS2"		
rRNA	481..>509		
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Query Match	96.6%;	Score 308;	DB 8; Length 509;
Best Local Similarity	100.0%;	Pred. No. 2,5e-159;	
Matches 308;	Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	3	AAATGCATTAAGTAAGTGAATTCGACGATTCAGTGAATCAATCAATCTTTGAAGCACA	62
Db	202	AAATGCATTAAGTAAGTGAATTCGACGATTCAGTGAATCAATCAATCTTTGAAGCACA	261
Qy	63	TTGGCCCGCCGACAGTATTCGCGCGGATCCTGTTGAGCGTCATTACAACCTCAGGCG	122
Db	262	TTGGCCCGCCGACAGTATTCGCGCGGATCCTGTTGAGCGTCATTACAACCTCAGGCG	321
Qy	123	CCCGGGCTTGGCGTTGGGATGCGCGAAGCCCCCTGCGGGCAACAACCGTCCCCCAA	182
Db	322	CCCGGGCTTGGCGTTGGGATGCGCGAAGCCCCCTGCGGGCAACAACCGTCCCCCAA	381
Qy	183	TACAGTGGCGGTCCCGCCGACGTTCCATGTGCTAGCTAACCCCTGGCACTGGAGA	242
Db	382	TACAGTGGCGGTCCCGCCGACGTTCCATGTGCTAGCTAACCCCTGGCACTGGAGA	441
Qy	243	GGCGCGCGGCAAGCCGCTAAAAACACCAACTTCTGAATGTTGACCTCGAATCAGTGAAGA	302

QY	303	ATACCGCG	310		
Db	502	ATACCGCG	509		
RESULT 8					
LOCUS	AY226096				
DEFINITION	AY226096				
ACCESSION	AY226096				
VERSION	AY226096.1				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
misc_RNA					
rRNA					
tRNA					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	28	AGAAATTCAGTGAATCATCGAATCTTTGGAACGACATGTCGCGCCGACGATTTCTGGCGGG	87		
Db	1	AGAAATTCAGTGAATCATCGAATCTTTGGAACGACATGTCGCGCCGACGATTTCTGGCGGG	60		
QY	88	CATGCGCTGTCGAGCGGTCAATTAACAACCTCAGAGCCCGCGGCGCTGGCGTGGGGAATCGGC	147		
Db	61	CATGCGCTGTCGAGCGGTCAATTAACAACCTCAGAGCCCGCGGCGCTGGCGTGGGGAATCGGC	120		
QY	148	GGAAGCCCCCTCGCGGCGCAACAAGCCGCTCCCCCAATTAACAGTGGCGGCTCCCGCGGACGCTT	207		
Db	121	GGAAGCCCCCTCGCGGCGCAACAAGCCGCTCCCCCAATTAACAGTGGCGGCTCCCGCGGACGCTT	180		
QY	208	CCATTGCGGTAAGAGCTTAACACCTCGCAACTGGAGAGCGCGCGGCGCAAGCGCGGTAAACAC	267		
Db	131	CCATTGCGGTAAGAGCTTAACACCTCGCAACTGGAGAGCGCGCGGCGCAAGCGCGGTAAACAC	240		
QY	268	CCAACTTGTGAATGTTGACCTTCGATCAGTGAATACCCGCTGAACCTTAA	319		
Db	241	CCAACTTGTGAATGTTGACCTTCGATCAGTGAATACCCGCTGAACCTTAA	292		
RESULT 9					
LOCUS	AF150466				
DEFINITION	AF150466				
ACCESSION	AF150466				

VERSION	AF150466.1	GI:7650164
KEYWORDS		
SOURCE	Nectria haematococca	
ORGANISM	Nectria haematococca	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
AUTHORS	Suga,H., Hasegawa,T., Mitui,H., Kageyama,K. and Hyakumachi,M.	
TITLE	Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region	
JOURNAL	Mycol. Res. 104 (10), 1175-1183 (2000)	
REFERENCE	2 (bases 1 to 480)	
AUTHORS	Suga,H., Hyakumachi,M. and Kageyama,K.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-May-1999) Molecular Genetics Research Center, Gifu University, Gifu 501-1112, Japan	
FEATURES	Location/Qualifiers	
source	1..480	
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misc_RNA	309..480	
	/product="internal transcribed spacer 2"	
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Best Local Similarity	100.0%; Pred. No. 3.1e-143;	
Matches 279; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	3 AAATGGCATAGTATGTGAATTGCAGATTTCATGTAATCTCGAATCTTTGAACGCACA	62
DB	202 AAATGGCATAGTATGTGAATTGCAGATTTCATGTAATCTCGAATCTTTGAACGCACA	261
QY	63 TTGGCGCCGCGCAGATTTCTGGCGGGGCATGCTGTTCGAGCGTCATTACAACCTTCAGGCC	122
DB	262 TTGGCGCCGCGCAGATTTCTGGCGGGGCATGCTGTTCGAGCGTCATTACAACCTTCAGGCC	321
QY	123 CCCGGCGCTGGCGCTTGGGGGATCGCGGAGGCCCTTCGCGGCACAGCGCGTCCGCCAA	182
DB	322 CCCGGCGCTGGCGCTTGGGGGATCGCGGAGGCCCTTCGCGGCACAGCGCGTCCGCCAA	381
QY	183 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTAGTACTTAACACTTCGCAATCGAGA	242
DB	382 TACAGTGGCGGTCCCGCGCAGCTTCCATTGCGTAGTACTTAACACTTCGCAATCGAGA	441
QY	243 GCGGCGGGCGCAGCGCGTAAACACCAACTTCGTAATG	281
DB	442 GCGGCGGGCGCAGCGCGTAAACACCAACTTCGTAATG	480
RESULT 10		
AF150467	480 bp	DNA linear
LOCUS	AF150467	linear
DEFINITION	Nectria haematococca strain SUF210 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	
ACCESSION	AF150467	
VERSION	AF150467.1	GI:7650165
KEYWORDS		
SOURCE	Nectria haematococca	
ORGANISM	Nectria haematococca	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
AUTHORS	Suga,H., Hasegawa,T., Mitui,H., Kageyama,K. and Hyakumachi,M.	
TITLE	Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region	

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

Mycol. Res. 104 (10), 1175-1183 (2000)
2 (bases 1 to 480)
Suga, H., Hyakumachi, M. and Kageyama, K.
Direct Submission
Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
Location/Qualifiers

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ORIGIN
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ORIGIN

Query Match	87.5%;	Score 279;	DB 8;	Length 480;
Best Local Similarity	100.0%;	Pred. No. 3.1e-143;		
Matches 279;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	3	AAATGCGATTAAGTAATGGAATTCAGAAATCAATCGAAATTTTGAACGCACA	62
Db	202	AAATGCGATTAAGTAATGGAATTCAGAAATCAATCGAAATTTTGAACGCACA	261
QY	63	TTGGCGCCCGCAGTAATTCGGCGGGCAGATGCGTTTCAGCGCTCATTTCAACCCTCAGAGCC	122
Db	262	TTGGCGCCCGCAGTAATTCGGCGGGCAGATGCGTTTCAGCGCTCATTTCAACCCTCAGAGCC	321
QY	123	CCCGGCGCTGGCGTTCGGGGGATTCGGCGGAAAGGCCCTCGCGGGCACAACGCCCTCCCCCAA	182
Db	322	CCCGGCGCTGGCGTTCGGGGGATTCGGCGGAAAGGCCCTCGCGGGCACAACGCCCTCCCCCAA	381
QY	183	TACAGTGGCGGTCCCGCGCAGACTTCATTGTCGTAAGTACCAACCTCGCACTGAGAGA	242
Db	382	TACAGTGGCGGTCCCGCGCAGACTTCATTGTCGTAAGTACCAACCTCGCACTGAGAGA	441
QY	243	GGGCGGCGGCACGCGCGTTAAACACCCCAACTTCGGAATG	281
Db	442	GGGCGGCGGCACGCGCGTTAAACACCCCAACTTCGGAATG	480

Result 11	AF440567	AF440567	AF440567	LOCUS	DEFINITION
		480 bp	DNA	linear	PLN 24-SEP-2003
					Neceria haemalococca isolate CS-1 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

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1. .150
/product="internal transcribed spacer 1"
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misc_RNA
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/product="internal transcribed spacer 2"
ORIGIN

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ORIGIN

Query Match	87.5%	Score 279	DB 8	Length 480
Best Local Similarity	100.0%	Pred. No.	3,1e-143	
Matches 279	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	3	AAATGCGATTAAGTAAGTGAATTCGAGATTCAGTAATCGAATCTTTGAACGACA	62
Db	202	AAATGGGATTAAGTAAGTGAATTCGAGATTCAGTAATCGAATCTTTGAACGACA	261
QY	63	TTGGCGCCCGCAGATTAATTCGCGGGCATGCTGTTGAGCTCATTAACAACCTCAGGCC	122
Db	262	TTTCGCGCCCGCAGATTAATTCGCGGGCATGCTGTTGAGCTCATTAACAACCTCAGGCC	321
QY	123	CCGCGGACTGAGGATTGGGGGATCGGGGGAAGCCCCCTGGGGGCAAAAGCCGTCCTCCCAA	182
Db	322	CCGCGGACTGAGGATTGGGGGATCGGGGGAAGCCCCCTGGGGGCAAAAGCCGTCCTCCCAA	381
QY	183	TACAGTGGCGGATCCCGCGCAGCTTCATTCGTAAGTAGTAAACCTCGCAACTGGAGA	242
Db	382	TACAGTGGCGGATCCCGCGCAGCTTCATTCGTAAGTAGTAAACCTCGCAACTGGAGA	441
QY	243	GGCGCGCGGCAACGCGCTTAACACCCCACTTCGAATG	281
Db	442	GGCGCGCGGCAACGCGCTTAACACCCCACTTCGAATG	480

RESULT 12	
AY429049	
LOCUS	AY429049
DEFINITION	Chactonium globosum isolate Cg2 18S ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AY429049
VERSION	AY429049.1
	569 bp DNA linear
	PLN 30-NOV-2003

TITLE	Genetic analysis of pathogenic and nonpathogenic <i>Fusarium oxysporum</i> from tomato plants
JOURNAL	Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE	2 (bases 1 to 480)
AUTHORS	Bao, J. R., Fravel, D. R. and Laarovich, G.
TITLE	Direct Submission
JOURNAL	Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES	location/Qualifiers
SOURCE	1 480

Query Match 83.4%; Score 266; DB 8; Length 569;

Best Local Similarity 99.7%; Pred. No. 5.1e-136;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 62
DB 212 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 271
QY 63 TTGGGCGCGGCGGATTTGCGGCGGCGGATTCGAGCGCATTAACCTTCAGGCC 122
DB 272 TTGGGCGCGGCGGATTTGCGGCGGCGGATTCGAGCGCATTAACCTTCAGGCC 331
QY 123 CCGGGGCTGGCGGTGGGGAATCGGCGGAAGCCCCCTGGGCGGACAAAGCCGTCGCCAAA 182
DB 332 CCGGGGCTGGGCGGTGGGGAATCGGCGGAAGCCCCCTGGGCGGACAAAGCCGTCGCCAAA 391
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTAAGTAACTTGAACCTTCGCACTGGAGA 242
DB 392 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTAAGTAACTTGAACCTTCGCACTGGAGA 451
QY 243 GCGGCGGCGGCGGCGGTAACCACTTCGAAATTCGAACTTCGAACTTCGAACTTCGAACTTCGAA 302
DB 452 GCGGCGGCGGCGGCGGTAACCACTTCGAAATTCGAACTTCGAACTTCGAACTTCGAACTTCGAA 511
QY 303 ATACCGGCTGAACCTTAA 319
DB 512 ATACCGGCTGAACCTTAA 528

RESULT 13
LOCUS AY273332 501 bp DNA linear PLN 30-OCT-2003
DEFINITION Uncultured ascomycete clone 77A6 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
VERSION AY273332
KEYWORDS AY273332.1 GI:34420179

SOURCE .
ORGANISM uncultured ascomycete
uncultured ascomycete
Eukaryota; Fungi; Ascomycota; environmental samples.
REFERENCE 1 (bases 1 to 501)
Roose-Amaaleg,C., Brygoo,Y. and Harry,M.
Marked discrepancy between fungal diversity in soil-feeding
termitaries and tropical soils
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 501)
Roose-Amaaleg,C., Brygoo,Y. and Harry,M.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2003) UFR Sciences Universite Paris 12,
UMR137-LBSE, Avenue du General de Gaulle, Creteil cedex 94010,
France

FEATURES
source
1. .501
Location/Qualifiers
/organism="uncultured ascomycete"
/mol_type="genomic DNA"
/isolation_source="termitarie of Cubitermes sp. 1 (forest
dominated by Aucoamea klaineana)"
/db_xref="taxon:175243"
/clone="T7A6"
/environmental_sample
/country="Gabon: Doda, La Lope"
<1. .141
/note="contains 18S ribosomal RNA and internal transcribed
spacer 1"
rRNA 142. .292
/product="5.8S ribosomal RNA"
misc_RNA 293. .501
/note="contains internal transcribed spacer 2 and 28S
ribosomal RNA"

ORIGIN
Query Match 56.7%; Score 181; DB 8; Length 501;

Best Local Similarity 99.3%; Pred. No. 7.8e-89;
Matches 281; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 62
DB 188 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 247
QY 63 TTGGGCGCGGCGGATTTGCGGCGGCGGATTCGAGCGCATTAACCTTCAGGCC 122
DB 248 TTGGGCGCGGCGGATTTGCGGCGGCGGATTCGAGCGCATTAACCTTCAGGCC 307
QY 123 CCGGGGCTGGCGGTGGGGAATCGGCGGAAGCCCCCTGGGCGGACAAAGCCGTCGCCAAA 182
DB 308 CCGGGGCTGGCGGTGGGGAATCGGCGGAAGCCCCCTGGGCGGACAAAGCCGTCGCCAAA 367
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTAAGTAACTTGAACCTTCGCACTGGAGA 242
DB 368 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTAAGTAACTTGAACCTTCGCACTGGAGA 427
QY 243 GCGGCGGCGGCGGCGGTAACCACTTCGAAATTCGAACTTCGAACTTCGAACTTCGAACTTCGAA 285
DB 428 GCGGCGGCGGCGGCGGTAACCACTTCGAAATTCGAACTTCGAACTTCGAACTTCGAACTTCGAA 470

RESULT 14
LOCUS AF132801 478 bp DNA linear PLN 20-JAN-2000
DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal
RNA, and internal transcribed spacer 2, complete sequence.
VERSION AF132801
KEYWORDS AF132801.1 GI:4809015

SOURCE .
ORGANISM Fusarium solani
Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
Molecular identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
Plant Dis. 84 (1), 83-89 (2000)
2 (bases 1 to 478)
Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1999) Plant Pathology, Iowa State University,
Room 351 Beesey Hall, Ames, IA 50011, USA

FEATURES
source
1. .478
Location/Qualifiers
/organism="Fusarium solani"
/mol_type="genomic DNA"
/isolate="P185"
/specific_host="Glycine max"
/db_xref="taxon:169388"
/tissue_type="mycelium"
/country="USA: Iowa, Lee County"
1. .149
/product="internal transcribed spacer 1"
/note="ITS1"
rRNA 150. .306
/product="5.8S ribosomal RNA"
misc_RNA 307. .478
/product="internal transcribed spacer 2"
/note="ITS2"

ORIGIN
Query Match 49.2%; Score 157; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 62
DB 201 AAATGCGATTAAGTATGTAATTCGAAATTCAGTAATCATCGAATCTTTGAACGACA 260

QY 63 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTGTTCAGCGTCATTACAACTCTCAGGCC 122
 |||||
 Db 261 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTGTTCAGCGTCATTACAACTCTCAGGCC 320
 |||||
 QY 123 CCCGGGCTTGCGGTGGGGATCGCGGAAAGCCCCCTG 159
 |||||
 Db 321 CCCGGGCTTGCGGTGGGGATCGCGGAAAGCCCCCTG 357
 |||||

RESULT 15

AF150459

LOCUS

DEFINITION

478 bp DNA linear PLN 05-JAN-2001
 Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S
 ribosomal RNA gene, and internal transcribed spacer 2, complete
 sequence.

ACCESSION AF150459.1 GI:7650157
 VERSION AF150459

KEYWORDS
 SOURCE Nectria haematococca

ORGANISM Nectria haematococca
 Nectria haematococca
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
 Suga,H., Haegeawa,T., Mitsu,H., Kageyama,K. and Hyakumachi,M.
 Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
 based on the rDNA-ITS region

Mycol. Res. 104 (10), 1175-1183 (2000)

2 (bases 1 to 478)
 Suga,H., Hyakumachi,M. and Kageyama,K.

REFERENCE Direct Submission
 Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
 University, Gifu 501-1112, Japan

JOURNAL

TITLE

FEATURES

source

1..478
 /organism="Nectria haematococca"
 /mol_type="genomic DNA"
 /strain="K-1"
 /db_xref="taxon:140110"
 /note="anamorph: Fusarium solani"
 1..149
 /product="internal transcribed spacer 1"
 150..307
 /product="5.8S ribosomal RNA"
 308..478
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 49.2%; Score 157; DB 8; Length 478;
 Best local similarity 100.0%; Pred. No. 1,7e-75;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAATGCGATTAAGTATGGAATTCAGAAATTCAGTAATCGAATCTTTGAAGCACA 62
 |||||
 Db 201 AAATGCGATTAAGTATGGAATTCAGAAATTCAGTAATCGAATCTTTGAAGCACA 260
 |||||
 QY 63 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTGTTCAGCGTCATTACAACTCTCAGGCC 122
 |||||
 Db 261 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTGTTCAGCGTCATTACAACTCTCAGGCC 320
 |||||
 QY 123 CCCGGGCTTGCGGTGGGGATCGCGGAAAGCCCCCTG 159
 |||||
 Db 321 CCCGGGCTTGCGGTGGGGATCGCGGAAAGCCCCCTG 357
 |||||

Search completed: October 1, 2004, 09:56:21

Job time : 1626.37 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:41:36 ; Search time 267.27 Seconds
(without alignments)
5070.430 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319
Sequence: 1 gaatacgagtaagtaatgt.....ggaataccgcgtgaactaa 319

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 212409041 residues

Word size : 10

Total number of hits satisfying chosen parameters: 606458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N Geneseq, 29Jan04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	319	100.0	319	2	AAV70850 Internal
2	107	33.5	382	3	AAa72783 5.8s rRNA
3	107	33.5	502	3	AAa61893 Fusarium
4	107	33.5	504	2	AAAT05400 Fusarium
5	107	33.5	504	2	AAV62591 Fusarium
6	107	33.5	504	2	AAV59028 F. culmorum
7	107	33.5	504	4	AAa808426 Internal
8	107	33.5	521	7	ACC50000 Internal
9	107	33.5	522	7	ACC49999 Internal
10	107	33.5	534	7	ACC50002 Internal
11	107	33.5	545	2	AAV62593 Fusarium
12	107	33.5	545	2	AAV59030 F. moniliforme
13	107	33.5	546	2	AAV62596 Fusarium
14	107	33.5	546	2	AAV59007 F. poae
15	107	33.5	2293	4	AAV516211 Fusarium
16	107	33.5	647	6	ABV78700 C. crassii
17	106	33.2	661	6	ABV78721 C. sinensis
18	106	33.2	389	3	AAZ92490 Rhizoctonia
19	94	29.5	569	2	AAAT65101 T. harzia
20	94	29.5	569	2	AAAT65099 T. harzia
21	94	29.5	582	2	AAAT65100 T. harzia
22	94	29.5	310	2	AAV70851 Internal
23	79	24.8	310	2	AAV70851 Internal

24	73	22.9	545	2	AAAT05403 Microdoch
25	71	22.3	561	2	AAV59009 F. avenae
26	71	22.3	659	6	ABV78724 C. sinensis
27	70	21.9	537	3	AAZ91725 Roseillini
28	69	21.6	343	2	AAV70871 Internal
29	69	21.6	344	2	AAV70870 Internal
30	68	21.3	377	6	ABa94559 Truncated
31	68	21.3	377	6	ABa94564 Consensus
32	68	21.3	377	6	ABa94561 Truncated
33	68	21.3	377	6	ABa94560 Truncated
34	68	21.3	415	4	AAAT75169 Consensus
35	68	21.3	415	4	AAAT75170 Consensus
36	68	21.3	451	4	AAZ22436 Internal
37	68	21.3	466	8	ADA273221 P. micros
38	68	21.3	534	2	AAAT05398 Mycosphae
39	68	21.3	534	2	AAAT62505 Mycosphae
40	68	21.3	534	6	ABa94562 DNA seqe
41	68	21.3	537	6	ABa01153 Deuteromy
42	68	21.3	540	2	AAAT05399 Mycosphae
43	68	21.3	540	2	AAAT62506 Mycosphae
44	68	21.3	540	6	ABa94563 DNA seqe
45	68	21.3	548	2	AAAT05394 Septoria

ALIGNMENTS

RESULT 1	AAV70850 standard; DNA; 319 BP.
ID	AAV70850
XX	AAV70850;
AC	26-FEB-1999 (first entry)
DT	Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; R. circinellioideus F. circinellioideus; Rhizopus oryzae; R. microsporus; M. circinellioideus F. circinellioideus; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
KW	Fusarium solani.
XX	MO9850584-A2.
OS	12-NOV-1998.
XX	01-MAY-1998; 98MO-US008926.
XX	02-MAY-1997; 97US-0045400P.
PR	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	Morrison CJ, Reiss E, Aidorevich L, Choi JS;
XX	WPI, 1999-034737/03.
DR	New nucleic acid probes for filamentous fungi - for detecting e.g.
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT	species.
XX	Claim 1; Page 12; 45pp; English.
PS	The present sequence represents an internal transcribed spacer 2 (ITS2)
XX	and adjacent regions. Probes can be derived from the present sequence
CC	which are species-specific. The specification also describes ITS2
CC	sequence-derived probes for identifying a species selected from
CC	Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,

invention in combination with an AIDS antiviral agent, an immunomodulator and an antineoplastic agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of HIV infection. A wide range of state of HIV infection may be treated: CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); CC both asymptomatic and asymptomatic HIV infection; and actual or potential CC exposure to HIV. The compounds may be used to isolate HIV integrase CC mutants which are potentially useful as screening tools for antiviral CC compounds. The compounds may also be used to establish or determine the CC site at which other antivirals bind to HIV integrase (e.g., by CC competitive inhibition). The present sequence represents the ribosomal CC DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp. CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003 CC to standardize OS field)

Sequence 502 BP, 127 A, 144 C, 118 G, 113 T, 0 U, 0 Other;

Query Match 33.5%; Score 107; DB 3; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAATGCGATAGTAATGTAATTCAGAAATTCAGTGAATTCGAAATCTTTGAACGCAC 61
 DB 195 AAATGCGATAGTAATGTAATTCAGAAATTCAGTGAATTCGAAATCTTTGAACGCAC 254

OY 62 ATTGCGCCCGCCAGTATTCCTGGCGGCATGCTGCTTTGAGCGTCATT 108
 DB 255 ATTGCGCCCGCCAGTATTCCTGGCGGCATGCTGCTTTGAGCGTCATT 301

RESULT 4
 AAT05400
 ID AAT05400 standard; DNA; 504 BP.
 AC AAT05400;
 DT 04-JUN-1996 (first entry)
 DB *Fusarium culmorum* internal transcribed spacer sequence.
 XX Plant pathogen; fungus; *Septoria nodorum*; *Septoria tritici*; *Fusarium*;
 KW *Pseudocercospora*; *herpotrichoides*; *Mycosphaerella fijiensis*; PCR;
 KW *Mycosphaerella muscicola*; amplification; primer; ribosomal RNA gene;
 KW internal transcribed region; strain; capture; colourimetric assay;
 KW isolate; development; population; random amplified polymorphic DNA; ss.
 OS *Fusarium culmorum*.
 XX **W09529260-A2**
 PN 02-NOV-1995.
 XX 19-APR-1995; 95WO-US004712.
 PF 25-APR-1994; 94US-00233608.
 PR (CTBA) CTBA GEIGY AG.
 PA Liqon JM, Beck J;
 PI WPI; 1995-383005/49.
 DR DNA encoding intervening transcribed sequence - used for detection of
 FT plant fungal pathogens.
 PT Claim 1; Page 54-55; 65pp; English.
 XX A novel method for the detection of plant pathogenic strains of fungi
 CC e.g. *Septoria nodorum*, *S. tritici*, *Pseudocercospora herpotrichoides*,
 CC *Mycosphaerella fijiensis*, *M. muscicola* or *Fusarium* spp, involves the PCR
 CC amplification of sequences found in the internal transcribed region (ITS)
 CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAO94359-93
 CC and AAT05357-72. These primers are derived from the ITS sequences of

these fungi (AAT05394-T05404 and AAO94398) and are strain specific. The CC amplification products of the reactions using these primers can be used CC with the capture primers AAT05378-93 in colourimetric assays. The primers CC and ITS DNAs can be used for the detection of specific fungal pathogen CC isolates and in monitoring disease development in plant populations

Sequence 504 BP, 133 A, 132 C, 113 G, 122 T, 0 U, 4 Other;

Query Match 33.5%; Score 107; DB 2; Length 504;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAATGCGATAGTAATGTAATTCAGAAATTCAGTGAATTCGAAATCTTTGAACGCAC 61
 DB 211 AAATGCGATAGTAATGTAATTCAGAAATTCAGTGAATTCGAAATCTTTGAACGCAC 270

OY 62 ATTGCGCCCGCCAGTATTCCTGGCGGCATGCTGCTTTGAGCGTCATT 108
 DB 271 ATTGCGCCCGCCAGTATTCCTGGCGGCATGCTGCTTTGAGCGTCATT 317

RESULT 5
 AAV62591
 ID AAV62591 standard; DNA; 504 BP.
 AC AAV62591;
 DT 17-DEC-1998 (first entry)
 DE *Fusarium culmorum* PCR amplified ITS region consensus DNA sequence.
 XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
 KW *Fusarium culmorum*; *Fusarium graminearum*; *Fusarium moniliforme*; plant;
 KW *Septoria avenae*; *Microdochium nivale*; *Fusarium poae*; *Fusarium avenaceum*;
 KW PCR; nucleic acid detection; ss.
 OS *Fusarium culmorum*.
 XX Key Location/Qualifiers
 FH 1. 12
 FT misc_feature /*tag= a
 FT /note= "3' end of small subunit rRNA gene"
 FT misc_feature 13. 161
 FT /*tag= b
 FT /note= "ITS 1"
 FT misc_feature 162.. 318
 FT /*tag= c
 FT /note= "5.8S rRNA gene"
 FT misc_feature 319.. 472
 FT /*tag= d
 FT /note= "ITS 2"
 FT misc_feature 473.. 504
 FT /*tag= e
 FT /note= "5' end of large subunit rRNA gene"
 PN US5814453-A.
 XX 29-SEP-1998.
 PD 02-JUL-1997; 97US-00887480.
 PF 19-APR-1995; 95WO-US004712.
 PR 15-OCT-1996; 96US-00722187.
 PA (NOVS) NOVARTIS FINANCE CORP.
 PI Beck J;
 DR WPI; 1998-541745/46.
 XX DNA isolated from fungal RNA, and its internal transcribed spacer
 PT sequence - used for detecting fungal pathogens in plant tissue.

PS Claim 2; Fig 3; 56bp; English.

XX This represents the consensus DNA sequence of the internal transcribed
CC spacer (ITS) region that was PCR amplified from *Fusarium culmorum*
CC isolates, R-5106, R-5126 and R-5146. The invention provides a DNA
CC molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
CC pathogen, where the DNA molecule consists of an ITS sequence selected
CC from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium*
CC moniliforme, *Septoria avenae* or *Microdochium nivale*. A method for
CC detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*
CC *avenaeum* and *M. nivale* isolates is also provided. The method comprises
CC isolating DNA from a plant leaf infected with at least one of the above
CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
CC PCR using specific primers from within these sequences. The pathogen(s)
CC are detected by visualising the amplified part of the ITS sequence

XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 33.5%; Score 107; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATAGTATGTAATGCAAGATTGAGTATGATCATGAACTTTGAAAGCAGC 61
DB 211 AAAATGCGATAGTATGTAATGCAAGATTGAGTATGATCATGAACTTTGAAAGCAGC 270
QY 62 ATGGCGCCCGCAGTATTCGCGGCGCATGCGCTGTTGAGCGTCATT 108
DB 271 ATGGCGCCCGCAGTATTCGCGGCGCATGCGCTGTTGAGCGTCATT 317

RESULT 6
AAV59028
ID AAV59028 standard; DNA; 504 BP.
XX
AC AAV59028;
XX
DT 25-MAR-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE F. culmorum internal transcribed spacer.
XX
KM Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.
XX
OS *Fusarium culmorum*.
XX
FH Key Location/Qualifiers
FT misc_feature 13..161
FT /*tag= a
FT /note= "ITS1"
FT misc_feature 319..472
FT /*tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
PD 27-OCT-1998.
XX
PF 04-AUG-1997; 97US-00905314.
XX
PR 04-AUG-1997; 97US-00905314.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Beck JJ;
XX
DR WPI; 1998-593995/50.
XX
PT Wheat pathogen internal transcribed spacer sequences - used as a basis
PT for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.

PS Disclosure; Col 21-22; 20pp; English.

XX This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*
CC *avenaeum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.)

XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 33.5%; Score 107; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATAGTATGTAATGCAAGATTGAGTATGATCATGAACTTTGAAAGCAGC 61
DB 211 AAAATGCGATAGTATGTAATGCAAGATTGAGTATGATCATGAACTTTGAAAGCAGC 270
QY 62 ATGGCGCCCGCAGTATTCGCGGCGCATGCGCTGTTGAGCGTCATT 108
DB 271 ATGGCGCCCGCAGTATTCGCGGCGCATGCGCTGTTGAGCGTCATT 317

RESULT 7
AAS08426
ID AAS08426 standard; DNA; 504 BP.
XX
AC AAS08426;
XX
DT 26-SEP-2001 (first entry)
XX
DE Internal transcribed spacer, ITS, region #16.
XX
KM Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;
KM Sharp eyespot; fungal pathotype identification; isolate 62215.
XX
OS *Fusarium culmorum*.
XX
PN WO200151653-A1.
XX
PD 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-EP000172.
XX
PF 11-JAN-2000; 2000US-00481293.
XX
PR (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PA Beck JJ, Barnett CJ;
XX
PI WPI; 2001-442154/47.
XX
DR New internal transcribed spacer DNA sequences, useful for identifying
PT fungal pathogen, particularly *Rhizoctonia cerealis*, and for monitoring
PT disease development in plant population.
XX
PS Disclosure; Page 31; 35pp; English.
XX
XX The sequence is an internal transcribed spacer (ITS) region from *Fusarium*
CC *culmorum*, isolate 62215. The ITS DNA sequences are useful for detecting
CC *Rhizoctonia cerealis*, a fungal pathogen of wheat causing Sharp eyespot,
CC for monitoring disease development in plant population, and for providing
CC detailed information on the development and spread of specific pathogen
CC races over extended geographical areas. The DNA sequences are
CC specifically used as primers in PCR-based analysis for the identification
CC of fungal pathotypes

XX
SQ Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;

Query Match 33.5%; Score 107; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 61
DB 214 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 273
OY 62 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 108
DB 274 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 320

RESULT 8
ACCS0000
ID ACC50000 standard; DNA; 521 BP.
AC ACC50000;
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #2.
DE
XX Mitochondria; fungal pathogen; ds.
XX
XX Gibberella zeae.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JI, Barnett CJ;
XX
XX WPI; 2003-363229/34.
XX
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
XX Claim 5; Page 38; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 7; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 61
DB 228 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 287
OY 62 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 108
DB 288 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 334

RESULT 9
ACCS0000
ID ACC49999 standard; DNA; 522 BP.

XX
AC ACC49999;
XX
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence.
DE
XX Mitochondria; fungal pathogen; ds.
XX
XX Fusarium subglutinans.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JI, Barnett CJ;
XX
XX WPI; 2003-363229/34.
XX
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
XX Claim 5; Page 38; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 7; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 61
DB 228 AAAATGCGATGAATGATGCAATTCAGATGATCATGCAATCTTTGAACGCAC 287
OY 62 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 108
DB 288 ATTGGCGCCGCGCAGATTTCTGGCGGCGCATGCTGTTGAGCGTCATT 334

RESULT 10
ACCS0002
ID ACC50002 standard; DNA; 522 BP.
AC ACC50002;
XX
XX 27-OCT-2003 (revised)
XX
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #4.
DE
XX Mitochondria; fungal pathogen; ds.
XX
XX Gibberella moniliformis.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.

XX Claim 2; Fig 3; 56pp; English.

CC This represents the DNA sequence of the internal transcribed spacer (ITS)
 CC region that was PCR amplified from *Fusarium moniliforme*. The invention
 CC provides a DNA molecule isolated from the ribosomal RNA gene region of a
 CC fungal pathogen, where the DNA molecule consists of an ITS sequence
 CC selected from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*,
 CC *Fusarium moniliforme*, *Septoria avenae* or *Microdochium nivale*. A method
 CC for detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*
 CC *avenaceum* and *M. nivale* isolates is also provided. The method comprises
 CC isolating DNA from a plant leaf infected with at least one of the above
 CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
 CC PCR using specific primers from within these sequences. The pathogen(s)
 CC are detected by visualizing the amplified part of the ITS sequence.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCATAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 61
 DB 228 AAAATGCATAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 287
 OY 62 ATTGGCCCCCGCAGTATTCTGGCGGCATGCTCTTTCGAGGTCATT 108
 DB 288 ATTGGCCCCCGCAGTATTCTGGCGGCATGCTCTTTCGAGGTCATT 334

RESULT 13

AAVS9030
 ID AAVS9030 standard; DNA; 545 BP.

XX AAVS9030;

XX 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1999 (first entry)

XX F. moniliforme internal transcribed spacer.

XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
 KW fungal pathogen identification; infection identification; ss.

XX Gibberella fujikuroi.

XX Key Location/Qualifiers

FT misc_feature 31..178
 FT /*tag= a
 FT /note= "ITS1"
 FT 336..488
 FT /*tag= b
 FT /note= "ITS2"

XX US5827695-A.

XX 27-OCT-1998.

XX 04-AUG-1997; 97US-00905314.

XX 04-AUG-1997; 97US-00905314.

XX (NOVS) NOVARTIS FINANCE CORP.

XX Beck JU;

XX WPI; 1998-593995/50.

XX Wheat pathogen internal transcribed spacer sequences - used as a basis
 PT for primers for the species-specific polymerase chain reaction detection

PT of the pathogens.

XX Disclosure: Col 23-26; 20pp; English.

CC This sequence represents an internal transcribed spacer (ITS) sequence of
 CC the invention. The primer pairs, based on the ITS sequences, are used for
 CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
 CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*
 CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
 CC strains of fungi show different symptoms during infection, which may or
 CC may not be due to infection. Early identification of the strain causing
 CC the infection allows early, and more specific fungicidal treatment.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCATAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 61
 DB 228 AAAATGCATAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 287
 OY 62 ATTGGCCCCCGCAGTATTCTGGCGGCATGCTCTTTCGAGGTCATT 108
 DB 288 ATTGGCCCCCGCAGTATTCTGGCGGCATGCTCTTTCGAGGTCATT 334

RESULT 14

AAV62596
 ID AAV62596 standard; DNA; 546 BP.

XX AAV62596;

XX 17-DEC-1998 (first entry)

XX *Fusarium poae* PCR amplified ITS region consensus DNA sequence.

XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
 KW *Fusarium culmorum*; *Fusarium graminearum*; *Fusarium moniliforme*; plant;
 KW *Septoria avenae*; *Microdochium nivale*; *Fusarium poae*; *Fusarium avenaceum*;
 XX PCR; nucleic acid detection; ss.

XX *Fusarium poae*.

XX Key Location/Qualifiers

FT misc_feature 1..30
 FT /*tag= a
 FT /note= "3' end of small subunit rRNA gene"
 FT 31..180
 FT /*tag= b
 FT /note= "ITS 1"
 FT 181..337
 FT /*tag= c
 FT /note= "5.8S rRNA gene"
 FT 338..489
 FT /*tag= d
 FT /note= "ITS 2"
 FT 490..546
 FT /*tag= e
 FT /note= "5' end of large subunit rRNA gene"

XX US5814453-A.

XX 29-SEP-1998.

XX 02-JUL-1997; 97US-00887480.

XX 19-APR-1995; 95MO-US004712.

XX 15-OCT-1996; 96US-00722187.

PA (NOVS) NOVARTIS FINANCE CORP.
 XX Beck JJ;
 PI WPI, 1998-541745/46.
 XX DNA isolated from fungal RNA, and its internal transcribed spacer
 PT sequence - used for detecting fungal pathogens in plant tissue.
 XX Example; Col 87-88; 56pp; English.
 XX This represents the consensus DNA sequence of the internal transcribed
 CC spacer (ITS) region that was PCR amplified from *Fusarium poae* isolates, T
 CC -427, T-534 and T-756. The invention provides a DNA molecule isolated
 CC from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the
 CC DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of
 CC *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium moniliforme*, *Septoria*
 CC *avenae* or *Microdochium nivale*. A method for detecting *F. graminearum*, *F.*
 CC *culmorum*, *F. moniliforme*, *F. poae*, *F. avenaceum* and *M. nivale* isolates is
 CC also provided. The method comprises isolating DNA from a plant leaf
 CC infected with at least one of the above pathogens and amplifying parts of
 CC the ITS sequence of the pathogen(s) by PCR using specific primers from
 CC within these sequences. The pathogen(s) are detected by visualising the
 CC amplified part of the ITS sequence
 SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
 Query Match 33.5%; Score 107; DB 2; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAAATGCGATTAAGTAATGTAATTCGCAATTCGTAATCATCGAATCTTTGAACGAC 61
 Db 230 AAAATGCGATTAAGTAATGTAATTCGCAATTCGTAATCATCGAATCTTTGAACGAC 289
 QY 62 ATTGGCCCGCCGAGTATTCGCGGGCATGCGCTGTTCGAGCGTCATT 108
 Db 290 ATTGGCCCGCCGAGTATTCGCGGGCATGCGCTGTTCGAGCGTCATT 336

RESULT 15
 AAVS9007
 ID AAVS9007 standard; DNA; 546 BP.
 AC AAVS9007;
 XX
 XX 25-MAR-2003 (revised)
 DT 06-JAN-1999 (first entry)
 XX
 DE F. poae internal transcribed spacer.
 XX
 XX Internal transcribed spacer; ITS; *Microdochium*; *Fusarium*; wheat pathogen;
 KW fungal pathogen identification; infection identification; ss.
 XX
 XX *Fusarium poae*.
 OS
 XX
 XX Key Location/Qualifiers
 FH misc_feature 31..180
 FT /*tag= a
 FT /note= "ITS1"
 FT misc_feature 338..489
 FT /*tag= b
 FT /note= "ITS2"
 FT
 FT
 PN US5827695-A.
 PD 27-OCT-1998.
 XX
 XX 04-AUG-1997; 97US-00905314.
 PF
 XX 04-AUG-1997; 97US-00905314.
 PR
 XX (NOVS) NOVARTIS FINANCE CORP.
 PA

XX Beck JJ;
 PI WPI, 1998-593995/50.
 XX
 DR Wheat pathogen internal transcribed spacer sequences - used as a basis
 PT for primers for the species-specific polymerase chain reaction detection
 PT of the pathogens.
 XX Claim 1; Col 25-26; 20pp; English.
 XX
 XX This sequence represents an internal transcribed spacer (ITS) sequence of
 CC the invention. The primer pairs, based on the ITS sequences, are used for
 CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
 CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*
 CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
 CC strains of fungi show different symptoms during infection, which may or
 CC may not be due to infection. Early identification of the strain causing
 CC the infection allows early, and more specific fungicidal treatment.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
 Query Match 33.5%; Score 107; DB 2; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAAATGCGATTAAGTAATGTAATTCGCAATTCGTAATCATCGAATCTTTGAACGAC 61
 Db 230 AAAATGCGATTAAGTAATGTAATTCGCAATTCGTAATCATCGAATCTTTGAACGAC 289
 QY 62 ATTGGCCCGCCGAGTATTCGCGGGCATGCGCTGTTCGAGCGTCATT 108
 Db 290 ATTGGCCCGCCGAGTATTCGCGGGCATGCGCTGTTCGAGCGTCATT 336

Search completed: October 1, 2004, 09:02:48
 Job time : 274.27 secs

RESULT 2
ITG-09-997-490-93

US-08-905-314A-19

Query Match 33.5%; Score 107; DB 1; Length 504;

Best Local Similarity 100.0%; Pred. No. 9.9e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 61

Db 211 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 270

Qy 62 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 108

Db 271 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 317

RESULT 4

US-08-722-187-82

Sequence 82, Application US/08722187

Patent No. 5955274

GENERAL INFORMATION:

APPLICANT: ligon, James M

APPLICANT: Beck, James J

TITLE OF INVENTION: Detection of Fungal Pathogens Using the

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: NY

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722,187

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/233,608

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988

REFERENCE/DOCKET NUMBER: CGC 1739

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8666

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHEITICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..504

OTHER INFORMATION: /note= "DNA sequence for the

OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum

OTHER INFORMATION: {fcuim.con}"

US-08-722-187-82

Query Match 33.5%; Score 107; DB 2; Length 504;

Best Local Similarity 100.0%; Pred. No. 9.9e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 61

Db 211 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 270

Db 211 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 270

Qy 62 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 108

Db 271 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 317

RESULT 5

US-09-481-293-32

Sequence 32, Application US/09481293

Patent No. 6485907

GENERAL INFORMATION:

APPLICANT: Beck, James

APPLICANT: Barnett, Jason

TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis

FILE REFERENCE: PB/5-31135P1

CURRENT APPLICATION NUMBER: US/09/481,293

CURRENT FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 32

LENGTH: 504

TYPE: DNA

ORGANISM: Fusarium culmorum

US-09-481-293-32

Query Match 33.5%; Score 107; DB 4; Length 504;

Best Local Similarity 100.0%; Pred. No. 9.9e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 61

Db 214 AAAATGCATAGTAATGTAATTCAGAAATTCAGTAATCATGAAATCTTTGAACGCAC 273

Qy 62 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 108

Db 274 ATTGGCCCCGCGAGTATTCTGGCGGCGATGCTGTTCGAGCGTCATT 320

RESULT 6

PCT-US95-04712-82

Sequence 82, Application PC/TUS9504712

GENERAL INFORMATION:

APPLICANT: ligon, James M

APPLICANT: Beck, James J

TITLE OF INVENTION: Detection of Fungal Pathogens Using the

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: NY

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04712

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/233,608

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988

REFERENCE/DOCKET NUMBER: CGC 1739

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8666

TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fcultm.com)"
PCT-US95-04712-82

Query Match 33.5%; Score 107; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCGATGAATGATGTAATGCAGAATTCAGTGAATCAGAACTTTGAAGCAC 61
Db 211 AAAATGCGATGAATGATGTAATGCAGAATTCAGTGAATCAGAACTTTGAAGCAC 270

Qy 62 ATTGCGCCCGCAGATTCTGGCGGCGCATGCTGTTGAGCGTCATT 108
Db 271 ATTGCGCCCGCAGATTCTGGCGGCGCATGCTGTTGAGCGTCATT 317

RESULT 7
US-08-887-480-84
Sequence 84, Application US/08887480
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 581445artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: PCRPMON1
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-887-480-84

Query Match 33.5%; Score 107; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCGATGAATGATGTAATGCAGAATTCAGTGAATCAGAACTTTGAAGCAC 61
Db 228 AAAATGCGATGAATGATGTAATGCAGAATTCAGTGAATCAGAACTTTGAAGCAC 287

Qy 62 ATTGCGCCCGCAGATTCTGGCGGCGCATGCTGTTGAGCGTCATT 108
Db 288 ATTGCGCCCGCAGATTCTGGCGGCGCATGCTGTTGAGCGTCATT 334

RESULT 8
US-08-905-314A-21
Sequence 21, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689

US-08-887-480-96
 Sequence 96, Application US/08087480
 Patent No. 5814453
 GENERAL INFORMATION:
 APPLICANT: Beck, James J
 TITLE OF INVENTION: Detection of Fungal Pathogens Using the
 TITLE OF INVENTION: Polymerase Chain Reaction
 NUMBER OF SEQUENCES: 96
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 5814453artis Corporation
 STREET: 520 White Plains Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/887,480
 FILING DATE:

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Query Match          33.5%; Score 107; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2  AAATGCGATAGTAATGATGTAATTCAGAAATTCAGTAATCATCGAACTTTGAACGCAC 61
        AAAATGCGATAGTAATGTAATTCAGAAATTCAGTAATCATTCGAACTTTGAACGCAC
Db      230 AAAATGCGATAGTAATGTAATTCAGAAATTCAGTAATCATTCGAACTTTGAACGCAC 289

Oy      62  ATTGCGCCCGCCAGTATTTCTGGCCGGCATGCTCTTTGAGCGTCATT 108
        ATTGCGCCCGCCAGTATTTCTGGCCGGCATGCTCTTTGAGCGTCATT
Db      290 ATTGCGCCCGCCAGTATTTCTGGCCGGCATGCTCTTTGAGCGTCATT 336

RESULT 10
US-08-905-314A-22
; Sequence 22, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 5827695artis Corporation Patent Department
;

```

```
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
IMMEDIATE SOURCE:
CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
pCRFpoaeT756(3-1)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-22

Query Match 33.5%; Score 107; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAAGCAGC 61
DB 230 AAAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAAGCAGC 289

QY 62 ATTGCGCCCGCCAGTATTCGTGCGCGCATGCTGTTGAGCGTCATT 108
DB 290 ATTGCGCCCGCCAGTATTCGTGCGCGCATGCTGTTGAGCGTCATT 336

RESULT 11
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US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match 33.5%; Score 107; DB 3; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.6e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAAGCAGC 61
DB 1971 AAAATGCGATTAAGTATGTAATTCGAGATTCAGTGAATCATCGAATCTTTGAAGCAGC 2030

QY 62 ATTGCGCCCGCCAGTATTCGTGCGCGCATGCTGTTGAGCGTCATT 108
DB 2031 ATTGCGCCCGCCAGTATTCGTGCGCGCATGCTGTTGAGCGTCATT 2077

RESULT 12
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-7
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Fri Oct 1 16:15:49 2004

us-10-046-955-6.01g10.rn1

Page 8

Qy 90 TGCCTGTTCGAGCGTCATT 108
|||
Db 88 TGCCTGTTCGAGCGTCATT 106
|||

Search completed: October 1, 2004, 11:12:56
Job time : 53.744 secs


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Db      1  GAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 60
Qy      61  CATTGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATTAACACCTTGAAG 120
Db      61  CATTGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATTAACACCTTGAAG 120
Qy      121  CCCCCGGGCGCTGGGATCGGCGGAAAGCCCGCTGGCGGGGACAAAGCCGTCGCCCA 180
Db      121  CCCCCGGGCGCTGGGATCGGCGGAAAGCCCGCTGGCGGGGACAAAGCCGTCGCCCA 180
Qy      181  AATACAGTGGCGGATCGGCGGAGCTTCCATTGCGTATGCTAACAACCTCGCAACTGGA 240
Db      181  AATACAGTGGCGGATCGGCGGAGCTTCCATTGCGTATGCTAACAACCTCGCAACTGGA 240
Qy      241  GAGGCGGCGCGCCGACGCGCGTAAACACCCGAATCTTGAATGTTGACTTCGAATCAGGTAG 300
Db      241  GAGGCGGCGCGCCGACGCGCGTAAACACCCGAATCTTGAATGTTGACTTCGAATCAGGTAG 300
Qy      301  GAATACCCGCTGAACCTTAA 319
Db      301  GAATACCCGCTGAACCTTAA 319

RESULT 2
US-09-961-755A-6
; Sequence 6, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6

Query Match      33.5%; Score 107; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 287
Qy      62  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 108
Db      288  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 334

RESULT 3
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA

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; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

Query Match      33.5%; Score 107; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 287
Qy      62  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 108
Db      288  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 334

RESULT 4
US-09-961-755A-8
; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match      33.5%; Score 107; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 287
Qy      62  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 108
Db      288  ATTGGCGCCCGCCGATATTCCTGGCGGGGATGCGCTGTTGAGCGTCATT 334

RESULT 5
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match      33.5%; Score 107; DB 10; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 AAAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGAC 61
Db 228 AAAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGAC 287
Qy 62 ATTGCGCCCGCCAGTAATTCGCGCGGCAATGCGTGTTCGAGCGTCATT 108
Db 288 ATTGCGCCCGCCAGTAATTCGCGCGGCAATGCGTGTTCGAGCGTCATT 334

RESULT 6
US-10-046-955-7

; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliiana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match 24.8%; Score 79; DB 15; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.7e-35;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 AATTCAGTAATCATTCGAATTTTGAACGCAATTCGCGCCCGCAGTAATTTGGCGGCA 89
Db 28 AATTCAGTAATCATTCGAATTTTGAACGCAATTCGCGCCCGCAGTAATTTGGCGGCA 87
Qy 90 TGCGTTCGAGCGTCATT 108
Db 88 TGCGTTCGAGCGTCATT 106

RESULT 7
US-10-046-955-27

; Sequence 27, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliiana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926

; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-27

Query Match 21.6%; Score 69; DB 15; Length 343;
Best Local Similarity 100.0%; Pred. No. 2.9e-29;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGACA 62
Db 1 AAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGACA 60
Qy 63 TTGCGCCCG 71
Db 61 TTGCGCCCG 69

RESULT 8
US-10-046-955-26

; Sequence 26, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliiana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-26

Query Match 21.6%; Score 69; DB 15; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.9e-29;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGACA 62
Db 2 AAATGCATTAAGTAATGTAATTCAGAAATTCAGTAATCGAATCTTTGAACGACA 61
Qy 63 TTGCGCCCG 71
Db 62 TTGCGCCCG 70

RESULT 9
US-09-961-663-14

; Sequence 14, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:

APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 377
TYPE: DNA
ORGANISM: Mycosphaerella sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(377)
OTHER INFORMATION: Truncated DNA sequence for the Internal
OTHER INFORMATION: Transcribed Spacer of a fungus amplified from
OTHER INFORMATION: banana sample "Capeteire-babin 2".
US-09-961-663-14

Query Match 21.3%; Score 68; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 62
DB 91 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 150

QY 63 TTGGCCCC 70
DB 151 TTGGCCCC 158

RESULT 10
US-09-961-663-15
Sequence 15, Application US/09961663
Patent No. US20020115084A1
GENERAL INFORMATION:
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 377
TYPE: DNA
ORGANISM: Mycosphaerella sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(377)
OTHER INFORMATION: Truncated DNA sequence for the Internal
OTHER INFORMATION: Transcribed Spacer of fungus amplified from banana
OTHER INFORMATION: sample "Matouba bas 3"
US-09-961-663-15

Query Match 21.3%; Score 68; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 62
DB 91 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 150
QY 63 TTGGCCCC 70

DB 151 TTGGCCCC 158

RESULT 11
US-09-961-663-16
Sequence 16, Application US/09961663
Patent No. US20020115084A1
GENERAL INFORMATION:
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 377
TYPE: DNA
ORGANISM: Mycosphaerella sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(377)
OTHER INFORMATION: Truncated DNA sequence for the Internal
OTHER INFORMATION: Transcribed Spacer of a fungus amplified from
OTHER INFORMATION: banana sample "Temoin Infest Forte"
US-09-961-663-16

Query Match 21.3%; Score 68; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 62
DB 91 AATGCGATAGTATGTAATTCGAGATTCGATGATCGAATCTTTGAACGACA 150

QY 63 TTGGCCCC 70
DB 151 TTGGCCCC 158

RESULT 12
US-09-961-663-19
Sequence 19, Application US/09961663
Patent No. US20020115084A1
GENERAL INFORMATION:
APPLICANT: Barnett, Jason
TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
FILE REFERENCE: PB/5-31382A
CURRENT APPLICATION NUMBER: US/09/961,663
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/211902
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 377
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: (1)-(377)
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: sequence of Mycosphaerella sp. ITS sequences shown
OTHER INFORMATION: in SEQ ID NO:14-16.
US-09-961-663-19

Query Match 21.3%; Score 68; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 62
Db 91 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 150
QY 63 TTGGCCCC 70
Db 151 TTGGCCCC 158

RESULT 13
US-10-356-320-1
; Sequence 1, Application US/10356320
; Publication No. US20040009573A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Ford, Eugene
; APPLICANT: James, Harper K.
; TITLE OF INVENTION: Pestalotiopsis Microsporia Isolates and Compounds Derived
; TITLE OF INVENTION: Therefrom
; FILE REFERENCE: A-72093 (470425-4)
; CURRENT APPLICATION NUMBER: US/10/356,320
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/352,254
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Pestalotiopsis sp. NG12-30
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301
; DATABASE ENTRY DATE: 2002-06-02
; RELEVANT RESIDUES: (1)..(466)
US-10-356-320-1

Query Match 21.3%; Score 68; DB 16; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 62
Db 194 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 253
QY 63 TTGGCCCC 70
Db 254 TTGGCCCC 261

RESULT 14
US-09-961-663-17
; Sequence 17, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, James
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: PB/5-31382A
; CURRENT APPLICATION NUMBER: US/09/961,663
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/211902
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Mycosphaerella fijiensis
US-09-961-663-17

Query Match 21.3%; Score 68; DB 9; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 62
Db 222 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 281
QY 63 TTGGCCCC 70
Db 282 TTGGCCCC 289

RESULT 15
US-09-961-663-18
; Sequence 18, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, James
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: PB/5-31382A
; CURRENT APPLICATION NUMBER: US/09/961,663
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/211902
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Mycosphaerella musicola
US-09-961-663-18

Query Match 21.3%; Score 68; DB 9; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 62
Db 231 AATGCGATTAAGTATGATTCGATTCAGATTCATCGAATCTTTGAACGCACA 290
QY 63 TTGGCCCC 70
Db 291 TTGGCCCC 298

Search completed: October 1, 2004, 11:22:42
Job time : 295.049 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:04:24 : Search time 2163.01 Seconds
(without alignments)
4404.059 Million cell updates/sec

Title: US-10-046-955-6
Perfect score: 319
Sequence: 1 gaaatgcgtaagtaagt.....ggaataccgcgtgacttaa 319

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5727071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
5: em_estba:*
6: em_estba:*
7: em_estba:*
8: em_estba:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrc:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	29.5	735	14	CF880267 trico81xc
2	94	29.5	739	14	CF870552 trico24xb
3	94	29.5	755	14	CF870665 trico24xj
4	94	29.5	796	14	CB900742 trico24xb

Result No.	Score	Query Match	Length	ID	Description
5	94	29.5	808	14	CB900860 trico24xj
6	94	29.5	840	14	CB907036 trico81xc
7	71	22.3	169	12	BM870292 mgms009xu
8	59	18.5	147	14	CF800463 ghrm331 6
9	59	18.5	190	12	BM347000 A1_3D11 m
10	59	18.5	374	14	CB012091 LB03D01 m
11	57	17.9	359	14	CB011883 LB03N02 m
12	57	17.9	789	28	BZ782051 A1SP1C26
13	52	16.3	791	28	BZ782064 A1SP2C19
14	52	16.3	795	28	BZ782081 A1SP2C4 M
15	52	16.3	840	28	BZ782314 A2AP1C47
16	42	13.2	120	9	A1327878 j0606a1.f
17	42	13.2	141	9	A1327879 j0606a1.f
18	42	13.2	213	9	A1209736 t7c08a1.f
19	42	13.2	318	9	A1213025 y6f01a1.f
20	41	12.9	704	13	BQ751285 EST631848
21	41	12.9	725	13	BQ752001 EST632564
22	41	12.9	806	13	BQ751015 EST631578
23	41	12.9	806	13	BQ751484 EST632047
24	36	11.3	150	12	BM361006 A00318-F
25	36	11.3	150	12	BM361064 A00414-R
26	36	11.3	157	12	BM361387 A00705-R
27	36	11.3	157	12	BM361430 A00748-R
28	35	11.0	140	12	BP517053 BP517053
29	35	11.0	146	12	BP508427 BP508427
30	35	11.0	214	10	BP251183 EST418443
31	35	11.0	268	14	CF780131 tad04c11
32	35	11.0	298	14	CA303199 ta040e02
33	35	11.0	320	28	AZ925653 4910_e234
34	35	11.0	332	14	CA301641 ta06a11
35	35	11.0	332	14	CA303270 ta06a11
36	35	11.0	360	28	AZ923094 4908_g687
37	35	11.0	370	14	CD566941 tgc12f11
38	35	11.0	376	14	CD567121 tab47a02
39	35	11.0	384	28	BZ304161 KD2793.q1
40	35	11.0	392	28	AZ923588 4908_gf22
41	35	11.0	407	28	AZ923857 4908_gf22
42	35	11.0	414	14	CA301545 ta08b008
43	35	11.0	419	14	CA301933 ta01a07
44	35	11.0	420	14	CA303244 ta05c12
45	35	11.0	422	14	CA302907 ta04b10

ALIGNMENTS

RESULT 1
CF880267
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF880267 735 bp mRNA linear EST 31-OCT-2003
trico81xc18.b2.T.reesei mycelial culture, Version 6 October 2003
Hypocrea jecorina CDNA clone trico81xc18, mRNA sequence.
CF880267
CF880267.1 GI:38134949
EST.
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 735)
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,
Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and
Dean,R.A.
Analysis of the protein processing and secretion pathways in a
Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.

FEATURES
source
1. 735
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric081xc18"
/dev_stage="mycelia"
/clone_1lb="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 29.5%; Score 94; DB 14; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 62
|||||
50 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 109
|||||
QY 63 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 96
|||||
Db 110 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 143
|||||

RESULT 2
CF870552 739 bp mRNA linear EST 31-OCT-2003
LOCUS
DEFINITION
Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.
ACCESSION
CF870552 GI:38125234
VERSION
CF870552.1 GI:38125234
SOURCE
Hypocrea jecorina (anamorph: Trichoderma reesei)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1 (bases 1 to 739)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL
Unpublished (2003)
COMMENT
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
location/Qualifiers
1. 739
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric024xb14"
/dev_stage="mycelia"
/clone_1lb="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 29.5%; Score 94; DB 14; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 62
|||||
Db 43 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 102
|||||
QY 63 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 96
|||||
Db 103 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 136
|||||

RESULT 3
CF870665 755 bp mRNA linear EST 31-OCT-2003
LOCUS
DEFINITION
tric024xb14.T.reesei mycelial culture, Version 6 October 2003
ACCESSION
CF870665 GI:38125347
VERSION
CF870665.1 GI:38125347
KEYWORDS
EST.
SOURCE
Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1 (bases 1 to 755)
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL
Unpublished (2003)
COMMENT
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
location/Qualifiers
1. 755
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric024xb14"
/dev_stage="mycelia"
/clone_1lb="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 29.5%; Score 94; DB 14; Length 755;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 62
|||||
Db 43 AATGCGATAGTAAATGTAATGCAATTCAGATTCGAATCTTTGAACGACA 102
|||||
QY 63 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 96
|||||
Db 103 TTGGCCCGCCAGTATTTCTGGCGGCGATGCTGT 136
|||||

RESULT 4
CB900742 796 bp mRNA linear EST 02-JUN-2003
LOCUS
DEFINITION
tric024xb14.T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.
ACCESSION
CB900742
VERSION
CB900742.1 GI:30115400
KEYWORDS
EST.

Tel: (650) 846-7635
 Fax: (650) 621-7817
 Email: Pforeman@genencor.com
 Seq primer: LT-F1 primer.
 Location/Qualifiers
 1..808
 /organism="Hypocrea jecorina"
 /mol_type="mRNA"
 /strain="QM6a"
 /db_xref="taxon:51453"
 /clone="trico24x104"
 /dev_string="mycelia"
 /clone_lib="T.reesei mycelial culture, Version 3 april"
 /note="Vector: PREP3J, Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
 Query Match 29.5%; Score 94; DB 14; Length 808;
 Best Local Similarity 100.0%; Pred. No. 1,2e-38;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 AATGGCATAGTATGGAATTCGACAAATTCATGATCATCATGATCTTTGAACGACA 62
 Db 96 AATGGCATAGTATGGAATTCGACAAATTCATGATCATCATGATCTTTGAACGACA 155

Oy 63 TTGGCGCCGCCAGTATTCGGCGGCATGCCTGT 96
 Db 156 TTGGCGCCGCCAGTATTCGGCGGCATGCCTGT 189

RESULT 6 840 bp mRNA linear EST 02-JUN-2003
 LOCUS CB907036
 DEFINITION trico81xc18 T.reesei mycelial culture, Version 3 april Hypocrea
 ACCESSION J9607036
 VERSION CB907036
 KEYWORDS
 SOURCE
 ORGANISM
 Hypocrea jecorina (anamorph: Trichoderma reesei)
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 1 (bases 1 to 840)
 Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Engner,S.,
 Dunn-Coleman,N.S., Goeddegebur,F., Houlek,T.D., England,G.J.,
 Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
 Olivaates,H.A., Teunissen,P.V., Yao,J. and Ward,M.
 Transcriptional regulation of biomass-degrading enzymes in the
 filamentous fungus Trichoderma reesei
 J. Biol. Chem. 278 (34), 31988-31997 (2003)
 22803314
 12788920
 Contact: Pamela K. Foreman
 Genencor Intl.
 925 Page Mill Road, Palo Alto, CA 94304, USA
 Tel: (650) 846-7635
 Fax: (650) 621-7817
 Email: Pforeman@genencor.com
 Seq primer: LT-F1 primer.
 Location/Qualifiers
 1..840
 /organism="Hypocrea jecorina"
 /mol_type="mRNA"
 /strain="QM6a"
 /db_xref="taxon:51453"
 /clone="trico81xc18"
 /dev_string="mycelia"
 /clone_lib="T.reesei mycelial culture, Version 3 april"
 /note="Vector: PREP3J, Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

FEATURES
 source

ORIGIN

Query Match 29.5%; Score 94; DB 14; Length 840;
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCACA 62
 |||||
 DB 155 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCACA 214
 |||||

QY 63 TTGGCCCCGCGAGTATTCGGCGGCATGCTGT 96
 |||||
 DB 215 TTGGCCCCGCGAGTATTCGGCGGCATGCTGT 248
 |||||

RESULT 7
 BM870292 169 bp mRNA linear EST 06-MAY-2003
 LOCUS mgns009xj23f.b Magnaporthe grisea NS Uni-Zap XR library Magnaporthe
 DEFINITION grisea cDNA clone mgns009xj23 5', mRNA sequence.
 BM870292
 VERSION BM870292.2 GI:30404719
 SOURCE EST.
 ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 169)
 Ebohle,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
 Bhatterai,K. and Dean,R.A.
 Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea
 TITLE Unpublished (2002)
 JOURNAL On Mar 7, 2002 this sequence version replaced gi:19237974.
 COMMENT Contact: Ebohle DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebohle@tamu.edu
 Chromatogram file of this sequence is available, see contact
 person; Best nr hit (April, 22, 2003) gb|AL79278.1| unknown
 [Saccharomyces cerevisiae] 79 1e-14
 PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgns009 row: J column: 23
 Seq primer: T3.

FEATURES
 source Location/Qualifiers
 1..169
 /organism="Magnaporthe grisea"
 /mol_type="mRNA"
 /strain="Guy11"
 /db_xref="taxon:148305"
 /clone="mgns009xj23"
 /sex="Mati-2 hermaphrodite"
 /cell_type="mycelium"
 /clone_lib="Magnaporthe grisea NS Uni-Zap XR library"
 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and
 predominantly 5' reads. T7 primer on XhoI side of insert.
 Nitrogen starvation library. Cells were inoculated into
 minimal medium and grown for two days with shaking (150
 rpm) at room temperature. Culture was harvested, blended,
 inoculated into minimal medium as above for 24 h. Cells
 were harvested, washed with water and inoculated into
 minimal medium base lacking nitrogen source for 6 h.
 Sequences were processed by one of two methods. Where a
 full-length alignment to the M. grisea genome sequence was
 available, the EST sequence was trimmed according to the
 alignment, otherwise sequence quality was assessed using
 phredPhrap version 991019 and trimmed according to phd
 files (0.05) and for vector segs."

ORIGIN
 Query Match 22.3%; Score 71; DB 12; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1.5e-26;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCACA 62
 |||||
 DB 39 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCACA 98
 |||||

QY 63 TTGGCCCCGCC 73
 |||||
 DB 99 TTGGCCCCGCC 109
 |||||

RESULT 8
 CF800463 147 bp mRNA linear EST 04-NOV-2003
 LOCUS 6HRM331 6HR Nitrogen-limited Schizophyllum library Schizophyllum
 DEFINITION commune cDNA 5', mRNA sequence.
 CF800463
 VERSION CF800463.1 GI:37818860
 SOURCE EST.
 ORGANISM Schizophyllum commune
 Schizophyllum commune
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Agaricales; Schizophyllaceae; Schizophyllum.
 1 (bases 1 to 147)
 Foster,K.D., Belsler,A.E., Buchanan,S., Huck,M., Devoll,T.,
 Hittinger,C.T., Green,A., Lilly,W.W. and Gatchman,A.C.
 Expressed sequence tags from Schizophyllum commune nitrogen-replete
 and nitrogen-limited libraries, 2003
 TITLE Unpublished (2003)
 JOURNAL
 COMMENT Contact: Gatchman AC
 Biology Department
 Southeast MO State University
 1 University Plaza, Cape Girardeau, MO 63701, USA
 Tel: 5736512361
 Fax: 5739866433
 Email: agatchman@semo.edu
 Seq primer: T3
 POLYA=Yes.

FEATURES
 source Location/Qualifiers
 1..147
 /organism="Schizophyllum commune"
 /mol_type="mRNA"
 /strain="4-40"
 /db_xref="taxon:5334"
 /issue_type="mycelium"
 /clone_lib="6HR Nitrogen-limited Schizophyllum library"
 /note="Vector: lambda Zap; Site 1: EcoRI; Site 2: XhoI;
 4-day-old mycelia of Schizophyllum commune were
 transferred from minimal (nitrogen-replete) medium to
 low-nitrogen medium. RNA was extracted six hours after
 transfer and cDNAs prepared."

ORIGIN
 Query Match 18.5%; Score 59; DB 14; Length 147;
 Best Local Similarity 100.0%; Pred. No. 3.4e-20;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCAC 61
 |||||
 DB 32 AATGCGATTAAGTAATGTGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCAC 90
 |||||

RESULT 9
 BM347000 190 bp mRNA linear EST 07-JUN-2002
 LOCUS Al_3D11 Heterobasidion annosum infection stage cDNA library
 DEFINITION Heterobasidion annosum cDNA clone Al_3D11 similar to putative
 ribosomal RNA protein [Arabidopsis thaliana], mRNA sequence.
 BM347000

VERSION BM347000.1 GI:18083915
KEYWORDS EST.
SOURCE Heterobasidion annosum
ORGANISM Heterobasidion annosum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Heterobasidion; Heterobasidion
annosum species complex.
1 (bases 1 to 190)
REFERENCE Karlsson,M., Olson,A. and Stenlid,J.
AUTHORS Expressed sequences from the basidiomycetous tree pathogen
TITLE Heterobasidion annosum during early infection of Scots pine
JOURNAL Fungal Genet. Biol. 39 (1), 51-59 (2003)
MEDLINE 22627971
PUBMED 12742063
COMMENT Contact: Magnus Karlsson
Forest Mycology & Pathology
Swedish University of Agricultural Sciences
Box 7026, SE-750 07, Uppsala, Sweden
Tel: +46 18 671806
Fax: +46 18 673599
Email: Magnus.Karlsson@mykopat.slu.se
Seq primer: 58#8217;Triplex2 MK Seq.
Location/Qualifiers
1. .190
/organism="Heterobasidion annosum"
/mol_type="mRNA"
/strain="TC 32-1 (P)"
/db_xref="taxon:13563"
/clone="A1_3D11"
/tissue_type="Mycelia"
/dev_stage="Mycelia after 6 h & 72 h of challenge with
pine seedling roots"
/clone_lib="Heterobasidion annosum infection stage cDNA
library"
/note="Vector: Lambda; Heterobasidion annosum mycelia were
challenged by pinus sylvestris seedling roots for 6 h &
72 h and the cDNA library was made from a mix of the two
stages"

ORIGIN
Query Match 18.5%; Score 59; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAATCGGATAGTATGTAATGCAAGATTCAGTCAATCATGCAATCTTTGAACGAC 61
|||||
Db 52 AAATCGGATAGTATGTAATGCAAGATTCAGTCAATCATGCAATCTTTGAACGAC 110
|||||

RESULT 10
LOCUS CB012091 374 bp mRNA linear EST 30-JUN-2003
DEFINITION Lb08D01 mycelium of Laccaria bicolor grown for three weeks
ACCESSION CB012091
VERSION CB012091.1 GI:32334717
KEYWORDS EST.
SOURCE Laccaria bicolor
ORGANISM Laccaria bicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Laccaria.
1 (bases 1 to 374)
REFERENCE Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D.,
AUTHORS Tagu,D., Frey-Klett,P., Duplessis,S., Chalot,M., Podila,G. and
TITLE Analysis of expressed sequence tags from the ectomycorrhizal
JOURNAL basidiomycetes Laccaria bicolor and Pisolithus microcarpus
COMMENT New Phytol. 159 (1), 117-129 (2003)
Contact: Martin FM
Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80

Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert length: 374 Std Error: 0.00
Seq primer: Fornat 5' AAGCGCCCATGTTGTTGTAACC.
Location/Qualifiers
1. .374
/organism="Laccaria bicolor"
/mol_type="mRNA"
/cultiivar="S238N"
/db_xref="taxon:29883"
/dev_stage="three-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for three
weeks"
/note="Organ: free-living vegetative mycelium; Vector:
pTriplex2; Laccaria bicolor Maire Orton; cDNA library from
mycelium of Laccaria bicolor grown for three weeks on
agar-plates containing high sugar (20 g/l glucose, 5 g/l
maltose) Pachlewski medium. The cDNA library was
constructed from 1 ug of total RNA using the SMART cDNA
synthesis kit (Clontech, Palo Alto, CA, USA) according to
the manufacturer's instructions. The resulting cDNA was
packed into lambda phages using the Gigapack III Gold
packaging kit (Stratagene, La Jolla, CA). The pTriplex2
phagemid clones in Escherichia coli were obtained by
using the mass in vivo excision protocol according to the
manufacturer's instructions (Clontech)."

ORIGIN
Query Match 18.5%; Score 59; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAATCGGATAGTATGTAATGCAAGATTCAGTCAATCATGCAATCTTTGAACGAC 61
|||||
Db 229 AAATCGGATAGTATGTAATGCAAGATTCAGTCAATCATGCAATCTTTGAACGAC 287
|||||

RESULT 11
LOCUS CB011883 359 bp mRNA linear EST 30-JUN-2003
DEFINITION Lb03N02 mycelium of Laccaria bicolor grown for three weeks
ACCESSION CB011883
VERSION CB011883.1 GI:32334509
KEYWORDS EST.
SOURCE Laccaria bicolor
ORGANISM Laccaria bicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Laccaria.
1 (bases 1 to 359)
REFERENCE Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D.,
AUTHORS Tagu,D., Frey-Klett,P., Duplessis,S., Chalot,M., Podila,G. and
TITLE Analysis of expressed sequence tags from the ectomycorrhizal
JOURNAL basidiomycetes Laccaria bicolor and Pisolithus microcarpus
COMMENT New Phytol. 159 (1), 117-129 (2003)
Contact: Martin FM
Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert length: 359 Std Error: 0.00
Seq primer: Fornat 5' AAGCGCCCATGTTGTTGTAACC.
Location/Qualifiers
1. .359
/organism="Laccaria bicolor"
/mol_type="mRNA"
/cultiivar="S238N"
/db_xref="taxon:29883"
/dev_stage="three-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for three

survey sequence.

ACCESSION BZ782081 GI:28960886

VERSION BZ782081.1

KEYWORDS GSS

SOURCE Microbotryum violaceum

ORGANISM Microbotryum violaceum
Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
Microbotryomycetidae; Microbotryales; Microbotryaceae;
Microbotryum

REFERENCE 1 (bases 1 to 795)
Hood, M.E., Antonovics, J. and Koskella, B.
Shared forces of sex chromosome evolution in haploids and diploids
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Department of Biology
University of Virginia
Glimer Hall, Charlottesville, VA 22903, USA
Tel: 434 243 5077
Fax: 434 982 5626
Email: michael.hood@virginia.edu
random fragment isolated from A1 mating type chromosome; BLASTx
similarity to Transcript Antisense to Ribosomal RNA and BLASTn
similarity to nuclear ribosomal RNA
Class: shotgun
High quality sequence stop: 795.

FEATURES
source
1..795
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="100-15lamole.1"
/db_xref="taxon:5272"
/clone="A1SP2C4"
/cell_type="sporidia"
/dev_stage="post-meiotic"
/clone_lib="Microbotryum mating type chromosome and
autosome random fragments"
/note="Field Collected; specific host=Silene latifolia;
country=Italy; common name= anther smut; synonym=Ustilago
violacea; Chromosome-specific bands were gel-isolated from
electrophoretic karyotypes, triple digested (Real, MscI,
and DraI), size-fractionated by electrophoresis for
fragments between 200 to 1000 bp, cloned, and sequenced."

ORIGIN

Query Match 16.3%; Score 52; DB 28; Length 795;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 60
|||||
Db 99 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 150

RESULT 15
BZ782314/c 840 bp DNA linear GSS 14-MAR-2003

LOCUS A2AP1C47 Microbotryum mating type chromosome and autosome random
fragments Microbotryum violaceum genomic clone A2AP1C47, genomic
survey sequence.

ACCESSION BZ782314

VERSION BZ782314.1 GI:28961356

KEYWORDS GSS

SOURCE Microbotryum violaceum

ORGANISM Microbotryum violaceum
Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
Microbotryomycetidae; Microbotryales; Microbotryaceae;
Microbotryum

REFERENCE 1 (bases 1 to 840)
Hood, M.E., Antonovics, J. and Koskella, B.
Shared forces of sex chromosome evolution in haploids and diploids
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Department of Biology

University of Virginia
Glimer Hall, Charlottesville, VA 22903, USA
Tel: 434 243 5077
Fax: 434 982 5626
Email: michael.hood@virginia.edu
random fragment isolated from autosomes; BLASTx similarity to
Transcript Antisense to Ribosomal RNA and BLASTn similarity to
nuclear ribosomal RNA
Class: shotgun
High quality sequence stop: 840.

FEATURES
source
1..840
Location/Qualifiers
/organism="Microbotryum violaceum"
/mol_type="genomic DNA"
/strain="100-15lamole.1"
/db_xref="taxon:5272"
/clone="A2AP1C47"
/cell_type="sporidia"
/dev_stage="post-meiotic"
/clone_lib="Microbotryum mating type chromosome and
autosome random fragments"
/note="Field Collected; specific host=Silene latifolia;
country=Italy; common name= anther smut; synonym=Ustilago
violacea; Chromosome-specific bands were gel-isolated from
electrophoretic karyotypes, triple digested (Real, MscI,
and DraI), size-fractionated by electrophoresis for
fragments between 200 to 1000 bp, cloned, and sequenced."

ORIGIN

Query Match 16.3%; Score 52; DB 28; Length 840;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 60
|||||
Db 742 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 691

Search completed: October 1, 2004, 11:11:02
Job time : 2167.01 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 549.986 Seconds
(without alignments)
2394.501 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
Sequence: 1 aaatgcgcatgaatcatgtga.....ggataccgcgtgaactta 310

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001as:.*
5: Geneseq2001bs:.*
6: Geneseq2002s:.*
7: Geneseq2003as:.*
8: Geneseq2003bs:.*
9: Geneseq2003cs:.*
10: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	2	AAV70851 Internal
2	306.8	99.0	2293	4	AA516211 Fungus ge
3	302.8	97.7	534	7	ACC50001 Internal
4	265.8	85.7	502	3	AAA61893 Fungarium
5	249.8	80.6	561	2	AAV59009 F. avenac
6	248.6	80.2	659	6	ABV78724 C. sinens
7	240.2	77.5	319	2	AAV70850 Internal
8	194.4	62.7	522	7	ACC49999 Internal
9	194.4	62.7	522	7	ACC50002 Internal
10	193.8	62.5	661	6	ABV78721 C. sinens
11	193.4	62.4	582	2	AAV65100 F. moniliforme
12	187.6	60.5	546	2	AAV62596 Fungarium
13	187.6	60.5	546	2	AAV59007 F. poae 1
14	186.6	60.2	504	2	AAV62591 Fungarium
15	186.6	60.2	504	2	AAV62592 Fungarium
16	186.6	60.2	504	2	AAV59028 F. culmor
17	186.6	60.2	504	2	AAV59011 Fungomopsis
18	183.2	59.1	545	2	AAV62593 Fungarium
19	183.2	59.1	545	2	AAV59030 F. moniliforme
20	180.4	58.2	503	2	AAV62592 Fungarium
21	180.4	58.2	503	2	AAV59029 F. gramin
22	180.4	58.2	503	2	AAV59029 F. gramin
23	180.4	58.2	503	2	AAV59029 F. gramin

24	179.2	57.8	521	7	ACC50000 Internal
25	175	56.5	569	2	AAV65101 T. harzia
26	174.2	56.2	504	2	AAV65099 T. harzia
27	168.2	54.3	569	2	AAV65099 T. harzia
28	166.2	53.6	545	2	AAV65099 T. harzia
29	163.8	52.8	608	2	AAV65099 T. harzia
30	157.8	50.9	537	3	AAV65099 T. harzia
31	151	48.7	632	6	ABV78706 C. sinens
32	151	48.7	632	6	ABV78706 C. sinens
33	151	48.7	664	6	ABV78703 C. sinens
34	151	48.7	667	6	ABV78712 C. sinens
35	149.4	48.2	615	5	AAV76260 Cordyceps
36	149.4	48.2	625	6	ABV78718 C. sinens
37	149.4	48.2	659	6	ABV78715 C. sinens
38	147.8	47.7	549	3	AAV91723 Rosellinia
39	147.8	47.7	549	3	AAV91724 Rosellinia
40	141.8	45.7	382	3	AAV72783 5.8S rRNA
41	139	44.8	605	2	AAV90108 Eutypella
42	137.6	44.4	537	6	ABA01153 Muscodor
43	136.2	43.9	652	7	ABZ20765 Muscodor
44	136	43.9	365	2	AAV70847 Sequence
45	136	43.9	587	2	AAV43269 Sequence

ALIGNMENTS

RESULT 1	AAV70851 standard; DNA; 310 BP.
ID	AAV70851
AC	AAV70851;
DT	17-OCT-2003 (revised)
DT	26-FEB-1999 (first entry)
XX	Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;
KW	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;
KW	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Pennicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	Gibberella fujikuroi.
OS	W09850584-A2.
XX	12-NOV-1998.
PD	01-MAY-1998; 98WO-US008926.
PF	02-MAY-1997; 97US-0045400P.
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PA	Morrison CJ, Reiss B, Aldorevich L, Choi JS;
PI	WPI; 1999-034737/03.
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT	species.
XX	Claim 1; Page 12; 45pp; English.
PS	The present sequence represents an internal transcribed spacer 2 (ITS2)
XX	and adjacent regions. Probes can be derived from the present sequence
CC	which are species-specific. The specification also describes ITS2
CC	sequence-derived probes for identifying a species selected from

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CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinalis, F. circinalis, Rhizopus oryzae, R.
CC microsporus, R. circinalis, R. stolonifer, Rhizomucor pusillus, Ascidia
CC corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph
CC of Scedosporium apiospermum), Penicillium notatum, or Sporothrix
CC schenckii. The probes can be used for differentiating filamentous fungal
CC species from each other and from other medically important fungi.
CC (Updated on 17-Oct-2003 to standardise OS field)
XX
SQ Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;
Query Match 100.0%; Score 310; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.3e-98;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATGCATAGTATGATGATGCAAAATTCAGTGAATCATCTTTGAACGACA 60
DB 1 AAATGCATAGTATGATGATGCAAAATTCAGTGAATCATCTTTGAACGACA 60
QY 61 TTGGGCGCCGCAATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCGAACCC 120
DB 61 TTGGGCGCCGCAATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCGAACCC 120
QY 121 CCGGCGTTGTGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGGCAATCTAGTG 180
DB 121 CCGGCGTTGTGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGGCAATCTAGTG 180
QY 181 GCGGTCCTGCTGAGCTTCATTCAGTAGTAAACCTTCGCACTGTAAGCGCGCG 240
DB 181 GCGGTCCTGCTGAGCTTCATTCAGTAGTAAACCTTCGCACTGTAAGCGCGCG 240
QY 241 GCGCAACCGCTTAAACCCCACTTCGATGTTGACCTGGAATCAGTGAATACCG 300
DB 241 GCGCAACCGCTTAAACCCCACTTCGATGTTGACCTGGAATCAGTGAATACCG 300
QY 301 CTGAACCTTAA 310
DB 301 CTGAACCTTAA 310
RESULT 2
AAS16211
ID AAS16211 standard; DNA; 2293 BP.
XX
AC AAS16211;
XX
DT 29-JAN-2002 (first entry)
XX
DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
XX
KM Gibberellin, 18S rRNA; internal transcribed spacer region; ITS1; ITS2;
KM 5.8S rRNA; LTB-1027; species differentiation; GA_4; GA_3; GA_7;
KM flowering; fruit cell elongation; apple; pear; grape; fruit;
KM russet control; fungus; ds.
XX
OS Gibberella fujikuroi.
XX
FH Key Location/Qualifiers
FT misc_feature 1..1774
FT FT /*tag= a
FT FT /note= "18S rRNA gene"
FT FT 1775..1921
FT FT /*tag= b
FT FT /note= "ITS1 region"
FT FT 1922..2078
FT FT /*tag= c
FT FT /note= "5.8S rRNA gene"
FT FT 2079..2243
FT FT /*tag= d
FT FT /note= "ITS2 region"
FT FT 2244..2293
FT FT misc_feature /*tag= e

```

```

FT FT /note= "28S rRNA gene"
XX
XX US6287800-B1.
XX
XX 11-SBP-2001.
XX
XX 23-AUG-2000; 2000US-00645073.
XX
XX 31-AUG-1999; 99US-0151770P.
XX
XX (GALL/) GALLIAZZO J L.
XX (LEEM/) LEE M D.
XX
XX Galliazzo JL, Lee MD;
XX WPI; 2001-662197/76.
XX
XX A new method for producing a mixture of gibberellins from Gibberella
PT fujikuroi results in high titers of GA4 and GA7 useful to promote
PT flowering and fruit growth in the fruit growing industry.
XX
XX Example 4; Col 9-12; 7pp; English.
XX
XX This sequence represents a genomic DNA sequence containing the 18S rRNA
CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC rRNA sequences from a mutant strain of Gibberella fujikuroi (LTB-1027) of
CC the invention. This region of DNA is highly variable and can be used for
CC species and strain differentiation. The LTB-1027 mutant produces a
CC mixture of gibberellins which is at least 70 % GA_4 and GA_7.
CC Gibberellin GA_4 and GA_7 promote flowering and fruit cell elongation,
CC and are used by growers of apples, pears and grapes to produce larger
CC fruits and earlier harvests. The mixture of GA_3, GA_4 and GA_7 achieved
CC using the method of this invention should be particularly useful in the
CC apple industry where GA_4 has been found more effective in russet control
CC and in promoting fruit set. This method produces GA_4 and GA_7 in much
CC higher titers than prior art methods
XX
SQ Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;
Query Match 99.0%; Score 306.8; DB 4; Length 2293;
Best Local Similarity 99.4%; Pred. No. 1.7e-96;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAATGCATAGTATGATGATGCAAAATTCAGTGAATCATCTTTGAACGACA 60
DB 1972 AAATGCATAGTATGATGATGCAAAATTCAGTGAATCATCTTTGAACGACA 2031
QY 61 TTGGGCGCCGCAATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCGAACCC 120
DB 2032 TTGGGCGCCGCAATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCGAACCC 2091
QY 121 CCGGCGTTGTGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGGCAATCTAGTG 180
DB 2092 CCGGCGTTGTGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGGCAATCTAGTG 2151
QY 181 GCGGTCCTGCTGAGCTTCATTCAGTAGTAAACCTTCGCACTGTAAGCGCGCG 240
DB 2152 GCGGTCCTGCTGAGCTTCATTCAGTAGTAAACCTTCGCACTGTAAGCGCGCG 2211
QY 241 GCGCAACCGCTTAAACCCCACTTCGATGTTGACCTGGAATCAGTGAATACCG 300
DB 2212 GCGCAACCGCTTAAACCCCACTTCGATGTTGACCTGGAATCAGTGAATACCG 2271
QY 301 CTGAACCTTAA 310
DB 2272 CTGAACCTTAA 2281
RESULT 3
ACCS0001
ID ACCS0001 standard; DNA; 534 BP.
XX
XX ACCS0001,

```


QY 239 GGGGCAAGCCGTTAAACCCCACTTCTGAATGTGACCTCGATCAGTAGAATACC 238
 Db 436 GGGGCAAGCCGTTAAACCCCACTTCTGAATGTGACCTCGATCAGTAGAATACC 435
 QY 299 CGCTGAA 305
 Db 496 CGCTGAA 502

RESULT 5

AAV59009 standard; DNA; 561 BP.

QY 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1999 (first entry)

DE F. avenaceum internal transcribed spacer.

KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
 KM fungal pathogen identification; infection identification; ss.

OS Gibberella avenacea.

Key Location/Qualifiers
 FT misc_feature 31..181
 FT /*tag= a
 FT /note= "ITS1"
 FT misc_feature 339..504
 FT /*tag= b
 FT /note= "ITS2"

US5827695-A.

27-OCT-1998.

04-AUG-1997; 97US-00905314.

04-AUG-1997; 97US-00905314.

(NOVS) NOVARTIS FINANCE CORP.

Beck JJ;

WPI; 1998-593995/50.

Wheat pathogen internal transcribed spacer sequences - used as a basis
 for primers for the species-specific polymerase chain reaction detection
 of the pathogens.

Claim 1; Col 29-30; 20pp; English.

This sequence represents an internal transcribed spacer (ITS) sequence of
 the invention. The primer pairs, based on the ITS sequences, are used for
 the PCR amplification detection of wheat Microdochium and Fusarium fungal
 pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
 avenaceum, F. poae, F. moniliforme or F. roseum. The two different
 strains of fungi show different symptoms during infection, which may or
 may not be due to infection. Early identification of the strain causing
 the infection allows early, and more specific fungicidal treatment.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)

Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;

Query Match 80.6%; Score 249.8; DB 2; Length 561;
 Best Local Similarity 91.6%; Pred. No. 8.2e-77;
 Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

1 AATGCGATTAAGTATGTGATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACACA 60

Db 232 AATGCGATTAAGTATGTGATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACACA 291
 QY 61 TTGCGCCCGCAGATATTTGCGCGGCATCCTGTTGAGCGTCATTTCAACCTCAAGCC 120
 Db 292 TTGCGCCCGCAGATATTTGCGCGGCATCCTGTTGAGCGTCATTTCAACCTCAAGCC 351
 QY 121 CCGGGTTTGTGTTGGGATTCGGCAAGCCCTTGGCGC-AAGCCGGCCCGGAATCTAGT 179
 Db 352 CCGGGTTTGTGTTGGGATTCGGCAAGCCCTTGGCGC-AAGCCGGCCCGGAATCTAGT 411
 QY 180 GCGGTCCTGCTGACACTTCCATTGGGTAGTAAACCTCGCAACTGTACGGGCG 239
 Db 412 GCGGTCCTGCTGACACTTCCATTGGGTAGTAAACCTCGCAACTGTACGGGCG 471
 QY 240 CCGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGTAGAATACC 299
 Db 472 CCGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGTAGAATACC 530
 QY 300 GCTGAATCTTAA 310
 Db 531 GCTGAATCTTAA 541

RESULT 6

ABV78724 standard; rRNA; 659 BP.

ABV78724;

14-JAN-2003 (first entry)

DE C. sinensis rRNA sequence #23.

KW Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;
 KM Cordyceps sinensis; ss.

OS Cordyceps sinensis.

PN JP2002204696-A.

23-JUL-2002.

12-JAN-2001; 2001JP-00004805.

12-JAN-2001; 2001JP-00004805.

(HEAL-) HEALTHWAY KK.

(KANE/) KANESHIRO N.

WPI; 2002-639075/69.

Ribosome RNA gene base sequence of Cordyceps sinensis for classification
 of seeds of Cordyceps sinensis.

26; Page 25; 33pp; Japanese.

The invention relates to a novel base sequence which is part of a fully
 defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.
 CC The base sequences can be used for the classification of Cordyceps
 CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
 CC invention

Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;

Query Match 80.2%; Score 248.6; DB 6; Length 659;
 Best Local Similarity 91.6%; Pred. No. 2.3e-76;
 Matches 285; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

1 AATGCGATTAAGTATGTGATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACACA 60
 Db 260 AATGCGATTAAGTATGTGATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACACA 319

Query Match 62.7%; Score 194.4; DB 7; Length 522;
Best Local Similarity 84.3%; Pred. No. 26-57; Mismatches 36; Indels 12; Gaps 3;
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AATGCGATTAAGTAAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAAAGCACA 60
DB 229 AATGCGATTAAGTAAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAAAGCACA 288
QY 61 TTGCGCCGCCAGTATTTCTGCGCGGCAATGCTGTTGAGCGTCAATTTCAACCTCAAGCC 120
DB 289 TTGCGCCGCCAGTATTTCTGCGCGGCAATGCTGTTGAGCGTCAATTTCAACCTCAAGCC 348
QY 121 CCCGGGTTGGTGTGGGATGGGCAAGCCCTTGGGCAAGCCGCCCGCAATTTACTAG 180
DB 349 C-----AGTTGGTGGGATGGGCAAGCCCTTGGGCAAGCCGCCCGCAATTTACTAG 398
QY 181 GCGGCTCGCTGCACTTCATTTGAGTAAATCCCTGCAACTGTTACGGCGGC 240
DB 399 GCGGCTCGCTGCACTTCATTTGAGTAAATCCCTGCAACTGTTACGGCGGC 457
QY 241 GCGCAAGCGGTTAAACCCCACTTCTGAAATGTTGACCTCGATGAGTAAATACCG 300
DB 458 GCGCAAGCGGTTAAACCCCACTTCTGAAATGTTGACCTCGATGAGTAAATACCG 516
QY 301 CTGAC 306
DB 517 CTGAC 522

RESULT 11
ABV78721
ID ABV78721 standard; rRNA, 661 BP.
XX AC ABV78721;
XX DT 14-JAN-2003 (first entry)
XX DE C. sinensis rRNA sequence #20.
XX KW Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;
XX KW Cordyceps sinensis; ss.
XX OS Cordyceps sinensis.
XX PN JP2002204696-A.
XX PD 23-JUL-2002.
XX PE 12-JAN-2001; 2001JP-00004805.
XX PR 12-JAN-2001; 2001JP-00004805.
XX PA (HEAL-) HEALTHWAY KK.
XX PA (KANE/) KANESHIRO N.
XX DR WPI; 2002-639075/69.
XX PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
XX PT of seeds of Cordyceps sinensis.
XX PS 23; Page 24; 33pp; Japanese.
XX CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.
CC The base sequence can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
CC invention
XX SQ Sequence 661 BP, 176 A; 192 C; 168 G; 123 T; 0 U; 2 Other;
Query Match 62.5%; Score 193.8; DB 6; Length 661;
Best Local Similarity 83.6%; Pred. No. 3.66-57;

Matches 260; Conservative 0; Mismatches 37; Indels 14; Gaps 3;
QY 1 AATGCGATTAAGTAAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAAAGCACA 60
DB 269 AATGCGATTAAGTAAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAAAGCACA 328
QY 61 TTGCGCCGCCAGTATTTCTGCGCGGCAATGCTGTTGAGCGTCAATTTCAACCTCAAGCC 120
DB 329 TTGCGCCGCCAGTATTTCTGCGCGGCAATGCTGTTGAGCGTCAATTTCAACCTCAAGCC 388
QY 121 CCCG-GGTTGGTGTGGGATGGGCAAGCCCTTGGGCAAGCCGCCCGCAATTTACTAG 179
DB 389 CCAGGCGGCTGTGTGGGAGCCGGC-----CCGGCGGCCCGCCCAATTTGAGGT 437
QY 180 GCGGCTCGCTGCACTTCATTTGAGTAAATCCCTGCAACTGTTACGGCGGC 239
DB 438 GCGGCTCGCTGCACTTCATTTGAGTAAATCCCTGCAACTGTTACGGCGGC 495
QY 240 GCGCAAGCGGTTAAACCCCACTTCTGAAATGTTGACCTCGATGAGTAAATACCG 299
DB 496 GCGTCAAGCGGTTAAACCCCACTTCTGAAATGTTGACCTCGATGAGTAAATACCG 555
QY 300 GCTGAACCTTAA 310
DB 556 GCTGAACCTTAA 566

RESULT 12
AAT65100
ID AAT65100 standard; DNA, 582 BP.
XX AC AAT65100;
XX DT 17-OCT-2003 (revised)
XX DT 17-FEB-1998 (first entry)
XX DE T. harzianum IMI 352940 5.8 S rRNA gene regions ITS1-ITS4.
XX KW ITS1-ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzianum;
XX KW liquid formulation; T. viride; gene recipient; increase activity;
XX KW biological control agent; plant disease; biodegradation;
XX KW biofixation; leaching; ss.
XX OS Hypocrea lixii; strain IMI 352940.
XX PN WO9716974-A1.
XX PD 15-MAY-1997.
XX PE 06-NOV-1996; 96WO-ES000206.
XX PR 07-NOV-1995; 95ES-00002266.
XX PA (UYSA-) UNIV SALAMANCA.
XX PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX PT Monte Vazquez E, Grondona Espana I, Garcia Ancha I;
XX DR WPI; 1997-280728/25.
XX PT Liquid formulation of Trichoderma harzianum and Trichoderma viride
XX PT strains - are used as biological control agents against diseases of
XX PT plants and plant material and as biofixation agents.
XX PS Disclosure; Page 26; 37pp; Spanish.
XX CC The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC gene from the filamentous fungi Trichoderma harzianum strain IMI 352940.
CC A novel liquid formulation based on strains of T. harzianum and T.
CC viride, has the following composition (w/v%): 0.1-6 sorbitol; 0.02-2
CC K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4; 0.02-2 copper;
CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2
CC manganese; and a biological component comprising at least one of: T.

CC harzianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352941 (3 x 105 to 10 x 107 conidia/ml), T. harzianum CECT 20179 and/or T. viride CECT 20178. The Trichoderma fungi, alone or in combination, are used as gene recipients to increase activity of the formulation as a biological control agent against diseases of plants and plant material and biological entitles causing biodegradation, and as a biofixation (leaching) agent. It is particularly used e.g. in agriculture, forestry and gardening; for controlling microorganisms which damage food and its packaging; construction materials, raw materials and manufactured products. The antagonistic capacity of the four types of T. harzianum and one type of T. viride over other soil fungi makes them useful for control of plant diseases. Use of this formulation allows reduced application of polluting chemical pesticides and is thus more eco-friendly. (updated on 17-OCT-2003 to standardise OS field)

CC XX Sequence 582 BP, 129 A; 178 C; 142 G; 133 T; 0 U; 0 Other;

Query Match 62.4%; Score 193.4; DB 2; Length 582;
Best Local Similarity 85.9%; Pred. No. 4.7e-57;
Matches 274; Conservative 0; Mismatches 36; Indels 9; Gaps 5;

QY 1 AATGCCATTAATGATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 264 AATGCCATTAATGATGTAATTCAGTGAATCATCGAATCTTTGAACGCACA 323

QY 61 TTGGCCCGCCGACGATTTCTGGCGGGGCAATGCTGTTCAGAGGTCTTTCACACCTCAAGCC 120
Db 324 TTGGCCCGCCGACGATTTCTGGCGGGGCAATGCTGTTCAGAGGTCTTTCACACCTCAAGCC 383

QY 121 C-----CCGGTTTGTTGGTTGGGATCGCAAGCCCTT-GCGGCACCGCGCCCGAAT 174
Db 384 CCGCCGCCCGCCCGCGGTTGGGATCGCCCTTCCTTAGCGGATGCGCCGTCCGAAT 443

QY 175 CTATGCGCGGTCTGCTGCTGACCTTCCATTGCTAGTG-G-TAAACCTCCCACTGTAC 223
Db 444 ACAATGGGCTCTGCGCGACCCCTCTCTGCGCAGTGTTCACACTCCCATCGGAGC 503

QY 234 GCGCGCGGCCA-AGCGTTAAACCCCACTCTG-AATGTGACCTCGGATCAGGTAG 291
Db 504 GCGCGCGGTCCACGCGCTTTAAACCCCACTCTGAAATGTGACCTCGGATCAGGTAG 563

QY 292 GAATACCCGCTGAACCTTAA 310
Db 564 GAATACCCGCTGAACCTTAA 582

RESULT 13
AAV62596 standard; DNA, 546 BP.
XX AAV62596;
XX
DT 17-DEC-1998 (first entry)
XX Fusarium poae PCR amplified ITS region consensus DNA sequence.
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KM Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
KM PCR; nucleic acid detection; ss.
XX
XX Fusarium poae.
OS
FH Key location/Qualifiers
FT misc_feature 1..30
FT /tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 31..180
FT /tag= b
FT /note= "ITS 1"
FT misc_feature 181..337
FT /tag= c

FT /note= "5.8S rRNA gene"
FT misc_feature 338..489
FT /tag= d
FT /note= "ITS 2"
FT misc_feature 490..546
FT /tag= e
FT /note= "5' end of large subunit rRNA gene"
FN US5814453-A.
PD 29-SEP-1998.
XX
PF 02-JUL-1997; 97US-00887480.
XX
XX 19-APR-1995; 95MO-US004712.
PR 15-OCT-1996; 96US-00722187.
XX
XX (NOVS) NOVARTIS FINANCE CORP.
PA Beck UJ;
XX WPI; 1998-541745/46.
DR
XX DNA isolated from fungal RNA, and its internal transcribed spacer
PT sequence - used for detecting fungal pathogens in plant tissue.
XX Example; Col 87-88; 56bp; English.
XX
CC This represents the consensus DNA sequence of the internal transcribed
CC spacer (ITS) region that was PCR amplified from Fusarium poae isolates, T
CC -427, T-534 and T-756. The invention provides a DNA molecule isolated
CC from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the
CC DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of
CC Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria
CC avenae or Microdochium nivale. A method for detecting F. graminearum, F.
CC culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is
CC also provided. The method comprises isolating DNA from a plant leaf
CC infected with at least one of the above pathogens and amplifying parts of
CC the ITS sequence of the pathogen(s) by PCR using specific primers from
CC within these sequences. The pathogen(s) are detected by visualising the
CC amplified part of the ITS sequence
XX
SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;

Query Match 60.5%; Score 187.6; DB 2; Length 546;
Best Local Similarity 84.5%; Pred. No. 4.9e-55;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

QY 1 AATGCCATTAATGATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
Db 231 AATGCCATTAATGATGTAATTCAGTGAATCATCGAATCTTTGAACGCACA 290

QY 61 TTGGCCCGCCGACGATTTCTGGCGGGGCAATGCTGTTCAGAGGTCTTTCACACCTCAAGCC 120
Db 291 TTGGCCCGCCGACGATTTCTGGCGGGGCAATGCTGTTCAGAGGTCTTTCACACCTCAAGCC 350

QY 121 CCGGGTTTGTTGGTTGGGATCGCAAGCCCTTGGGGAAGCGCCCGCGAATTAATAGT 180
Db 351 C---AGCTTGGTGGG-----ATCTGTGGCAACACAGTCCCAAAATGATG 398

QY 181 GCGGTCTGCTGACGCTTCATTTGCGTAGTAGTAACCCCTCGCAACGTGTACCGCGGC 240
Db 399 GCGGTCAAG-TGACGCTTCATTTGCGTAGTAGTAACCCCTCGCAACGTGTGTACGTAATCGTGC 457

QY 241 GCGCAAGCGCTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTAGGAATACCG 300
Db 458 GCGCAAGCGCTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTAGGAATACCG 516

QY 301 CTGAACCTTAA 310
Db 517 CTGAACCTTAA 526

RESULT 14
AAV53007
ID AAV59007 standard; DNA; 546 BP.
XX
AC AAV59007;
XX
DT 25-MAR-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE F. poae internal transcribed spacer.
XX
KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KW fungal pathogen identification; infection identification; ss.
XX
OS Fusarium poae.
XX
FH Key Location/Qualifiers
FT misc_feature 31..180
FT /tag= a
FT /note= "ITS1"
FT misc_feature 338..489
FT /tag= b
FT /note= "ITS2"
XX
PN US5827695-A.
XX
PD 27-OCT-1998.
XX
PF 04-AUG-1997; 97US-00905314.
XX
PR 04-AUG-1997; 97US-00905314.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Beck JJ;
XX
DR WPI; 1998-593995/50.
XX
PT Wheat pathogen internal transcribed spacer sequences - used as a basis
PT for primers for the species-specific polymerase chain reaction detection
PT of the pathogens.
XX
PS Claim 1; Col 25-26; 20pp; English.
XX
CC This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat Microdochium and Fusarium fungal
CC pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
CC avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;
Query Match 60.5%; Score 187.6; DB 2; Length 546;
Best Local Similarity 84.5%; Pred. No. 4.9e-55;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

1 AAATGCGATGAATGGAATTCGAAATTCAGTATTCATTCGAATCTTGAACGCACA 60
231 AAATGCGATGAATGGAATTCGAAATTCAGTATTCATTCGAATCTTGAACGCACA 290
61 TTGGGCCCCGCAATTCGCGGCGCATGCTGTTCAGCGTCAATTCGAACCTCAAGCC 120
291 TTGGGCCCCGCAATTCGCGGCGCATGCTGTTCAGCGTCAATTCGAACCTCAAGCC 350
121 CCCGGGTTGTGTGGGGAATCGGCAAGCCCTTGGCGGCAAGCCGCGCGGAATCTAGTG 180
351 C---AGCTTGGTGTGGG-----ATCTGTGTGCAAAACAGTCCCAAAATTCGATTG 398

181 GCGGTCGTGCAGACTTCATTCGATGATGATTAACCTCGCAACTGATGCGGCGC 240
399 GCGGTACAG-TCGAGCTTCATACGCTGATTAATTCACATCGTTCATCGTAATCTGCG 457
241 GCGCAAGCGGTTAAACCCCAACTTCGATGATGTTGACCTCGGATCAGGTAGAAATACCCG 300
458 GCGCAAGCGGCTTAAAC-CCCAACTTCGATGATGTTGACCTCGGATCAGGTAGAAATACCCG 516
301 CTGAACCTTAA 310
517 CTGAACCTTAA 526

RESULT 15
AAT05400
ID AAT05400 standard; DNA; 504 BP.
XX
AC AAT05400;
XX
DT 04-JUN-1996 (first entry)
XX
DE Fusarium culmorum internal transcribed spacer sequence.
XX
KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KW Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
KW Mycosphaerella muscicola; amplification; primer; ribosomal RNA gene;
KW internal transcribed region; strain; capture; colourimetric assay;
KW isolate; development; population; random amplified polymorphic DNA; ss.
XX
OS Fusarium culmorum.
XX
PN WO9529260-A2.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US004712.
XX
PR 25-APR-1994; 94US-00233608.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Liqon JM, Beck JJ;
XX
DR WPI; 1995-383005/49.
XX
PT DNA encoding intervening transcribed sequence - used for detection of
PT plant fungal pathogens.
XX
PS Claim 1; Page 54-55; 65pp; English.
XX
CC A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,
CC Mycosphaerella fijiensis, M. muscicola or Fusarium spp. involves the PCR
CC amplification of sequences found in the internal transcribed region (ITS)
CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAG94359-93
CC and AAT05357-72. These primers are derived from the ITS sequences of
CC these fungi (AAT05394-T05404 and AAG94398) and are strain specific. The
CC amplification products of the reactions using these primers can be used
CC with the capture primers AAT05378-93 in colourimetric assays. The primers
CC and ITS DNAs can be used for the detection of specific fungal pathogen
CC isolates and in monitoring disease development in plant populations
XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
Query Match 60.2%; Score 186.6; DB 2; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.1e-54;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

1 AAATGCGATGAATGGAATTCGAAATTCAGTATTCATTCGAATCTTGAACGCACA 60
212 AAATGCGATGAATGGAATTCGAAATTCAGTATTCATTCGAATCTTGAACGCACA 271
61 TTGGGCCCCGCAATTCGCGGCGCATGCTGTTCAGGCGTCAATTCGAACCTCAAGCC 120

```

Db      272  TTGGCCCGCCAGATATTCTGGCGGGCATGCTGTTGAGGTCATTCAACCTCAAGCC 331
QY      121  CCCGGTTTGGTGTGGGGATCGCAAGCCCTTGGGCAAGCCGGCCCGAATCTAGTG 180
Db      332  C--AGCTTGGTGTGGG-----AGCTGCACTCCTGCTGCACCTCCCAAAATACATTG 380
QY      181  GCGGTCTCGCTGCAGTTCATTTGCTAGTAAACCTCGCACTGGTAAGCGGGCG 240
Db      381  GCGGTCACTGCGAGACTTCCATAGCGTAGTATTACATATCGTTACTGGTAATCGTGC 440
QY      241  GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGTAGAATACCCG 300
Db      441  GGCYAGCCCGTTAA--CCCCAATTCTGAATGTTGACCTCGATCAGTAGAATACCCG 499
QY      301  CTGAA 305
Db      500  CTGAA 504

```

Search completed: October 1, 2004, 03:41:03
 Job time : 551.986 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 2524.91 Seconds
(without alignments)
5321.503 Million cell updates/sec

Title: US-10-046-955-7
Perfect score: 310
Sequence: 1 aaatgcataagtaatgta.....ggaatacccgctgaacttaa 310

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_gts:*
12: gb_gy:*
13: gb_un:*
14: gb_vi:*
15: gb_vl:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_bcs:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rdd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_gy:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	6 AR206401	AR206401 Sequence
2	310	100.0	310	6 BD083592	BD083592 Nucleic a
3	310	100.0	310	6 AF117922	AF117922 Gdbere11
4	306.8	99.0	351	8 AF162903	AF162903 Fusarium
5	306.8	99.0	556	8 AF455422	AF455422 Gdbere11
6	306.8	99.0	556	8 AF455460	AF455460 Gdbere11
7	306.8	99.0	558	8 FPUORRNA	X94176 Fusarium fu
8	306.8	99.0	558	8 FPUORRNA	X94177 Fusarium pr
9	306.8	99.0	562	8 AY237110	AY237110 Fusarium
10	306.8	99.0	569	8 AF452163	AF452163 Pythium u
11	306.8	99.0	596	8 AF291061	AF291061 Fusarium
12	306.8	99.0	2293	6 AR168094	AR168094 Sequence
13	305.2	98.5	531	8 AF158303	AF158303 Fusarium
14	305.2	98.5	540	8 AF158304	AF158304 Fusarium
15	303.6	97.9	540	8 AF158302	AF158302 Fusarium
16	302.8	97.7	534	8 FPU34557	U34557 Fusarium fu
17	302.8	97.7	534	8 FPU34558	U34558 Fusarium pr
18	301.2	97.2	534	8 FPU61670	U61670 Fusarium an
19	301.2	97.2	534	8 FPU61693	U61693 Fusarium sp
20	300.8	97.0	502	8 AF165873	AF165873 Gdbere11
21	299.6	96.6	534	8 FPU34574	U34574 Fusarium ph
22	297.2	95.9	559	8 FREDRINA	X94169 Fusarium re
23	296.4	95.6	534	8 FPU34567	U34567 Fusarium sp
24	296.4	95.6	534	8 FPU61692	U61692 Fusarium sp
25	294.8	95.1	534	8 FPU34564	U34564 Fusarium sp
26	294.2	94.9	541	8 AF158307	AF158307 Fusarium
27	294.2	94.9	541	8 AF158309	AF158309 Fusarium
28	294.2	94.9	559	8 FDLARRNA	X94177 Fusarium dl
29	291	93.9	527	8 FPU61687	U61687 Fusarium gl
30	290.8	93.8	521	8 FPU61691	U61691 Fusarium sp
31	290.2	93.6	535	8 FPU34573	U34573 Fusarium ac
32	290	93.5	535	8 FPU34565	U34565 Fusarium re
33	289.2	93.2	522	8 FPU61678	U61678 Fusarium co
34	289	93.2	542	8 AF008920	AF008920 Fusarium
35	288.6	93.1	535	8 FPU34572	U34572 Fusarium dl
36	288.4	93.0	349	8 AF162897	AF162897 Fusarium
37	288.4	93.0	529	8 AF158312	AF158312 Fusarium
38	288.4	93.0	557	8 FNYGRRNA	X94174 Fusarium ny
39	284.4	91.7	533	8 FPU34568	U34568 Fusarium ny
40	284.4	91.7	533	8 FPU34575	U34575 Fusarium ud
41	278.2	89.7	543	8 FPU34581	U34581 Fusarium bu
42	272.4	87.9	532	8 FPU34560	U34560 Fusarium th
43	272.2	87.8	434	8 AY243055	AY243055 Ascomycet
44	270.8	87.4	520	8 FPU61690	U61690 Fusarium sp
45	270.8	87.4	1458	8 AF310981	AF310981 Fusarium

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	SEQUENCE	7 from patent US 6372430.	DNA	linear	PAT 20-JUN-2002
AR206401	AR206401	Sequence 7 from patent US 6372430.	AR206401	GI:21504992			
REFERENCE	1 (bases 1 to 310)						
AUTHORS	Morrison,C.O., Reles,E., Aidorevich,L. and Choi,J.Soo.						
TITLE	Nucleic acids for detecting Aspergillus species and other filamentous fungi						
JOURNAL	Patent: US 6372430-A 7 16-APR-2002;						

Pred. No. is the number of results predicted by chance to have a

Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 60
DB 1 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 60
QY 61 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 120
DB 61 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 120
QY 121 CCCGGGTTTGTGTGGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180
DB 121 CCCGGGTTTGTGTGGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180
QY 181 GCGGTCTGCTGACCTTCATTCGTTAGTAAACCTTCGCACTGTGATCGCGGCGC 240
DB 181 GCGGTCTGCTGACCTTCATTCGTTAGTAAACCTTCGCACTGTGATCGCGGCGC 240
QY 241 GCGCAAGCGGTTAAACCCCACTCTGATGTGACCTCGGATGAGTAAATACCGC 300
DB 241 GCGCAAGCGGTTAAACCCCACTCTGATGTGACCTCGGATGAGTAAATACCGC 300
QY 301 CTGAACCTTAA 310
DB 301 CTGAACCTTAA 310

RESULT 4
AF162903
LOCUS
DEFINITION

AF162903 351 bp DNA linear PLN 04-AUG-1999
Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence;
internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.

ACCESSION
AF162903.1 GI:5690392

VERSION
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea

Location/Qualifiers

1..351

/organism="Fusarium proliferatum"

/mol_type="genomic DNA"

/strain="6787"

/db_xref="taxon:42674"

<1..128

/product="5.8S ribosomal RNA"

/product="internal transcribed spacer 2"

294..351

/product="28S ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 351;
Best Local Similarity 99.4%; Pred. No. 1.2e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 60
DB 22 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 81
QY 61 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 120
DB 82 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 141

QY 121 CCCGGGTTTGTGTGGGGATCGGCAAGCCCTTGGCGGACCGGCCCGCAATCTAGTG 180
DB 142 CCCGGGTTTGTGTGGGGATCGGCAAGCCCTTGGCGGACCGGCCCGCAATCTAGTG 201
QY 181 GCGGTCTGCTGACCTTCATTCGTTAGTAAACCTTCGCACTGTGATCGCGGCGC 240
DB 202 GCGGTCTGCTGACCTTCATTCGTTAGTAAACCTTCGCACTGTGATCGCGGCGC 261
QY 241 GCGCAAGCGGTTAAACCCCACTCTGATGTGACCTCGGATGAGTAAATACCGC 300
DB 262 GCGCAAGCGGTTAAACCCCACTCTGATGTGACCTCGGATGAGTAAATACCGC 321
QY 301 CTGAACCTTAA 310
DB 322 CTGAACCTTAA 331

RESULT 5

AF455422

LOCUS

DEFINITION

AF455422 556 bp DNA linear PLN 16-JUN-2003
Gibberella fujikuroi isolate w518 small subunit ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene and internal transcribed spacer 2, complete
sequence; and large subunit ribosomal RNA gene, partial sequence.

ACCESSION
AF455422.1 GI:21666850

VERSION
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (04-DEC-2001) Laboratory for Mycology and Molecular
Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A
8036, Austria

Location/Qualifiers

1..556

/organism="Gibberella fujikuroi"

/mol_type="genomic DNA"

/isolate="w518"

/db_xref="taxon:5127"

<1..48

/product="small subunit ribosomal RNA"

49..247

/product="internal transcribed spacer 1"

248..353

/product="5.8S ribosomal RNA"

354..518

/product="internal transcribed spacer 2"

519..556

/product="large subunit ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 556;
Best Local Similarity 99.4%; Pred. No. 1.3e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 60
DB 247 AATGCGATAGTAATGCAAAATTCAGTCATCATGATCTTTGAACGCACA 306
QY 61 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 120
DB 307 TTGGCCCGCCGAGTATTCGGGGGAGTCCGTTGAGCGGATCTTCAACCCCTCAAGCC 366

QY 121 CCCGGTTTGGTGTGGGATCGCAAGCCCTTGGCGCAAGCCGCGGAAATCTAGTG 180
 Db 367 CCCGGTTTGGTGTGGGATCGGAGCCCTTGGCGCAAGCCGCGGAAATCTAGTG 426
 QY 181 GCGGTCTCGTGCAGCTTCATTTGGGTAGTAAACCCCTGGAACTGTAGCGGCGC 240
 Db 427 GCGGTCTCGTGCAGCTTCATTTGGGTAGTAAACCCCTGGAACTGTAGCGGCGC 486
 QY 241 GCGCAAGCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGGTAGAAATACCG 300
 Db 487 GCGCAAGCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGGTAGAAATACCG 546
 QY 301 CTGAACCTAA 310
 Db 547 CTGAACCTAA 556

RESULT 6

AF455460

LOCUS 556 bp DNA linear PLN 16-JUN-2003
 DEFINITION Gibberella fujikuroi isolate wb355 small subunit ribosomal RNA

gene, partial sequence; internal transcribed spacer 1, 5.8S
 ribosomal RNA gene and internal transcribed spacer 2, complete
 sequence; and large subunit ribosomal RNA gene, partial sequence.
 AF455460

AF455460.1 GI:21666892

ACCESSION

VERSION

KEYWORDS

ORGANISM

SOURCE

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

RESULT 7

FFURRNA

LOCUS 558 bp DNA linear PLN 14-JUN-2001
 DEFINITION Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S

internal transcribed spacer 1 (ITS1) and
 internal transcribed spacer 2 (ITS2).
 X94176.1 GI:1122868
 X94176 X9390

ACCESSION

VERSION

KEYWORDS

ORGANISM

SOURCE

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

FEATURES

source

1..558

/organism="Gibberella fujikuroi"

/mol_type="genomic DNA"

/strain="CBS 221.76"

/specific_host="rice"

/db_xref="taxon:5127"

1..30

/gene="18S rRNA"

<1..30

/gene="18S rRNA"

/product="18S ribosomal RNA"

31..177

/note="internal transcribed spacer 1, ITS1"

178..335

/gene="5.8 rRNA"

178..335

/gene="5.8 rRNA"

/product="5.8 ribosomal RNA"

336..500

/note="internal transcribed spacer 2, ITS2"

501..558

/gene="28S rRNA"

501..558

/gene="28S rRNA"

/product="28S ribosomal RNA"

501..558

/gene="28S rRNA"

/product="28S ribosomal RNA"

501..558

/gene="28S rRNA"

/product="28S ribosomal RNA"

501..558

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 558;
 Best Local Similarity 99.4%; Pred. No. 1.3e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
 DB 229 AATCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 288
 QY 61 TTGGCCCGCCGCAAGTATCTGCGCGGCGATCCCTGTTGAGCGTCAATTCACCCCTCAAGCC 120
 DB 289 TTGGCCCGCCGCAAGTATCTGCGCGGCGATCCCTGTTGAGCGTCAATTCACCCCTCAAGCC 348
 QY 121 CCCGGGTTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCCGGAATCTAGTG 180
 DB 349 CCCGGGTTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCCGGAATCTAGTG 408
 QY 181 GCGGTCTGCTGACGATTCATTCAGTGTAGTAAACCTCGCAACTGTGACGGCGC 240
 DB 409 GCGGTCTGCTGACGATTCATTCAGTGTAGTAAACCTCGCAACTGTGACGGCGC 468
 QY 241 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGACCTCGATCAGTAGGAATACCG 300
 DB 469 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGACCTCGATCAGTAGGAATACCG 528
 QY 301 CTGAACCTTAA 310
 DB 529 CTGAACCTTAA 538

RESULT 8

PPORRNA 558 bp DNA linear PLN 14-JUN-2001
 LOCUS FUSARIUM proliferatum 18S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).
 DEFINITION X94171.1 X93904

ACCESSION X94171.1 GI:1122873
 VERSION 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
 KEYWORDS FUSARIUM proliferatum
 SOURCE FUSARIUM proliferatum
 ORGANISM FUSARIUM proliferatum

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
 TITLE 1

REFERENCE Maalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.
 AUTHORS Discordant groupings of *Fusarium* spp. from sections *Elegans*,
 TITLE *lioseola* and *diastoma* a based on ribosomal ITS1 and ITS2 sequences
 JOURNAL Mycologia 88, 361-368 (1996)
 REFERENCE 2 (bases 1 to 558)

AUTHORS Maalwijk, C.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant
 PROTECTION, PO box 9060, 6700 GW Wageningen, NETHERLANDS
 COMMENT On Jun 15, 2001 this sequence version replaced gi:1103572.
 OVERLAPS with X78260.

FEATURES

source 1..558
 location/Qualifiers
 /organism="Fusarium proliferatum"
 /mol_type="genomic DNA"
 /strain="CBS 217.76"
 /specific_host="Cattleya"
 /db_xref="taxon:42674"
 1..30
 /gene="18S rRNA"
 <1..30
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 31..177
 /note="internal transcribed spacer 1, ITS1"

gene

178..335
 /gene="5.8 rRNA"

rRNA

178..335
 /gene="5.8 rRNA"
 /product="5.8 ribosomal RNA"

misc_feature

336..500
 /note="internal transcribed spacer 2, ITS2"

gene

501..558
 /gene="28S rRNA"

rRNA

501..558
 /gene="28S rRNA"
 /product="28S ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 558;
 Best Local Similarity 99.4%; Pred. No. 1.3e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
 DB 229 AATCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 288
 QY 61 TTGGCCCGCCGCAAGTATCTGCGCGGCGATCCCTGTTGAGCGTCAATTCACCCCTCAAGCC 120
 DB 289 TTGGCCCGCCGCAAGTATCTGCGCGGCGATCCCTGTTGAGCGTCAATTCACCCCTCAAGCC 348
 QY 121 CCCGGGTTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCCGGAATCTAGTG 180
 DB 349 CCCGGGTTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCCGGAATCTAGTG 408
 QY 181 GCGGTCTGCTGACGATTCATTCAGTGTAGTAAACCTCGCAACTGTGACGGCGC 240
 DB 409 GCGGTCTGCTGACGATTCATTCAGTGTAGTAAACCTCGCAACTGTGACGGCGC 468
 QY 241 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGACCTCGATCAGTAGGAATACCG 300
 DB 469 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGACCTCGATCAGTAGGAATACCG 528
 QY 301 CTGAACCTTAA 310
 DB 529 CTGAACCTTAA 538

RESULT 9

AY237110 562 bp DNA linear PLN 09-APR-2003
 LOCUS FUSARIUM sp. 03001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
 DEFINITION AY237110

ACCESSION AY237110 GI:29691499
 VERSION FUSARIUM sp. 03001
 KEYWORDS FUSARIUM sp. 03001
 SOURCE FUSARIUM sp. 03001

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*.
 TITLE 1 (bases 1 to 562)
 AUTHORS Afuntan, M.R. and Heiang, T.
 JOURNAL Direct Submission

COMMENT Submitted (14-FEB-2003) Environmental Biology, University of
 Guelph, Guelph, ON N1G 2W1, Canada
 OVERLAPS with X78260.

FEATURES

source 1..562
 location/Qualifiers
 /organism="Fusarium sp. 03001"
 /mol_type="genomic DNA"
 /isolate="03001"
 /db_xref="taxon:227081"
 <1..40
 /product="18S ribosomal RNA"
 41..186
 /product="internal transcribed spacer 1"
 187..345

misc_RNA
346..510
/product="5.8 ribosomal RNA"
/product="internal transcribed spacer 2"
511..>562
rRNA
/product="28S ribosomal RNA"

Query Match 99.0%; Score 306.8; DB 8; Length 562;
Best Local Similarity 99.4%; Pred. No. 1.3e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 239 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 298
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 120
DB 239 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 358
QY 121 CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTGGCGGCAAGCCGGCCCGGAATCTAGT 180
DB 359 CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTGGCGGCAAGCCGGCCCGGAATCTAGT 418
QY 181 GCGGTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACCGGCGC 240
DB 419 GCGGTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACCGGCGC 478
QY 241 GGGCAAGCCGTTAAACCCCAACTTCGTAAGTGTGACCTCGGATCAGATGAGTAATACCG 300
DB 479 GGGCAAGCCGTTAAACCCCAACTTCGTAAGTGTGACCTCGGATCAGATGAGTAATACCG 538
QY 301 CTGAACCTTAA 310
DB 539 CTGAACCTTAA 548

RESULT 10
AF452163 569 bp DNA linear PLN 27-DEC-2001
LOCUS Pythium ultimum var. sporangififerum isolate 308276R 18S ribosomal
DEFINITION RNA gene, partial sequence.
ACCESSION AF452163
VERSION AF452163.1 GI:17980882
KEYWORDS Pythium ultimum var. sporangififerum
SOURCE Pythium ultimum var. sporangififerum
ORGANISM Pythium
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

REFERENCE 1 (bases 1 to 569)
Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
Pythium species and a population identification using DNA markers
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 569)
Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2001) Plant Pathology, Pennsylvania State
University, 210 Buckhout Laboratory, University Park, PA 16802, USA

FEATURES
source
1..569
Location/Qualifiers
/organism="Pythium ultimum var. sporangififerum"
/mol_type="genomic DNA"
/variety="sporangififerum"
/isolate="308276R"
/db_xref="taxon:115421"
<1..569
/product="18S ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 569;
Best Local Similarity 99.4%; Pred. No. 1.3e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60

DB 246 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 305
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 120
DB 306 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 365
QY 121 CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTGGCGGCAAGCCGGCCCGGAATCTAGT 180
DB 366 CCCGGGTTGGTGTGGGGATCGGCAAGCCCTTGGCGGCAAGCCGGCCCGGAATCTAGT 425
QY 181 GCGGTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACCGGCGC 240
DB 426 GCGGTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACCGGCGC 485
QY 241 GGGCAAGCCGTTAAACCCCAACTTCGTAAGTGTGACCTCGGATCAGATGAGTAATACCG 300
DB 486 GGGCAAGCCGTTAAACCCCAACTTCGTAAGTGTGACCTCGGATCAGATGAGTAATACCG 545
QY 301 CTGAACCTTAA 310
DB 546 CTGAACCTTAA 555

RESULT 11
AF291061 596 bp DNA linear PLN 18-SEP-2001
LOCUS Fusarium proliferatum NRRL 31071 18S ribosomal RNA, partial
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and
internal transcribed spacer 2, complete sequence; 28S ribosomal
RNA, partial sequence.
ACCESSION AF291061
VERSION AF291061.1 GI:15637128
KEYWORDS Fusarium proliferatum
SOURCE Fusarium proliferatum
ORGANISM Fusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
fujikuroi complex.
REFERENCE 1 (bases 1 to 596)
Kwon,S.-I., van Dohnon,C.D. and Anderson,A.J.
Gene sequence analysis of an opportunistic wheat pathogen, an
isolate of Fusarium proliferatum
JOURNAL Can. J. Bot. 79 (9), 1115-1121 (2001)
AUTHORS 2 (bases 1 to 596)
Kwon,S.-I. and Anderson,A.J.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2000) Biology, Utah State University, Logan, UT
84322-5305, USA

FEATURES
source
1..596
Location/Qualifiers
/organism="Fusarium proliferatum"
/mol_type="genomic DNA"
/strain="NRRL 31071"
/specific_host="Triticum aestivum cv. Super Dwarf"
/db_xref="taxon:42674"
<1..596
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, 28S ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 596;
Best Local Similarity 99.4%; Pred. No. 1.3e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 267 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 326
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 120
DB 327 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTCCAGCGTCAITTCACCTCAAGCC 386

QY 121 CCCGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGT 180
 DB 387 CCCGGTTTGGTGGGGATCGCGAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGT 446
 QY 181 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 240
 DB 447 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 506
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 300
 DB 507 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 566
 QY 301 CTGAACCTTAA 310
 DB 567 CTGAACCTTAA 576

RESULT 12

LOCUS AR168094 2293 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 1 from patent US 6287800.
 ACCESSION AR168094
 VERSION AR168094.1 GI:17903914
 KEYWORDS
 SOURCE
 ORGANISM Unknown.
 REFERENCE Unpublished.
 AUTHORS Gallazo, J.L. and Lee, M.D.
 TITLE Production of high titers of gibberellins, GA4 and GA7, by
 Gibberella fujikuroi strain I7B-1027
 Patent: US 6287800-A 1 11-SEP-2001;
 FEATURES Location/Qualifiers
 source 1..2293
 /organism="Unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 6; Length 2293;
 Best Local Similarity 99.4%; Pred. No. 1.5e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAATGCGATAGTATGATGCAAAATTCAGTATCATTCGAATCTTTGAAGCACA 60
 DB 1972 AAATGCGATAGTATGATGCAAAATTCAGTATCATTCGAATCTTTGAAGCACA 2031
 QY 61 TTGGCCCGCCAGTATTCGCGGGCATGCTGTTCCAGCGTCATTTCAACCTCAAGCC 120
 DB 2032 TTGGCCCGCCAGTATTCGCGGGCATGCTGTTCCAGCGTCATTTCAACCTCAAGCC 2091
 QY 121 CCGGGTTTGGTGGGGATCGGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 180
 DB 2092 CCGGGTTTGGTGGGGATCGGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 2151
 QY 181 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 240
 DB 2152 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 2211
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 300
 DB 2212 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 2271
 QY 301 CTGAACCTTAA 310
 DB 2272 CTGAACCTTAA 2281

RESULT 13

LOCUS AF158303 531 bp DNA linear PLN 21-MAR-2000
 DEFINITION Fusarium sp. NRRL26794 18S ribosomal RNA gene, partial sequence;
 Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal

transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 AF158303
 AF158303.1 GI:7106206
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 1..531
 /organism="Fusarium sp. NRRL 26794"
 /mol_type="genomic DNA"
 /strain="NRRL26794"
 /db_xref="taxon:10621"
 <1..23
 /product="18S ribosomal RNA"
 24..169
 /product="Internal transcribed spacer 1"
 170..328
 /product="5.8S ribosomal RNA"
 329..493
 /product="Internal transcribed spacer 2"
 494..>531
 /product="28S ribosomal RNA"

ORIGIN

Query Match 98.5%; Score 305.2; DB 8; Length 531;
 Best Local Similarity 99.0%; Pred. No. 4e-84;
 Matches 307; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AAATGCGATAGTATGATGCAAAATTCAGTATCATTCGAATCTTTGAAGCACA 60
 DB 222 AAATGCGATAGTATGATGCAAAATTCAGTATCATTCGAATCTTTGAAGCACA 281
 QY 61 TTGGCCCGCCAGTATTCGCGGGCATGCTGTTCCAGCGTCATTTCAACCTCAAGCC 120
 DB 282 TTGGCCCGCCAGTATTCGCGGGCATGCTGTTCCAGCGTCATTTCAACCTCAAGCC 341
 QY 121 CCGGGTTTGGTGGGGATCGGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 180
 DB 342 CCGGGTTTGGTGGGGATCGGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 401
 QY 181 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 240
 DB 402 GCGGTCTGCTGACAGCTTCATTTGGGTAGTAAACCTTCGCACTGTACGGGGCC 461
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 300
 DB 462 GGGCAAGCCGTTAAACCCCAACTTCTGAATTTTACCTCGATCAGGTAGGAATACCG 521
 QY 301 CTGAACCTTAA 310
 DB 522 CTGAACCTTAA 531

RESULT 14

LOCUS AF158304 540 bp DNA linear PLN 21-MAR-2000
 DEFINITION Fusarium sp. NRRL28852 18S ribosomal RNA gene, partial sequence;
 Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.

```

ACCESSION   AF158304
VERSION     AF158304.1  GI:7106207
SOURCE      Fusarium sp. NRRL 28852
KEYWORDS    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE   1 (bases 1 to 540)
AUTHORS    O'Donnell, K., Nirenberg, H.I., Aoki, T. and Cigelink, E.
TITLE      A multigene phylogeny of the Gibberella fujikuroi species complex:
            detection of additional phylogenetically distinct species
JOURNAL    Mycoscience 41, 61-78 (2000)
REFERENCE   2 (bases 1 to 540)
AUTHORS    O'Donnell, K.
TITLE      Direct Submission
JOURNAL    Submitted (10-JUN-1999) Microbial Properties, NCAR-ARL, 1815
            University St., Peoria, IL 61604, USA
FEATURES    source
            1..540
            /organism="Fusarium sp. NRRL 28852"
            /mol_type="genomic DNA"
            /strain="NRRL28852"
            /db_xref="taxon:100620"
            <1..32
            /product="18S ribosomal RNA"
            33..178
            /product="internal transcribed spacer 1"
            179..337
            /product="5.8S ribosomal RNA"
            338..502
            /product="internal transcribed spacer 2"
            503..>540
            /product="28S ribosomal RNA"

ORIGIN
Query Match      98.5%; Score 305.2; DB 8; Length 540;
Best Local Similarity 99.0%; Pred. No. 4,1e-84;
Matches 307; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAACGACA 60
DB 231 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAACGACA 290
QY 61 TTGGCGCCGCGCATATTCGCGGGCATGCTGTTGAGGTCATTGCAACCTCAAGCC 120
DB 291 TTGGCGCCGCGCATATTCGCGGGCATGCTGTTGAGGTCATTGCAACCTCAAGCC 350
QY 121 CCGGGTTGGTGGGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB 351 CCGGGTTGGTGGGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 410
QY 181 GCGGTCGCTGCGAGCTTCATTGCGTAGTAAGTAACCTCGCAACTGTAGCGGCGC 240
DB 411 GCGGTCGCTGCGAGCTTCATTGCGTAGTAAGTAACCTCGCAACTGTAGCGGCGC 470
QY 241 GGCGAAGCGGTAAACCCCAACTTCGAATGTGACCTCGGATCAGTAAGATACCG 300
DB 471 GGCGAAGCGGTAAACCCCAACTTCGAATGTGACCTCGGATCAGTAAGATACCG 530
QY 301 CTGAACCTTAA 310
DB 531 CTGAACCTTAA 540

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KEYWORDS     Fusarium sp. NRRL 26427
SOURCE       Fusarium sp. NRRL 26427
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE    1 (bases 1 to 540)
AUTHORS      O'Donnell, K., Nirenberg, H.I., Aoki, T. and Cigelink, E.
TITLE        A multigene phylogeny of the Gibberella fujikuroi species complex:
            detection of additional phylogenetically distinct species
JOURNAL      Mycoscience 41, 61-78 (2000)
REFERENCE    2 (bases 1 to 540)
AUTHORS      O'Donnell, K.
TITLE        Direct Submission
JOURNAL      Submitted (10-JUN-1999) Microbial Properties, NCAR-ARL, 1815
            University St., Peoria, IL 61604, USA
FEATURES     source
            1..540
            /organism="Fusarium sp. NRRL 26427"
            /mol_type="genomic DNA"
            /strain="NRRL26427"
            /db_xref="taxon:100620"
            <1..32
            /product="18S ribosomal RNA"
            33..178
            /product="internal transcribed spacer 1"
            179..337
            /product="5.8S ribosomal RNA"
            338..502
            /product="internal transcribed spacer 2"
            503..>540
            /product="28S ribosomal RNA"

ORIGIN
Query Match      97.9%; Score 303.6; DB 8; Length 540;
Best Local Similarity 98.7%; Pred. No. 1.3e-83;
Matches 306; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAACGACA 60
DB 231 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAACGACA 290
QY 61 TTGGCGCCGCGCATATTCGCGGGCATGCTGTTGAGGTCATTGCAACCTCAAGCC 120
DB 291 TTGGCGCCGCGCATATTCGCGGGCATGCTGTTGAGGTCATTGCAACCTCAAGCC 350
QY 121 CCGGGTTGGTGGGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB 351 CCGGGTTGGTGGGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 410
QY 181 GCGGTCGCTGCGAGCTTCATTGCGTAGTAAGTAACCTCGCAACTGTAGCGGCGC 240
DB 411 GCGGTCGCTGCGAGCTTCATTGCGTAGTAAGTAACCTCGCAACTGTAGCGGCGC 470
QY 241 GGCGAAGCGGTAAACCCCAACTTCGAATGTGACCTCGGATCAGTAAGATACCG 300
DB 471 GGCGAAGCGGTAAACCCCAACTTCGAATGTGACCTCGGATCAGTAAGATACCG 530
QY 301 CTGAACCTTAA 310
DB 531 CTGAACCTTAA 540

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Search completed: October 1, 2004, 05:16:59
 Job time : 2528.41 secs

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RESULT 15
LOCUS    AF158302
DEFINITION
Fusarium sp. NRRL26427 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.
ACCESSION
AF158302
VERSION  AF158302.1  GI:7106205

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using BW model

Run on: October 1, 2004, 03:09:43 : Search time 102.159 Seconds
(without alignments)
1683.989 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aaatgcataatgaatgtga.....sgaataccgcgtgaactaa 310

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/6C_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	4	US-09-423-233-7
2	306.8	99.0	2293	3	US-09-645-073-1
3	249.8	80.6	561	1	US-08-905-314A-24
4	240.2	77.5	319	4	US-09-423-233-6
5	231	74.5	583	1	US-08-652-127C-8
6	225.2	72.6	531	1	US-08-652-127C-7
7	224.2	72.3	581	1	US-08-652-127C-6
8	197.8	63.8	594	1	US-08-652-127C-5
9	187.6	60.5	546	1	US-08-887-480-96
10	187.6	60.5	546	1	US-08-905-314A-22
11	186.6	60.2	504	1	US-08-887-480-82
12	186.6	60.2	504	1	US-08-905-314A-19
13	186.6	60.2	504	1	US-08-722-187-82
14	186.6	60.2	504	1	PCT-US95-04712-82
15	185	59.7	611	3	US-08-986-727-4
16	183.2	59.1	545	1	US-08-887-480-84
17	183.2	59.1	545	1	US-08-905-314A-21
18	180.4	58.2	503	1	US-08-887-480-83
19	180.4	58.2	503	1	US-08-905-314A-20
20	180.4	58.2	503	1	US-08-722-187-83
21	180.4	58.2	503	5	PCT-US95-04712-83
22	174.2	56.2	504	4	US-09-481-293-32
23	166.2	53.6	545	4	US-08-722-187-85
24	166.2	53.6	545	5	PCT-US95-04712-85
25	163.8	52.8	608	3	US-08-986-727-3
26	139	44.8	605	3	US-08-986-727-1
27	136	43.9	365	4	US-09-423-233-3

28	136	43.9	587	1	US-08-742-023-7	Sequence 7, Appli
29	136	43.9	587	3	US-08-968-505-7	Sequence 7, Appli
30	136	43.9	617	3	US-08-968-727-2	Sequence 2, Appli
31	131.4	42.4	364	4	US-09-423-233-2	Sequence 2, Appli
32	126.6	40.8	556	3	US-09-037-9908-7	Sequence 7, Appli
33	125.2	40.4	627	1	US-08-233-608-47	Sequence 47, Appli
34	125.2	40.4	627	1	US-08-887-480-47	Sequence 47, Appli
35	125.2	40.4	627	2	US-08-722-187-47	Sequence 47, Appli
36	125.2	40.4	627	5	PCT-US95-04712-47	Sequence 47, Appli
37	125	40.3	309	4	US-09-423-233-28	Sequence 28, Appli
38	124.4	40.1	536	4	US-09-517-790-5	Sequence 5, Appli
39	124.4	40.1	556	1	US-08-887-480-85	Sequence 85, Appli
40	124.4	40.1	556	1	US-08-905-314A-23	Sequence 23, Appli
41	124.4	40.1	580	3	US-08-742-023-6	Sequence 6, Appli
42	124.4	40.1	580	3	US-08-968-505-6	Sequence 6, Appli
43	123.6	39.9	626	1	US-08-233-608-3	Sequence 3, Appli
44	123.6	39.9	626	1	US-08-887-480-3	Sequence 3, Appli
45	123.6	39.9	626	2	US-08-722-187-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
NUMBER OF SEQUENCE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 8.5e-93;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAATGCATAATGAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
DB      1 AAATGCATAATGAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
QY      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCATTTCAACCTCAAGCC 120
DB      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCATTTCAACCTCAAGCC 120
QY      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCATTTCAACCTCAAGCC 120
DB      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCATTTCAACCTCAAGCC 120
QY      121 CCGCGGTTTGATGTTGGGATTCGCGAAGCCCTTCCGCGAAGCCGCCGCAAAATCTAGTG 180
DB      121 CCGCGGTTTGATGTTGGGATTCGCGAAGCCCTTCCGCGAAGCCGCCGCAAAATCTAGTG 180
QY      121 CCGCGGTTTGATGTTGGGATTCGCGAAGCCCTTCCGCGAAGCCGCCGCAAAATCTAGTG 180
DB      121 CCGCGGTTTGATGTTGGGATTCGCGAAGCCCTTCCGCGAAGCCGCCGCAAAATCTAGTG 180
QY      181 GCGGTCGCGTCAATTCGAGTAGTAAACCTTCGCAATCGGTAACCGGCGC 240
DB      181 GCGGTCGCGTCAATTCGAGTAGTAAACCTTCGCAATCGGTAACCGGCGC 240
QY      241 GCGCAACCGTAAACCCCAACTTCGAAATGTTGACCTCGATCAGTAAATACCGG 300
DB      241 GCGCAACCGTAAACCCCAACTTCGAAATGTTGACCTCGATCAGTAAATACCGG 300
QY      301 CTGAACCTAA 310
DB      301 CTGAACCTAA 310

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; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titerers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

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Query Match          99.0%; Score 306.8; DB 3; Length 2293;
Best Local Similarity 99.4%; Pred. No. 2.2e-91;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCGAATCTTTGAACGACA 60
DB 1972 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCGAATCTTTGAACGACA 2031
QY 61 TTGGCCCCCGGCAATGATTCGCGGGGCAATGCTGTTGCAAGCGTCAATCCCTGAAGCC 120
DB 2032 TTGGCCCCCGGCAATGATTCGCGGGGCAATGCTGTTGCAAGCGTCAATCCCTGAAGCC 2091
QY 121 CCCGGGTTTGGTGTGGGGGATTCGCGCAAGCCCTTGCGGCAAGCGGCGCGAATCTAGTG 180
DB 2092 CCCGGGTTTGGTGTGGGGGATTCGCGCAAGCCCTTGCGGCAAGCGGCGCGAATCTAGTG 2151
QY 181 GCGGTCCTGCTGCAGCTTCATTCAGTAGTAAACCCCTCGCAATGCTGTAAGCGCGCG 240
DB 2152 GCGGTCCTGCTGCAGCTTCATTCAGTAGTAAACCCCTCGCAATGCTGTAAGCGCGCG 2211
QY 241 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCGG 300
DB 2212 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCGG 2271
QY 301 CTGAACCTTAA 310
DB 2272 CTGAACCTTAA 2281

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RESULT 3
US-08-905-314A-24
; Sequence 24, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..181
; OTHER INFORMATION: /note="ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182..338
; OTHER INFORMATION: /note="5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 339..504
; OTHER INFORMATION: /note="ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 505..561
; OTHER INFORMATION: /note="5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

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Query Match          80.6%; Score 249.8; DB 1; Length 561;
Best Local Similarity 91.6%; Pred. No. 7.8e-73;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

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QY 1 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCGAATCTTTGAACGACA 60
DB 232 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCGAATCTTTGAACGACA 291
QY 61 TTGGCCCCCGGCAATGATTCGCGGGGCAATGCTGTTGCAAGCGTCAATCCCTGAAGCC 120
DB 292 TTGGCCCCCGGCAATGATTCGCGGGGCAATGCTGTTGCAAGCGTCAATCCCTGAAGCC 351
QY 121 CCCGGGTTTGGTGTGGGGGATTCGCGCAAGCCCTTGCGGCAAGCGGCGAATCTAGT 179
DB 352 CCCGGGTTTGGTGTGGGGGATTCGCGCAAGCCCTTGCGGCAAGCGGCGAATCTAGT 411
QY 180 GCGGTCCTGCTGCAGCTTCATTCAGTAGTAAACCCCTCGCAATGCTGTAAGCGCGG 239
DB 412 GCGGTCCTGCTGCAGCTTCATTCAGTAGTAAACCCCTCGCAATGCTGTAAGCGCGG 471
QY 240 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCG 299
DB 472 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCG 530
QY 300 GCTGAACCTTAA 310
DB 531 GCTGAACCTTAA 541

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RESULT 4
US-09-423-233-6
; Sequence 6, Application US/09423233

```

Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-09-423-233-6

Query Match 77.5%; Score 240.2; DB 4; Length 319;
Best Local Similarity 87.4%; Pred. No. 9,1e-70;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 1 AAATGCCATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
DB 3 AAATGCCATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 62
QY 61 TTGGCCCGCCAGTATTCGCGGCGCATGCTGTTCGAGCGTCATTTCACCCCTCAAGCC 120
DB 63 TTGGCCCGCCAGTATTCGCGGCGCATGCTGTTCGAGCGTCATTTCACCCCTCAAGCC 122
QY 121 CCCGGTTTGGTGTGGGATTCGGCAAGCCCTTGGCGC-----AAGCCGCGCCCGAAA 173
DB 123 CCCGGCTTGGGATTCGGGATTCGGGAGAGCCCTTGGCGGCAACGCCCGCCCAAA 182
QY 174 TCTAGTGGCGGTCTTCGTCGACGCTTCCATTTGGTATGTAATAACCTTCGCACTGGTAC 233
DB 183 TACAGTGGCGGTCTTCGTCGACGCTTCCATTTGGTATGTAATAACCTTCGCACTGGTAC 242
QY 234 GCGGCGCGCCAGCGCTTAAACCCCACTTCTGAATGTTGACCTCGGATCAGGTAGA 293
DB 243 GCGGCGCGCCAGCGCTTAAACCCCACTTCTGAATGTTGACCTCGGATCAGGTAGA 302
QY 294 ATACCCGCTGAACCTTAA 310
DB 303 ATACCCGCTGAACCTTAA 319

RESULT 5
US-08-652-127C-8
Sequence 8, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 583
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-8

Query Match 74.5%; Score 231; DB 1; Length 583;
Best Local Similarity 90.4%; Pred. No. 1,3e-66;
Matches 281; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

QY 1 AAATGCCATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
DB 257 AAATGCCATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 316
QY 61 TTGGCCCGCCAGTATTCGCGGCGCATGCTGTTCGAGCGTCATTTCACCCCTCAAGCC 120
DB 317 TTGGCCCGCCAGTATTCGCGGCGCATGCTGTTCGAGCGTCATTTCACCCCTCAAGCC 376
QY 121 CCCGGTTTGGTGTGGGATTCGGCAAGCCCTTGGCGCAGCCCGCGAAATCTAGTG 180
DB 377 CCCGGCTTGGTGTGGGATTCGGGAGAGCCCTTGGCGCAGCCCGCGAAATCTAGTG 435
QY 181 GCGGTCTCGTCGACGCTTCCATTCGTAAGTAAACCTTCGCACTGGTACCGCGCGC 240
DB 436 GCGGTCTCGTCGTAAGTATTCGTAAGTAAACCTTCGCACTGGTACCGCGCGC 492
QY 241 GCGCAAGCCGTTAAACCCCACTTCTGAATG-TTGACTTGGATCGTAAGTAATCCC 299
DB 493 GCGCAAGCCGTTAAACCCCACTTCTGAATG-TTGACTTGGATCGTAAGTAATCCC 552
QY 300 GCTGAACCTTAA 310
DB 553 GCTGAACCTTAA 563

RESULT 6
US-08-652-127C-7
Sequence 7, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-7

Query Match 72.6%; Score 225.2; DB 1; Length 531;
Best Local Similarity 88.8%; Pred. No. 9.9e-65;
Matches 277; Conservative 0; Mismatches 30; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAACGACA 60
DB 203 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAACGACA 262
QY 61 TTGCGCCCGCGCATATTCCTGGCGGCGATGCTGTTCAGCGCTCATTTCAACCTCAAGCC 120
DB 263 TTGCGCCCGCGCATATTCCTGGCGGCGATGCTGTTCAGCGCTCATTTCAACCTCAAGCC 322
QY 121 CCCGGGTTGGTGGTGGGATCGGCAAG-CCCTTCGGCGCAAGCGGCGCGAAATCTAGT 179
DB 323 CCCGGGTTGGTGGTGGGATCGGCAAG-CCCTTCGGCGCAAGCGGCGCGAAATCTAGT 382
QY 180 GCGGCTCTGCTGCAAGCTTCATTCGCTAGTATGTAACCCCTCGCACTGGTACGCGCG 239
DB 383 GCGGCTCTGCTGTAAGCTTCCTCTGCGTATGACACCTGCG--ACTGGAACAAGCG 439
QY 240 CGGCGAAGCGCTTAACCCCACTTCTG-AATGTTGACCTCGATCAGTAGAATACC 298
DB 440 CGGCGAAGCGCTTAACCCCACTTCTGAAAGGTTGACCTCGATCAGTAGAATACC 499
QY 299 CGCTGAACCTTAA 310
DB 500 CGCTGAACCTTAA 511

RESULT 7

US-08-652-127C-6

Sequence 6, Application US/08652127C

Patent No. 5792611

GENERAL INFORMATION:

APPLICANT: Richard C. Hamelin

TITLE OF INVENTION: DETECTION OF PLANT

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: George A. Seaby

STREET: 880 Wellington Street, Suite 708

CITY: Ottawa

COUNTRY: Canada

ZIP: K1R 6K7

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,127C

FILING DATE: May 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: George A. Seaby

REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898

TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 232-5815

TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 581

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6

Query Match 72.3%; Score 224.2; DB 1; Length 581;
Best Local Similarity 88.5%; Pred. No. 2.2e-64;
Matches 276; Conservative 1; Mismatches 30; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAACGACA 60
DB 253 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTGAATCATCATCTTTGAACGACA 312
QY 61 TTGCGCCCGCGCATATTCCTGGCGGCGATGCTGTTCAGCGCTCATTTCAACCTCAAGCC 120
DB 313 TTGCGCCCGCGCATATTCCTGGCGGCGATGCTGTTCAGCGCTCATTTCAACCTCAAGCC 372
QY 121 CCCGGGTTGGTGGTGGGATCGGCAAG-CCCTTCGGCGCAAGCGGCGCGAAATCTAGT 179
DB 373 CCCGGGTTGGTGGTGGGATCGGCAAG-CCCTTCGGCGCAAGCGGCGCGAAATCTAGT 432
QY 180 GCGGCTCTGCTGCAAGCTTCATTCGCTAGTATGTAACCCCTCGCACTGGTACGCGCG 239
DB 433 GCGGCTCTGCTGTAAGCTTCCTCTGCGTATGACACCTGCG--ACTGGAACAAGCG 489
QY 240 CGGCGAAGCGCTTAACCCCACTTCTG-AATGTTGACCTCGATCAGTAGAATACC 298
DB 490 CGGCGAAGCGCTTAACCCCACTTCTGAAAGGTTGACCTCGATCAGTAGAATACC 549
QY 299 CGCTGAACCTTAA 310
DB 550 CGCTGAACCTTAA 561

RESULT 8

US-08-652-127C-5

Sequence 5, Application US/08652127C

Patent No. 5792611

GENERAL INFORMATION:

APPLICANT: Richard C. Hamelin

TITLE OF INVENTION: DETECTION OF PLANT

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: George A. Seaby

STREET: 880 Wellington Street, Suite 708

CITY: Ottawa

COUNTRY: Canada

ZIP: K1R 6K7

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,127C

FILING DATE: May 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: George A. Seaby

REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898

TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 232-5815

TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 594

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-652-127C-5

Query Match 63.8%; Score 197.8; DB 1; Length 594;
 Best Local Similarity 85.0%; Pred. No. 1.1e-55;
 Matches 211; Conservative 0; Mismatches 37; Indels 11; Gaps 4;

QY 1 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGCAATCTTTTGAACGACA 60
 DB 258 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGCAATCTTTTGAACGACA 317
 QY 61 TTGCCCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 120
 DB 318 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCA 377
 QY 121 CC-----CGGATTGTTGGGATCGGCAAG-----CCCTTCGGGCAAGCCGCCCGCA 172
 DB 378 CTTTGGGAGAGCTTTGGTTGGGATCGGCGGCGTCTCCGGGTCGGCGCTCCCGCA 437
 QY 173 ATCTAGTGGCGGCTCTGCTGAGCTTCCATTGCGTAGTAAACCCCTCGCACTGTGA 232
 DB 438 ATCTAGTGGCGGCTCTGCTGAGCTTCCATTGCGTAGTAAACCCCTCGCTGAGT 495
 QY 233 CGCGCGCGGCGCCAGCCGTTAAACCCCACTTCTGAAT-GTTGACCTCGGATCGGTAG 291
 DB 496 CTCGGGTGGCGGCGCCAGTAAACCCCACTTCTTCTGTTGACCTCGAATCGGTAG 555
 QY 292 GAATACCGGCTGAACCTTAA 310
 DB 556 GACTACCGGCTGAACCTTAA 574

RESULT 9
 US-08-887-480-96
 ; Sequence 96, Application US/08887480
 ; Patent No. 5814453
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J
 ; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
 ; TITLE OF INVENTION: Polymerase Chain Reaction
 ; NUMBER OF SEQUENCES: 96
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5814453artis Corporation
 ; STREET: 520 White Plains Road
 ; CITY: Tarrytown
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10591
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,480
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/722,187
 ; FILING DATE: 15-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38, 241
 ; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8587
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 96:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 546 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; STRAIN: *Fusarium poae*

INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
 INDIVIDUAL ISOLATE: sequence)
 IMMEDIATE SOURCE:
 CLONE: PCRpoae1427(1-2), PCRpoae1534(2-2), and
 CLONE: PCRpoae1756(3-1)
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..310
 OTHER INFORMATION: /note= "3' end of small subunit
 OTHER INFORMATION: rRNA gene"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 31..180
 OTHER INFORMATION: /note= "ITS 1"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 338..489
 OTHER INFORMATION: /note= "ITS 2"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 490..546
 OTHER INFORMATION: /note= "5' end of large subunit
 OTHER INFORMATION: rRNA gene"
 US-08-887-480-96

Query Match 60.5%; Score 187.6; DB 1; Length 546;
 Best Local Similarity 84.5%; Pred. No. 2.5e-52;
 Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

QY 1 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGCAATCTTTTGAACGACA 60
 DB 231 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGCAATCTTTTGAACGACA 290
 QY 61 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 120
 DB 291 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 350
 QY 121 CGCGGATTGGTGTGGGAGATCGGCAAGCCCTTCGGGCAAGCCGCCGAAATCTAGTG 180
 DB 351 C---AGCTTGGTGTGG-----ATCTGTGCAACACAGTCCCAATTTGATTG 398
 QY 181 GCGGTCTGCTGAGCTTCCATTGCGTAGTAAACCCCTCGCACTGTGACGGCGC 240
 DB 399 GCGGTCAAG-TGAGCTTCCATTGCGTAGTAAACCCCTCGCACTGTGACGGCGC 457
 QY 241 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGGATCGAGTGAATACCCG 300
 DB 458 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGGATCGAGTGAATACCCG 516
 QY 301 CTGAACCTTAA 310
 DB 517 CTGAACCTTAA 526

RESULT 10
 US-08-905-314A-22
 ; Sequence 22, Application US/08905314A
 ; Patent No. 5827695
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 ; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5827695artis Corporation Patent Department
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA

ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: pCRFpoae1427(1-2), pCRFpoae1534(2-2), and
pCRFpoae1756(3-1)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-22

Query Match 60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 2.5e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATGAACTTTGAAGCAGC 60
DB 231 AATGCGATAGTATGTAATGCAAAATTCAGTGAATGAACTTTGAAGCAGC 290
QY 61 TTGGCCCGCCAGATTCGCGGGGCGATGCTGTGAGGCGTATTCACCTCAAGCC 120
DB 291 TTGGCCCGCCAGATTCGCGGGGCGATGCTGTGAGGCGTATTCACCTCAAGCC 350
QY 121 CCGGGGTTTGGTGTGGGGAATCGGCAAGCCCTTGCGGCAAGCCGCCGGAATCTAGTG 180
DB 351 C---AGCTTGATGTGGG-----ATCTGTGTGCAAAACACAGTCCCAATTTGATTG 398
QY 181 GCGGTCTCGTCGAGCTTCATTCGTAAGTAAGTAAACCTCGCAACTGGTACCGCGCC 240

DB 399 GCGGTACG-TGAGCTTCCATAGCGTAAATTACACATCGTACTGTAACTGCG 457
QY 241 GGCCAGCCGTTAAACCCCACTTGTGATGTTGACTCGATCAGTAGAATACCG 300
DB 458 GGCAGCCGTTAA-CCCACTTGTGATGTTGACTCGATCAGTAGAATACCG 516
QY 301 CTGAACCTTA 310
DB 517 CTGAACCTTA 526

RESULT 11
US-08-480-82
Sequence 82, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 581453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/BCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 319..472

OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-480-82

Query Match 60.2%; Score 186.6; DB 1; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AATCGATAGTAAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 60
DB 212 AATCGATAGTAAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 271
QY 61 TTGCGCCGCCAGTATTTCTGGCGGGGAGTCCCTGTTGAGCGTCAATTCACCCGCAAGCC 120
DB 272 TTGCGCCGCCAGTATTTCTGGCGGGGAGTCCCTGTTGAGCGTCAATTCACCCGCAAGCC 331
QY 121 CCCGGGTTGGTGGTGGGATGGGCAAGCCCTTGGCGCAAGCCGCCCGGAATCTAGTG 180
DB 332 C---AGCTTGTTGGG-----AGCTGAGTCTGCTGCTGCTCCCAATACATTG 380
QY 181 GCGGTCTGCTGACCTTCATTTGCGTAGTAAACCCCTGCAACTGTAGCGGCGC 240
DB 381 GCGGTCTGCTGACCTTCATTTGCGTAGTAAACCCCTGCAACTGTAGCGGCGC 440
QY 241 GGGCAAGCGGTTAAACCCCAACTTCTGTAATGTTGACCTCGATGAGTAGGAATACCG 300
DB 441 GGGCAAGCGGTTAAACCCCAACTTCTGTAATGTTGACCTCGATGAGTAGGAATACCG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

RESULT 12

US-08-905-314A-19

Sequence 19, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weig, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8589
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 319..472
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match 60.2%; Score 186.6; DB 1; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AATCGATAGTAAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 60
DB 212 AATCGATAGTAAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 271
QY 61 TTGCGCCGCCAGTATTTCTGGCGGGGAGTCCCTGTTGAGCGTCAATTCACCCGCAAGCC 120
DB 272 TTGCGCCGCCAGTATTTCTGGCGGGGAGTCCCTGTTGAGCGTCAATTCACCCGCAAGCC 331
QY 121 CCCGGGTTGGTGGTGGGATGGGCAAGCCCTTGGCGCAAGCCGCCCGGAATCTAGTG 180
DB 332 C---AGCTTGTTGGG-----AGCTGAGTCTGCTGCTGCTCCCAATACATTG 380
QY 181 GCGGTCTGCTGACCTTCATTTGCGTAGTAAACCCCTGCAACTGTAGCGGCGC 240
DB 381 GCGGTCTGCTGACCTTCATTTGCGTAGTAAACCCCTGCAACTGTAGCGGCGC 440
QY 241 GGGCAAGCGGTTAAACCCCAACTTCTGTAATGTTGACCTCGATGAGTAGGAATACCG 300
DB 441 GGGCAAGCGGTTAAACCCCAACTTCTGTAATGTTGACCTCGATGAGTAGGAATACCG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

RESULT 13

US-08-722-187-82

Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive

CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
US-08-722-187-82

Query Match 60.2%; Score 186.6; DB 2; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;
QY 1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 212 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 271
QY 61 TTGGCCCGCCAGATATTCGCGGGCAGTCCCTGTTGAGGCTCATTTCAACCTCAAGCC 120
DB 272 TTGGCCCGCCAGATATTCGCGGGCAGTCCCTGTTGAGGCTCATTTCAACCTCAAGCC 331
QY 121 CCCGGGTTTGTGTGGGGATCGCAAGCCCTTGCGGCAAGCCCGGCAAAATCTAGTG 180
DB 332 C---AGCTTGGTGTGGG-----AGCTGCACTCTGCTGCACCTCCCAATAATCATTTG 380
QY 181 GCGGTCGCTGCGAGCTTCCATTGCGTAGTAATGTAACCTTCGCACTGGTACGCGCGC 240
DB 381 GCGGTCGCTGCGAGCTTCCATTGCGTAGTAATGTAACCTTCGCACTGGTACGCGCGC 440
QY 241 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTGCGATCGAGTAGAATACCGG 300
DB 441 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTGCGATCGAGTAGAATACCGG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

RESULT 14
PCT-US95-04712-82
Sequence 82, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M

APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
PCT-US95-04712-82

Query Match 60.2%; Score 186.6; DB 5; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;
QY 1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 212 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 271
QY 61 TTGGCCCGCCAGATATTCGCGGGCAGTCCCTGTTGAGGCTCATTTCAACCTCAAGCC 120
DB 272 TTGGCCCGCCAGATATTCGCGGGCAGTCCCTGTTGAGGCTCATTTCAACCTCAAGCC 331
QY 121 CCCGGGTTTGTGTGGGGATCGCAAGCCCTTGCGGCAAGCCCGGCAAAATCTAGTG 180
DB 332 C---AGCTTGGTGTGGG-----AGCTGCACTCTGCTGCACCTCCCAATAATCATTTG 380
QY 181 GCGGTCGCTGCGAGCTTCCATTGCGTAGTAATGTAACCTTCGCACTGGTACGCGCGC 240
DB 381 GCGGTCGCTGCGAGCTTCCATTGCGTAGTAATGTAACCTTCGCACTGGTACGCGCGC 440
QY 241 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTGCGATCGAGTAGAATACCGG 300
DB 441 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTGCGATCGAGTAGAATACCGG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

Search completed: October 1, 2004, 08:05:40
Job time : 103.159 secs

RESULT 15

US-08-986-727-4

; Sequence 4, Application US/08986727

; Patent No. 6080543

; GENERAL INFORMATION:

; APPLICANT: ENGEL, Stacia R.

; APPLICANT: DESCENZO, Richard A.

; APPLICANT: IRELAN, Nancy A.

; TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/986,727

; FILING DATE: 08-DEC-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ekstrom, Richard C.

; REGISTRATION NUMBER: 37,027

; REFERENCE/DOCKET NUMBER: 009773-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 611 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-986-727-4

Query Match 59.7%; Score 185; DB 3; Length 611;
Best Local Similarity 83.1%; Pred. No. 1.9e-51;

Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;

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Oy 1 AAATCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
Db 283 AAATCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 342
Oy 61 TTGCGCCCGCCAGTAATTCGTGGCGGCATGCTGTTGAGCGTCATTTCAACCTCAAGCC 120
Db 343 TTGCGCCCTGTGTGTAATTCGGAGGGGCGATGCTGTTGAGCGTCATTTCAACCTCAAG-- 400
Oy 121 CCCGGGTTTGGTGTGGGATGCGCAAGCCCTTGGGCGAAGCCGCCGAATTAATG 180
Db 401 -CTGGCTTGTGATGGGCACTGCTCCCGCCCGGAGAGAGCCCTGAATTCAGTG 459
Oy 181 GCGGCTCGCTGACCTTCATTCGTAAGTAATAACCTCGCAACTG--GTAGCGGCG 238
Db 460 GCGAGCTGCG--CAGGACCCCGAGCGCACTGTAATTAACCTTCGCTCCGGAGGCGCTTGGC 517
Oy 239 GCGGCAAGCCGTTAAACCCCACTTCGTAATG--TTGACCTCGGATCAGGTAGGAATAC 297
Db 518 GGTGCGCTGCGGTAAACCCCACTTCGTAATGTTGACCTCGGATCAGGTAGGAATAC 577
Oy 298 CCGCTGAACCTTA 310
Db 578 CCGCTGAACCTTA 590
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1 AAATGGATAAGTAATGTGAATGCAAAATTCAGTGAATCATCGAATCTTGAACGCACA 60

Db 1 AATGCGATAGTATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60
Qy 61 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 120
Db 61 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 120
Qy 121 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 180
Db 121 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 180
Qy 181 GCGGTCGCGCGAGCTTCATTCAGTATGTAATTAACCTTCGCACTGGTAAGCGCGCG 240
Db 181 GCGGTCGCGCGAGCTTCATTCAGTATGTAATTAACCTTCGCACTGGTAAGCGCGCG 240
Qy 241 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAAATCCCG 300
Db 241 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAAATCCCG 300
Qy 301 CTGAACCTTA 310
Db 301 CTGAACCTTA 310

RESULT 2

US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match 97.7%; Score 302.8; DB 10; Length 534;
Best Local Similarity 99.3%; Pred. No. 3.5e-100;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATGCGATAGTATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60
Db 229 AATGCGATAGTATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 288
Qy 61 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 120
Db 289 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 348
Qy 121 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 180
Db 349 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 408
Qy 181 GCGGTCGCGCGAGCTTCATTCAGTATGTAATTAACCTTCGCACTGGTAAGCGCGCG 240
Db 409 GCGGTCGCGCGAGCTTCATTCAGTATGTAATTAACCTTCGCACTGGTAAGCGCGCG 468
Qy 241 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAAATCCCG 300
Db 469 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAAATCCCG 528
Qy 301 CTGAAC 306
Db 529 CTGAAC 534

RESULT 3

US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine U.
; APPLICANT: Reiss, Etrol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046.955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423.233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045.400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6

Query Match 77.5%; Score 240.2; DB 15; Length 319;
Best Local Similarity 87.4%; Pred. No. 2.6e-77;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

Qy 1 AATGCGATAGTATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60
Db 3 AATGCGATAGTATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 62
Qy 61 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 120
Db 63 TTGGCCCGCCAGTATTCGCGCGGCGATGCTGTTCAGAGGCTGATTTCAACCTCAAGCC 122
Qy 121 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 173
Db 123 CCGGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCCGGCCGGAATCTAGTG 182
Qy 174 TCTAGTGGCGGTCTGCTCGAGCTTTCATTCGCTAGTATTAACCTTCGCACTGGTAAG 233
Db 183 TCTAGTGGCGGTCTGCTCGAGCTTTCATTCGCTAGTATTAACCTTCGCACTGGTAAG 242
Qy 234 GCGGCGCGGCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAGA 293
Db 243 GCGGCGCGGCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTCGATCAGTATGAGA 302
Qy 294 ATACCCGCTGAACCTTA 310
Db 303 ATACCCGCTGAACCTTA 319

RESULT 4

US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0

SEQ ID NO 5
 LENGTH: 522
 TYPE: DNA
 ORGANISM: Fusarium subglutinans
 US-09-961-755A-5

Query Match 62.7%; Score 194.4; DB 10; Length 522;
 Best Local Similarity 84.3%; Pred. No. 2.1e-60;
 Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
 DB 229 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288
 QY 61 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 120
 DB 289 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 348
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180
 DB 349 C-----AGCTGGGTGGGATCGGCAAGTCGAGTCAATGCGCTTCCCAATTGATG 398
 QY 181 GCGGTCTGCTGCAGCTTCATTCGCTGTAAGTAAACCTTCGCACTGTGACGGCGC 240
 DB 399 GCGGTCAAG-TCGAGCTTCATGAGGTAGTAAACCTTCGTAATCTGTCGC 457
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 300
 DB 458 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 516
 QY 301 CTGAAC 306
 DB 517 CTGAAC 522

RESULT 5
 US-09-961-755A-8
 ; Sequence 8, Application US/09961755A
 ; Publication No. US20030113722A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, Jim
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
 ; FILE REFERENCE: 60055
 ; CURRENT APPLICATION NUMBER: US/09/961,755A
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 522
 ; TYPE: DNA
 ; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
 US-09-961-755A-8

Query Match 62.7%; Score 194.4; DB 10; Length 522;
 Best Local Similarity 84.3%; Pred. No. 2.1e-60;
 Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
 DB 229 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288
 QY 61 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 120
 DB 289 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 348
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180
 DB 349 C-----AGCTGGGTGGGATCGGCAAGTCGAGTCAATGCGCTTCCCAATTGATG 398
 QY 181 GCGGTCTGCTGCAGCTTCATTCGCTGTAAGTAAACCTTCGCACTGTGACGGCGC 240

DB 399 GCGGTCAAG-TCGAGCTTCATGAGGTAGTAAACCTTCGTAATCTGTCGC 457
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 300
 DB 458 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 516
 QY 301 CTGAAC 306
 DB 517 CTGAAC 522

RESULT 6
 US-09-961-755A-6
 ; Sequence 6, Application US/09961755A
 ; Publication No. US20030113722A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, Jim
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
 ; FILE REFERENCE: 60055
 ; CURRENT APPLICATION NUMBER: US/09/961,755A
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Gibberella zeae
 US-09-961-755A-6

Query Match 57.8%; Score 179.2; DB 10; Length 521;
 Best Local Similarity 83.3%; Pred. No. 7.9e-55;
 Matches 255; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

QY 1 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
 DB 229 AAATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288
 QY 61 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 120
 DB 289 TTGCGCCGCCGCAATATTCGCGGCGCATGCTGTTGAGCGTCATTTCACCTCAAGCC 348
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180
 DB 349 C---AGCTGGGTGGG-----AGCTGAGTCTGCTGCACTCCCAATAATG 397
 QY 181 GCGGTCTGCTGCAGCTTCATTCGCTGTAAGTAAACCTTCGCACTGTGACGGCGC 240
 DB 398 GCGGTCAAG-TCGAGCTTCATGAGGTAGTAAATCTGTAATCTGTCGC 456
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 300
 DB 457 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGTAAATACCG 515
 QY 301 CTGAAC 306
 DB 516 CTGAAC 521

RESULT 7
 US-10-121-740-2
 ; Sequence 2, Application US/10121740
 ; Publication No. US20030186425A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strobel, Gary
 ; APPLICANT: Manaker, Denise
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
 ; FILE REFERENCE: AQ 2019.40
 ; CURRENT APPLICATION NUMBER: US/10/121,740
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/283,902

PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 652
TYPE: DNA
ORGANISM: Muscudor albus
US-10-121-740-2

Query Match 43.9%; Score 136.2; DB 15; Length 652;
Best Local Similarity 71.7%; Pred. No. 5.3e-39;
Matches 223; Conservative 0; Mismatches 78; Indels 10; Gaps 3;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB AAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 388
QY 61 TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 120
DB TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 448
QY 121 CCCGGGTTTGATGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB CTGTGCTTAGCGTTGGGAGCC-----TACGGCACTGCGCGTAGCTCCCTAAAGTATG 503
QY 181 GCGGCTCGCTGAGCTTCATTCAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 239
DB GCGGAGTGGGTTTC---TCACTCTAGGCGTGAATGTAATGTAATGTAATGTAATGTTG 559
QY 240 CGGCGAAGCGGTTAAACCCCACTTGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 259
DB CGGCGGCTCGCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 619
QY 300 GCTGAACCTTAA 310
DB 620 GCTGAACCTTAA 630

RESULT 8
US-10-623-432-2
Sequence 2, Application US/10623432
Publication No. US20040141955A1
GENERAL INFORMATION:
APPLICANT: Strobel, Gary
APPLICANT: Manke, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
FILE REFERENCE: NO 2019.40
CURRENT APPLICATION NUMBER: US/10/623,432
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US/10/121,740
PRIOR FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 652
TYPE: DNA
ORGANISM: Muscudor albus
US-10-623-432-2

Query Match 43.9%; Score 136.2; DB 17; Length 652;
Best Local Similarity 71.7%; Pred. No. 5.3e-39;
Matches 223; Conservative 0; Mismatches 78; Indels 10; Gaps 3;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB AAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 388

QY 61 TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 120
DB TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 448
QY 121 CCCGGGTTTGATGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB CTGTGCTTAGCGTTGGGAGCC-----TACGGCACTGCGCGTAGCTCCCTAAAGTATG 503
QY 181 GCGGCTCGCTGAGCTTCATTCAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 239
DB GCGGAGTGGGTTTC---TCACTCTAGGCGTGAATGTAATGTAATGTAATGTAATGTTG 559
QY 240 CGGCGAAGCGGTTAAACCCCACTTGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 259
DB CGGCGGCTCGCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 619
QY 300 GCTGAACCTTAA 310
DB 620 GCTGAACCTTAA 630

RESULT 9
US-10-046-955-3
Sequence 3, Application US/10046955
Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Etrol
APPLICANT: Ahdorovich, Lilianna
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 365
TYPE: DNA
ORGANISM: Aspergillus niger
US-10-046-955-3

Query Match 43.9%; Score 136; DB 15; Length 365;
Best Local Similarity 69.0%; Pred. No. 4.7e-39;
Matches 218; Conservative 0; Mismatches 90; Indels 8; Gaps 2;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB AAATGCGATAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 111
QY 61 TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 120
DB TTGGGCGGCGCAGATTTCTGGCGGCGATGCTGTTGCAAGGTCATTTCAACCTCAAGCC 169
QY 121 CCCGGGTTTGATGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB CAAGGTTTGATGTTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 229
QY 181 GCGGCTCGCTGAGCTTCATTCAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 234
DB GCGGCGCAGCGCTCGCTGAGCTTCAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 289

Qy 235 CGGCGCGCCGCAAGCGCTTAAACCCCACTTCTGATGTGACCTCGATCGATGAGGAA 294
Db 290 CGGCGCGCCGCGAGCTTTCACACATTTTTCAGAGTTGACCTCGATGAGGAGGA 349
Qy 295 TACCGCTGAACCTTAA 310
Db 350 TACCGCTGAACCTTAA 365

RESULT 10
US-10-046-955-2
Sequence 2, Application US/10046955
Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Errol
APPLICANT: Aidorevich, Liliiana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT FILING DATE: 2002-06-04
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 364
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-046-955-2

Query Match 42.4%; Score 131.4; DB 15; Length 364;
Best Local Similarity 68.1%; Pred. No. 2.3e-37;
Matches 213; Conservative 0; Mismatches 96; Indels 4; Gaps 2;

Qy 1 AATGCGATGAATGATGAAATGCAAAATTCAGTGAATCATCGAATCTTGAAGCACA 60
Db 52 AATGCGATGAATGATGAAATGCAAAATTCAGTGAATCATCGAATCTTGAAGCACA 111
Qy 61 TTGGCGCGCCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTTGAACCTCAAGCC 120
Db 112 TTGGCGCGCCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTTGAACCTCAAG 170
Qy 121 CCCGCGTTTGGTGTGGGATTCGCGCAAGCCCTTGGCGCAAGCCCGCCGAAATCTAGTG 180
Db 171 CACGCGTTGTGTGTGGGCGCCCGCTCTCCCGGGGAGCGGCGCCGAAAGCGAGC 230
Qy 181 GCGGCTCTGCGACGCTTCAATTCGGA--GTAATAAACCTTCGCAACTGGAACGCG 237
Db 221 GCGGACCGCGCTCCGCTCTCGAGCGTATGGGCGTTCACCTGCTGTAGGCGCCGCC 290
Qy 238 GCGGCGCAAGCGCTTAAACCCCACTTCTGAATGTGACCTCGATCGATGAGGAAATAC 297
Db 291 GCGGCGCAAGCGACCACTTATTTTCTTAAGGTGACCTCGATCGATGAGGAAATAC 350
Qy 298 CCGCTGAACCTTAA 310
Db 351 CCGCTGAACCTTAA 363

RESULT 11
US-10-046-955-28
Sequence 28, Application US/10046955
Publication No. US20030129600A1

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Errol
APPLICANT: Aidorevich, Liliiana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT FILING DATE: 2002-06-04
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 28
LENGTH: 309
TYPE: DNA
ORGANISM: Penicillium notatum
US-10-046-955-28

Query Match 40.3%; Score 125; DB 15; Length 309;
Best Local Similarity 69.0%; Pred. No. 4.7e-35;
Matches 216; Conservative 0; Mismatches 90; Indels 7; Gaps 3;

Qy 1 AATGCGATGAATGATGAAATGCAAAATTCAGTGAATCATCGAATCTTGAAGCACA 60
Db 1 AATGCGATGAATGATGAAATGCAAAATTCAGTGAATCATCGAATCTTGAAGCACA 59
Qy 61 TTGGCGCGCCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTTGAACCTCAAGCC 120
Db 60 TTGGCGCGCCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTTGAACCTCAAGCA 119
Qy 121 CCCGCGTTTGGTGTGGGATTCGCGCAAGCCCTTGGCGCAAGCCCGCCGAAATCTAGTG 180
Db 120 C--GCTTGTGTGTGGGCGCCCGCTCTCGATCCGCGGAGCGGCGCCGAAAGCGAGC 176
Qy 181 GCGGCTCTGCGACGCTTCAATTCGGAATGGAATAAACCTTCGCAACTGGAACGCG 237
Db 177 GCGGACCGCGGTCCGCTCTCGAGCGTATGGGCGTTCGACCGCTCTAGGCGCGGC 236
Qy 238 GCGGCGCAAGCGCTTAAACCCCACTTCTGAATGTGACCTCGATCGATGAGGAAATAC 297
Db 237 GCGGCGTTCGCGATCAACCAATTTTATTCAGGTGACCTCGATCGATGAGGAAATAC 296
Qy 298 CCGCTGAACCTTAA 310
Db 297 CCGCTGAACCTTAA 309

RESULT 12
US-09-766-173C-4
Sequence 4, Application US/09766173C
Patent No. US20020172945A1
GENERAL INFORMATION:
APPLICANT: Carroll, George C.
TITLE OF INVENTION: Materials and Methods for Detection of
FILE REFERENCE: Oregon 99-09
CURRENT FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: PCT/US01/01735
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4
 ; LENGTH: 641
 ; TYPE: DNA
 ; ORGANISM: Guignardia citricarpa
 US-09-766-173C-4

Query Match 40.1%; Score 124.6; DB 9; Length 641;
 Best Local Similarity 64.6%; Pred. No. 9.4e-35;
 Matches 201; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
 DB 318 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 377
 QY 61 TTGGGCCCCGCGAGTATCTGCGCGGCGATGCTGTTGAGGCGTATTCACCCCTCAAGCC 120
 DB 378 TTGGGCCCCCTGGCATTCGCGGGCGCATGCTGTTGAGGCGTATTCACCCCTCAAGCT 437
 QY 121 CCGGCGTTTGGTGTGGGAGTCGCGAAGCCCTTGCGCGAAGCCGCGC-CCGAATCTAGT 179
 DB 438 CTGCTTGTATTTGGGCGACGTCGCGGACGCGCTGGAAGACCTCGGCGACGCGCT 497
 QY 180 GGGGCTCTGCTGCACTTCCTAGTTCGTAAGTAAACCTTCGCACTGTGACGCGCG 239
 DB 498 CTCAGCTTCGAGCGTAGTAGTAATAATATCTGCTTTGAGAGAGGGGCGCGCTGCGCGCG 557
 QY 240 CCGGCAAGCGGTAAACCCCACTCTGATGTGACCTCGATCAGTGAAGTAATACC 239
 DB 558 GACAATGACCTTCGCTCACTATTTTCCAAAGGTGACCTCGATCAGTGAAGTAATACC 617
 QY 300 GCTGAACCTTAA 310
 DB 618 GCTGAACCTTAA 628

RESULT 13
 US-10-121-740-4
 ; Sequence 4, Application US/10121740
 ; Publication No. US20030186425A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strobel, Gary
 ; APPLICANT: Manke, Denise
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
 ; FILE REFERENCE: AQ 2019.40
 ; CURRENT APPLICATION NUMBER: US/10/121,740
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/283,902
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/363,072
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 650
 ; TYPE: DNA
 ; ORGANISM: Muscodor roseus
 US-10-121-740-4

Query Match 40.1%; Score 124.2; DB 15; Length 650;
 Best Local Similarity 71.4%; Pred. No. 1.3e-34;
 Matches 222; Conservative 0; Mismatches 78; Indels 11; Gaps 4;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60
 DB 329 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 388
 QY 61 TTGGGCCCCGCGAGTATCTGCGCGGCGATGCTGTTGAGGCGTATTCACCCCTCAAGCC 120
 DB 389 TTGGGCCCCATTCATTTCTAGTGGGCGATGCTGTTGAGGCGTATTT-ACCACTTAAGCC 447
 QY 121 CCGGCGTTTGGTGTGGGAGTCGCGAAGCCCTTGCGCGAAGCCGCGCCGCAATCTAGTG 180

DB 448 CTGTGCTTAGGCGTGGAGGC-----TACGGCACTGCCCGTAGTCCCTTAAGTATG 502
 QY 181 GCGGTCTGCTGCAAGTTTCATTTGCTAGTATGTAATTAACCTTCGCACT-AGTAACGGGCG 239
 DB 503 GCGGAGTTGATTC---TACTCTAGGCGTATGTAATTAATCTGCTCTGTAAGGTTTC 558
 QY 240 CCGGCAAGCGGTAAACCCCAACTTCTGATGTTGACCTCGGATCAGGTAGGAATACC 299
 DB 559 CCGGCCCCCTCGTAAACCCCTTATATCAAGGTTGACCTCGGATCAGGTAGGAATACC 618
 QY 300 GCTGAACCTTAA 310
 DB 619 GCTGAACCTTAA 629

RESULT 14
 US-10-623-432-4
 ; Sequence 4, Application US/10623432
 ; Publication No. US20040141955A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strobel, Gary
 ; APPLICANT: Manke, Denise
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
 ; FILE REFERENCE: AQ 2019.40
 ; CURRENT APPLICATION NUMBER: US/10/623,432
 ; CURRENT FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: US/10/121,740
 ; PRIOR FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/283,902
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/363,072
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 650
 ; TYPE: DNA
 ; ORGANISM: Muscodor roseus
 US-10-623-432-4

Query Match 40.1%; Score 124.2; DB 17; Length 650;
 Best Local Similarity 71.4%; Pred. No. 1.3e-34;
 Matches 222; Conservative 0; Mismatches 78; Indels 11; Gaps 4;

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 QY 121 CCGGCGTTTGGTGTGGGAGTCGCGAAGCCCTTGCGCGAAGCCGCGCCGCAATCTAGTG 180
 DB 448 CTGTGCTTAGGCGTGGAGGC-----TACGGCACTGCCCGTAGTCCCTTAAGTATG 502
 QY 181 GCGGTCTGCTGCAAGTTTCATTTGCTAGTATGTAATTAACCTTCGCACT-AGTAACGGGCG 239
 DB 503 GCGGAGTTGATTC---TACTCTAGGCGTATGTAATTAATCTGCTCTGTAAGGTTTC 558
 QY 240 CCGGCAAGCGGTAAACCCCAACTTCTGATGTTGACCTCGGATCAGGTAGGAATACC 299
 DB 559 CCGGCCCCCTCGTAAACCCCTTATATCAAGGTTGACCTCGGATCAGGTAGGAATACC 618
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RESULT 15
 US-10-046-955-5
 ; Sequence 5, Application US/10046955

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: Publication No. US20030129600A1
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aidorevich, Liliانا
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: PRIORITY FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
: US-10-046-955-5

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 4340 Seconds

(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	60.0	739	14	CF870552 tric024xb
2	186	60.0	755	14	CF870665 tric024xj
3	186	60.0	796	14	CB900742 tric024xb
4	186	60.0	808	14	CB900860 tric024xj

5	139.8	45.1	735	14	CF880267	CF880267 tric081xc
6	139.8	45.1	840	14	CB907036	CB907036 tric081xc
7	120.2	38.8	704	13	BQ751285	BQ751285 EST631848
8	120.2	38.8	725	13	BQ752001	BQ752001 EST632564
9	120.2	38.8	806	13	BQ751015	BQ751015 EST631578
10	120.2	38.8	806	13	BQ751484	BQ751484 EST632047
11	118.6	38.3	745	13	BQ751971	BQ751971 EST632534
12	118.6	38.3	758	13	BQ751399	BQ751399 EST631962
13	116	37.4	169	12	BM870292	BM870292 mgm8009xj
14	113.6	36.6	774	13	BQ752136	BQ752136 EST632699
15	112	36.1	743	13	BQ751027	BQ751027 EST631590
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22	99.6	32.1	570	28	BZ293287	BZ293287 CG0248.r1
23	99.6	32.1	603	28	BZ296472	BZ296472 CG02071.r1
24	99.2	32.0	597	28	BZ293452	BZ293452 CG0344.f1
25	97.6	31.5	846	29	CNS07820	AL434652 T7 end of
26	97.6	31.5	893	29	CNS07956	AL435182 T7 end of
27	97.6	31.5	995	29	CNS07A08	AL435966 T7 end of
28	97.6	31.5	999	29	CNS07730	AL432204 T7 end of
29	97.6	31.5	1034	29	CNS07922	AL435957 T7 end of
30	97.6	31.5	1094	29	CNS0768E	AL431760 T7 end of
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36	96.2	31.0	1004	29	CNS06KCF	AL402853 T3 end of
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45	96	31.0	1042	29	CNS07CHZ	AL439197 T3 end of

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
tric024xb14.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION
CF870552
VERSION
CF870552.1 GI:38125234
KEYWORDS
SOURCE
ORGANISM
Hypocrea jecorina (anamorph: Trichoderma reesei)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
Diener S.B., Dankmeyer L., Dunn-Coleman N., Houfek T.D.,
Mitchell T.K., van Solingen P., Teunissen P.J.M., Ward M. and
Dean R.A.

TITLE
JOURNAL
COMMENT
Analysis of the protein processing and secretion pathways in a
Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.

FEATURES

source

Location/Qualifiers

1. .739
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 /note="Vector: PREP3Y; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 60.0%; Score 186; DB 14; Length 739;
 Best Local Similarity 80.9%; Pred. No. 1,1e-43;
 Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 60
 DB 43 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 102
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 QY 240 CGGCGAAGCCGTTAA---ACCCCAACTTGAATGTTGACTTCGATCAGTAGGAATA 296
 DB 282 CGGCGAAGCCGTTAAACCCCAACTTGAATGTTGACTTCGATCAGTAGGAATA 341
 QY 297 CCGGCTGAACCTTAA 310
 DB 342 CCGGCTGAACCTTAA 355

RESULT 2
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 LOCUS tric024xb14.b1 T.reesei mycelial culture, Version 6 October 2003
 DEFINITION Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.
 ACCESSION CF870665
 VERSION CF870665
 KEYWORDS
 SOURCE EST.
 ORGANISM GI:38125347
 Hypocrea jecorina (anamorph: Trichoderma reesei)
 Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 1 (bases 1 to 755)
 Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
 Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
 Dean, R.A.
 Analysis of the protein processing and secretion pathways in a
 Trichoderma reesei EST dataset
 Unpublished (2003)
 Contact: Ralph A. Dean
 Fungal Genomics Laboratory
 North Carolina State University
 Campus Box 7251, Raleigh, NC 27695, USA
 Tel: 919-513-0020
 Fax: 919-513-0024
 Email: ralph.dean@ncsu.edu
 Seq primer: Tr-F1 primer.
 Location/Qualifiers
 1. .755

FEATURES
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ORIGIN

Query Match 60.0%; Score 186; DB 14; Length 755;
 Best Local Similarity 80.9%; Pred. No. 1,1e-43;
 Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 60
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 QY 297 CCGGCTGAACCTTAA 310
 DB 342 CCGGCTGAACCTTAA 355

RESULT 3
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 LOCUS tric024xb14 T.reesei mycelial culture, Version 3 apr11 Hypocrea
 DEFINITION jecorina cDNA clone tric024xb14, mRNA sequence.
 ACCESSION CB900742
 VERSION CB900742
 KEYWORDS
 SOURCE EST.
 ORGANISM GI:30115400
 Hypocrea jecorina (anamorph: Trichoderma reesei)
 Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 1 (bases 1 to 796)
 Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
 Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
 Kelley, A.S., Weerman, H.J., Yao, J., and Ward, M.
 Oliveras, H.A., Teunissen, P.J., Yeo, J., and Ward, M.
 Transcriptional regulation of biomass-degrading enzymes in the
 filamentous fungus Trichoderma reesei
 J. Biol. Chem. 278 (34), 31988-31997 (2003)
 12788920
 Contact: Pamela K. Foreman
 Genencor Intl.
 925 Page Mill Road, Palo Alto, CA 94304, USA
 Tel: (650) 846-7635
 Fax: (650) 621-7817
 Email: Pforeman@genencor.com
 Seq primer: Tr-F1 primer.
 Location/Qualifiers
 1. .796

FEATURES
 source

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/clone_1lb="T.reesei mycelial culture, Version 3 april"
/note="Vector: PREPly, Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

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Query Match 60.0%; Score 186; DB 14; Length 796;
Best Local Similarity 80.9%; Pred. No. 1,1e-43;
Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;
QY 1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
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DB 220 CTTCCGGGGGGGT-CGGCGTTGGGATCGGCGCCCTTACCGGCGCGCCGAAATACAGTG 278
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DB 279 GCGGTCTCGGCGAGCCTCTCTCGGCGAGTAGTTGCACTCGCACCGGAGGCGCGCG 338
QY 240 CCGGCAAGCCGTTAA--ACCCCACTTCTGAATGTTGACTTGATCGATCAGTAGAATA 296
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QY 297 CCGGCTGAACCTTAA 310
DB 399 CCGGCTGAACCTTAA 412

RESULT 4
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DEFINITION tric024xj04 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric024xj04, mRNA sequence.
ACCESSION CB900860
VERSION CB900860.1 GI:30115518
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 808)
AUTHORS Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.O.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL JOURNAL
MEDLINE 22803314
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers

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/note="Vector: PREPly, Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

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Best Local Similarity 80.9%; Pred. No. 1,1e-43;
Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;
QY 1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
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DB 275 GCGGTCTCGGCGAGCCTCTCTCGGCGAGTAGTTGCACTCGCACCGGAGGCGCGCG 334
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DB 335 CCGGCAAGCCGTTAAACACCCCAACTGAAATGTTGACTTGATCAGTAGAATA 394
QY 297 CCGGCTGAACCTTAA 310
DB 395 CCGGCTGAACCTTAA 408

RESULT 5
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DEFINITION tric081xc18.b2 T.reesei mycelial culture, Version 6 October 2003
Hypocrea jecorina cDNA clone tric081xc18, mRNA sequence.
ACCESSION CF880267
VERSION CF880267.1 GI:38134949
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 735)
AUTHORS Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,
Dean,R.A.
Analysis of the protein processing and secretion pathways in a
Trichoderma reesei EST dataset
Unpublished (2003)
CONTACT: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers

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source 1..735
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culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations.."

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QY	181	GCGGTCTCGTCGACGCTTCATTCGCTAG-TAGTAAACCTTCGCAACTGTGACGCGCG	239
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Db	289	CGGCCA	294

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LOCUS	CB907036		
DEFINITION	CB907036	840 bp	mRNA linear EST 02-JUL-2005
DESCRIPTION	tr1c081xc18 T. reesei mycelial culture, Version 3 apr11 Hypocrea		
FEATURES	cgc ccna cdna clone tr1c081xc18, mRNA sequence.		

ORGANISM	SOURCE	KEYWORDS	VERSION	RELEASE
Hypocrea jecorina	Hypocrea jecorina (anamorph: Trichoderma reesei)	EST.	CB907036.1	GI:30121694
Hypocrea jecorina				

REFERENCE
1 (bases 1 to 840)
Foreman, P. K., Brown, D. E., Dankmeyer, L., Dean, R., Diener, S.,
Hypocreales; Hypocreaceae; Hypocrea.
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

TITLE	JOURNAL
Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus <i>Trichoderma reesei</i>	J. Biol. Chem. 278 (34), 31988-31997 (2003)

MEDLINE	22803314
PUBMED	12788920
COMMENT	Contact: Pamela K. Foreman

FEATURES	
source	Location/Qualifiers
	1. .840

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strain="OW6a"  
db_xref="taxon:51453"  
clone="tric081x18"  
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clone_lib="T_reseed_mycelial"  
note="Vector: pBESY, Site_1, Not I/Sal I, Mycelial  
3 apr 11"
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culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

Query Match	45.1%;	Score 139.8;	DB 14;	Length 840;
Best Local Similarity	78.0%;	Pred. No. 4.4e-30;		
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Db	215	TTGCGCCCGCAGATATCTGGCGGGCATGCTGTTCGAGGCTCATTTTCAACCTTCAAGCC	274
Qy	121	CCGGGATTGGGTGTTGGGGATTCGGCAAGCCCTTGCGGCAAGCGGCCCCGGAATCTAGTG	180
Db	275	CTTCCGGGGGGT- CGGTTTGGGGATTCGGCCCTTCAACGGGCGCCCCCGGAATCAAGNG	333
Qy	181	GGGGTCTCGTCGACGCTTCATTTGCGTAG- TAGTAAACCCCTCGCACTGTGACGGCGG	239
Db	334	GGGGTCTCGCGCACCTTTTCTTCGCGAGCTACTTGACACTCTACACCGGAGCGGGCG	393
Qy	240	CGGCCA	245
Db	394	CGGCCA	399

RESULT	
7	
BQ751285	
LOCUS	704 bp mRNA linear EST 18-JUL-2002
DEFINITION	EST631848 DSCCT Colletotrichum trifolii cDNA clone pDSCt4-17, mRNA sequence.
ACCESSION	DQ900000

ACCESSION	BO751285	GI:21906690
VERSION	BO751285.1	
KEYWORDS	EST.	
SOURCE	Colletotrichum trifolii	
ORGANISM	Colletotrichum trifolii	

REFERENCE

Samsø, D.A., Dickman, M., Town, C.D., Van Aken, S., Uteřacký, T.
1 (bases 1 to 704)

AUTHORS

Kudariyola; Fungi; Ascomycota; Pezizomycotina; Soridiomycetes;
Soridiomyces incertae sedis; Phyllachorales; Phyllochoreaceae;
mitosporic Phyllochoreaceae; Colletotrichum.

TITLE	JOURNAL	COMMENT
Ernst, R. and Placer, C.M. Ergs from mycelia of <i>Colletotrichum trifolii</i> race 1 Unpublished (2002)		
Other ERGs: EST631847		

UNIVERSITY OF MINNESOTA
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243

Email: debbys@puccini.crl.unm.edu
TIGR sequence name: MTSAD17TV More information is available at
www.medicaco.org

FEATURES	Location/Qualifiers
source	1. .704

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inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
/lab_host="DHSalpa"
/clone_id="DSC7"
/notes="Vector: Bluescript SK+, Site_1: EcoRI, Site_2:
EcoRI; isolate: 2992; cDNA was prepared from polyA+

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enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 704;
Best Local Similarity 74.2%; Pred. No. 2.4e-24;
Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

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Oy 33 AGTGAATCATGAACTTTTGAACGACATTTGGCCGCCGCAATTTCTGGCGGCGATGCT 92
Db 1 AGTGAATCATGAACTTTTGAACGACATTTGGCCGCCGCAATTTCTGGCGGCGATGCT 60
Oy 93 GTTCGAGCGTCATTTCAACCTTCAAGCCCGGGGTTTGTTGGGGAGATCGGCAAGCCCT 152
Db 61 GTTCGAGCGTCATTTCAACCTTCAAGCAC-----GCTTGGCGTTGGGCTTCCA 110
Oy 153 TGGCGCAAGCCGCGCCGAAATCTAGTGGCGTCTGC-TGCAGCTTCATTTGCGTAGTA 211
Db 111 CGGCTGAGTGGGGCCCTCAAGACAGTGGCGGACCTTGGCGGAGCTCTTTGGCTAGTA 170
Oy 212 GTAACCCCTCGCAACTGTGA--CGCGCGCGCGCAAGCCGTTAAACCCCACTTCT-- 267
Db 171 ACATACCACTCTGCGACCGGACCCGCAAGGCACTCTCTCGTTAAACCCCACTTTTGA 230
Oy 268 GAATGTGACCTCGGATCAGTAGAATACCCGCTGAACCTTA 310
Db 231 CAAGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTA 273
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RESULT 8
B0752001
LOCUS EST633564 DSCT Colletotrichum trifolii cDNA clone pDSCT9-22, mRNA
DEFINITION
ACCESSION B0752001
VERSION B0752001.1 GI:21907406
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
REFERENCE Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
AUTHORS Cheung,F. and Fraser,C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST632563
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTS412TV More information is available at:
www.medicago.org
Seq primer: (gta ACA CGA CTC Act ACA 999 C).
Location/Qualifiers

FEATURES
source 1..725
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/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCT9-22"
/tissue_type="mycelia"

/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/clone_id="DSCT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 725;
Best Local Similarity 74.2%; Pred. No. 2.4e-24;
Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

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Oy 33 AGTGAATCATGAACTTTTGAACGACATTTGCCGCCGCAATTTCTGGCGGCGATGCT 92
Db 1 AGTGAATCATGAACTTTTGAACGACATTTGCCGCCGCAATTTCTGGCGGCGATGCT 60
Oy 93 GTTCGAGCGTCATTTCAACCTTCAAGCCCGGGGTTTGTTGGGGAGATCGGCAAGCCCT 152
Db 61 GTTCGAGCGTCATTTCAACCTTCAAGCAC-----GCTTGGCGTTGGGCTTCCA 110
Oy 153 TGGCGCAAGCCGCGCCGAAATCTAGTGGCGTCTGC-TGCAGCTTCATTTGCGTAGTA 211
Db 111 CGGCTGAGTGGGGCCCTCAAGACAGTGGCGGACCTTGGCGGAGCTCTTTGGCTAGTA 170
Oy 212 GTAACCCCTCGCAACTGTGA--CGCGCGCGCGCAAGCCGTTAAACCCCACTTCT-- 267
Db 171 ACATACCACTCTGCGACCGGACCCGCAAGGCACTCTCGTTAAACCCCACTTTTGA 230
Oy 268 GAATGTGACCTCGGATCAGTAGAATACCCGCTGAACCTTA 310
Db 231 CAAGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTA 273
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RESULT 9
B0751015
LOCUS EST631578 DSCT Colletotrichum trifolii cDNA clone pDSCT2-7, mRNA
DEFINITION
ACCESSION B0751015
VERSION B0751015.1 GI:21906420
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
REFERENCE Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
AUTHORS Cheung,F. and Fraser,C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST631577
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAB07TV More information is available at:
www.medicago.org
Seq primer: (gta ACA CGA CTC Act ACA 999 C).
Location/Qualifiers

FEATURES

1..725
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/mol_type="mRNA"
/strain="race 1"
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/clone="pDSCT9-22"
/tissue_type="mycelia"

source

1. .806
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 /mol_type="mRNA"
 /strain="race 1"
 /db_xref="taxon:5466"
 /clone="pDST2-7"
 /tissue_type="mycelia"
 /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
 /lab_host="DH5alpha"
 /clone_lib="DST"
 /note="Vector: pBluescript SK+, Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into lambda gtl from Stragene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 806;
 Best Local Similarity 74.2%; Pred. No. 2.5e-24;
 Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTAATCATGAAATCTTTGAAGCAGATTGCGCCGCAATATCTGGCGGAGTCCT 92
 DB 1 AGTAATCATGAAATCTTTGAAGCAGATTGCGCCGCAATATCTGGCGGAGTCCT 60
 QY 93 GTTGAGGCGTATTTCAACCTCAAGCCCCGGGTTGGTGGGATGGCAAGCCT 152
 DB 61 GTTGAGGCGTATTTCAACCTCAAGCACC-----GTTGGGTTGGGCGTTTCCA 110
 QY 153 TCGCGCAGCGCGCCGCAATCTAGTGGCGTCTCGC-TGCAGCTTCATTGGGTAGTA 211
 DB 111 CGCGTGAAGTGGGCGCTCAAGAGACAGTGGGAGACCTCTGGGAGCCTCTTTCGTAGTA 170
 QY 212 GTTAAACCTCTGCAACTGTGA--CGCGCGCGGCGCAAGCGGTAAACCCCAATTCT-- 267
 DB 171 ACATACCACTCTGCAAGCGGAGCGGAGCCTCTGCGGTAAACCCCAATTCTTA 230
 QY 268 GAATGTTGACCTCGGATCAGTAGAATACCGCGTGAATTAA 310
 DB 231 CAAGGTTGACCTCGGATCAGTAGAATACCGCGTGAATTAA 273

RESULT 10 806 bp mRNA linear EST 18-JUL-2002
 BQ751484
 LOCUS EST632047 DSCR Colletoletrichum trifolii cDNA clone pDST5-48, mRNA
 DEFINITION
 ACCESSION BQ751484
 VERSION BQ751484.1 GI:21906889
 KEYWORDS EST.
 SOURCE Colletoletrichum trifolii
 ORGANISM Colletoletrichum trifolii
 Bkaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Mitosporic Phyllachoraceae; Colletoletrichum.
 1 (bases 1 to 806)
 CHEUNG, F. and FRASER, C.M., Town, C.D., Van Aken, S., Uteback, T.,
 Samac, D.A.,
 ESTS from mycelia of Colletoletrichum trifolii race 1
 Unpublished (2002)
 Other ESTs: EST632046
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENTFEATURES
source

Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debby@puccini.crl.umn.edu
 TIGR sequence name: MTSAB48TV More information is available at:
 www.medicago.org
 Seq primer: (grA Aba Cga Ctc Aba ggg C).
 Location/Qualifiers
 1. .806
 /organism="Colletoletrichum trifolii"
 /mol_type="mRNA"
 /strain="race 1"
 /db_xref="taxon:5466"
 /clone="pDST5-48"
 /tissue_type="mycelia"
 /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
 /lab_host="DH5alpha"
 /clone_lib="pDST"
 /note="Vector: pBluescript SK+, Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into lambda gtl from Stragene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 806;
 Best Local Similarity 74.2%; Pred. No. 2.5e-24;
 Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTAATCATGAAATCTTTGAAGCAGATTGCGCCGCAATATCTGGCGGAGTCCT 92
 DB 1 AGTAATCATGAAATCTTTGAAGCAGATTGCGCCGCAATATCTGGCGGAGTCCT 60
 QY 93 GTTGAGGCGTATTTCAACCTCAAGCCCCGGGTTGGTGGGATGGCAAGCCT 152
 DB 61 GTTGAGGCGTATTTCAACCTCAAGCACC-----GTTGGGTTGGGCGTTTCCA 110
 QY 153 TCGCGCAGCGCGCCGCAATCTAGTGGCGTCTCGC-TGCAGCTTCATTGGGTAGTA 211
 DB 111 CGCGTGAAGTGGGCGCTCAAGAGACAGTGGGAGACCTCTGGGAGCCTCTTTCGTAGTA 170
 QY 212 GTTAAACCTCTGCAACTGTGA--CGCGCGCGGCGCAAGCGGTAAACCCCAATTCT-- 267
 DB 171 ACATACCACTCTGCAAGCGGAGCGGAGCCTCTGCGGTAAACCCCAATTCTTA 230
 QY 268 GAATGTTGACCTCGGATCAGTAGAATACCGCGTGAATTAA 310
 DB 231 CAAGGTTGACCTCGGATCAGTAGAATACCGCGTGAATTAA 273

RESULT 11 745 bp mRNA linear EST 18-JUL-2002
 BQ751971
 LOCUS EST632534 DSCR Colletoletrichum trifolii cDNA clone pDST9-3, mRNA
 DEFINITION
 ACCESSION BQ751971
 VERSION BQ751971.1 GI:21907376
 KEYWORDS EST.
 SOURCE Colletoletrichum trifolii
 ORGANISM Colletoletrichum trifolii
 Bkaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Mitosporic Phyllachoraceae; Colletoletrichum.
 1 (bases 1 to 745)
 CHEUNG, F. and FRASER, C.M., Town, C.D., Van Aken, S., Uteback, T.,
 Samac, D.A.,
 ESTS from mycelia of Colletoletrichum trifolii race 1
 Unpublished (2002)
 Other ESTs: EST632534
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

TITLE
JOURNAL
COMMENT

ESTs from mycelia of *Colletotrichum trifolii* race 1
Unpublished (2002)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@pucini.crl.umn.edu
TIGR sequence name: MTS103TV More information is available at:
www.medicago.org
Seq primer: (gta Aca CGA CTC Aca 995 C).
Location/Qualifiers

FEATURES

source

1..745
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/db_xref="taxon:5466"
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/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC7"
/note="Vector: pluescript SK+; Site_1: EcoRI, Site_2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified after EcoRI lysis. The cDNA inserts were gel purified after EcoRI digestion and ligated into pluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.3%; Score 118.6; DB 13; Length 745;
Best Local Similarity 73.9%; Pred. No. 7.2e-24;
Matches 209; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

33 AGTAATCATGAACTTTGAAGCAGCATGGCGGCGGAGTTCGGGGGATGCT 92
1 AGTAATCATGAACTTTGAAGCAGCATGGCGGCGGAGTTCGGGGGATGCT 60
93 GTTCGAGCGTATTCACCTTCAAGCCCGGGTTGGTGGGATCGGCAAGCCT 152
61 GTTCGAGCGTATTCACCTTCAAGC-----GCTTGGCGTTGGGCTTCA 110
153 TCGGCAAGCGGCGGCGGAAATCTAGTGGCGTCTCG-TCAGCTTCATTCGAGTA 211
111 CGGCTGACGTGGGCGCTCAAGACAGTGGCGGAGCCTCGCGAGCCTCTTTGGGTAGTA 170
212 GTAACCCCTCGCACTGTA--CGCGCGGCGGCAAGCGCTTAAACCCCACTTC-- 267
171 ACATACCACTTCGACCGGAGCGGAGGAGCACTTCCTCGTAAACCCCAATTTTAA 230
268 GAATGTGACCTCGAGTCAAGTGAATACCCGCTGAATTA 310
231 CAAGTTGACCTCGAGTCAAGTGAATACCCGCTGAATTA 273

RESULT 12
BO751399 758 bp mRNA linear EST 18-JUL-2002
LOCUS EST613962 DSC7 Colletotrichum trifolii cDNA clone pDSC7-95, mRNA
DEFINITION
ACCESSION BO751399
VERSION BO751399.1 GI:21906804
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes: Sordariomycetes incertae sedis: Phyllachorales: Phyllachoraceae: mitosporic Phyllachoraceae, Colletotrichum.
1 (bases 1 to 758)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Chung, F., and Fraser, C.M.
ESTs from mycelia of *Colletotrichum trifolii* race 1
Unpublished (2002)
Other ESTs: EST631961
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@pucini.crl.umn.edu
TIGR sequence name: MTSAD95TV More information is available at:
www.medicago.org
Seq primer: (gta Aca CGA CTC Aca 995 C).
Location/Qualifiers

FEATURES

source

1..758
/organism="Colletotrichum trifolii"
/mol_type="mRNA"
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/clone="pDSC7-95"
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/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC7"
/note="Vector: pluescript SK+; Site_1: EcoRI, Site_2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 38.3%; Score 118.6; DB 13; Length 758;
Best Local Similarity 73.9%; Pred. No. 7.3e-24;
Matches 209; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

33 AGTAATCATGAACTTTGAAGCAGCATGGCGGCGGAGTTCGGGGGATGCT 92
1 AGTAATCATGAACTTTGAAGCAGCATGGCGGCGGAGTTCGGGGGATGCT 60
93 GTTCGAGCGTATTCACCTTCAAGCCCGGGTTGGTGGGATCGGCAAGCCT 152
61 GTTCGAGCGTATTCACCTTCAAGC-----GCTTGGCGTTGGGCTTCA 110
153 TCGGCAAGCGGCGGCGGAAATCTAGTGGCGTCTCG-TCAGCTTCATTCGAGTA 211
111 CGGCTGACGTGGGCGCTCAAGACAGTGGCGGAGCCTCGGAGGAGCCTTTGGGTAGTA 170
212 GTAACCCCTCGCACTGTA--CGCGCGGCGGCAAGCGCTTAAACCCCACTTC-- 267
171 ACATACCACTTCGACCGGAGCGGAGGAGGAGCACTTCCTCGTAAACCCCAATTTTAA 230
268 GAATGTGACCTCGAGTCAAGTGAATACCCGCTGAATTA 310
231 CAAGTTGACCTCGAGTCAAGTGAATACCCGCTGAATTA 273

RESULT 13
BM870292 169 bp mRNA linear EST 06-MAY-2003
LOCUS BM870292

DEFINITION mgns009xj23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns009xj23 5', mRNA sequence.

ACCESSION BM870292 GI:30404719

VERSION EST.

KEYWORDS Magnaporthe grisea (anamorph: Pyricularia grisea)

SOURCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 169)
Ebbold, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea

TITLE Unpublished (2002)

JOURNAL On Mar 7, 2002 this sequence version replaced gi:19237974.

COMMENT Contact: Ebbold DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 4832
Email: d-ebbold@tamu.edu
Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) gb|AL79278.1| unknown [Saccharomyces cerevisiae] 79 1e-14

PCR primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgns009 row: J column: 23
Seq primer: T3.

FEATURES
source
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location/Qualifiers
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgns009xj23"
/sex="Mati-2 hermaphrodite"
/cell_type="mycelium"
/clone_id="Magnaporthe grisea NS Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN
Query Match 37.4%; Score 116; DB 12; Length 169;
Best Local Similarity 96.0%; Pred. No. 2e-23;
Matches 115; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

D 1 AAATGCATTAAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAGCACA 60
D 39 AAATGCATTAAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAGCACA 98
Q 61 TTGGCCCGCCGCAATTTCTGGCGCGCATGCGCTTTGAGGCTATTCAACCTCAAGCC 120
D 99 TTCCGCCCGCCGCAATTTCTGGCGCGCATGCGCTTTGAGGCTATTCAACCTCAAGCC 158
Q 121 CCGC 124
D 159 TCGG 162

RESULT 14
B0752136
LOCUS
DEFINITION 774 bp mRNA linear EST 18-JUL-2002
EST632699 DSCOT Colletotrichum trifolii cDNA clone pDSC10-23, mRNA sequence.

ACCESSION B0752136
VERSION B0752136.1 GI:21907541

KEYWORDS EST.

SOURCE Colletotrichum trifolii

ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

REFERENCE 1 (bases 1 to 774)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1

TITLE Unpublished (2002)

JOURNAL Other ESTs: EST632698

COMMENT Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAMJ23TV More information is available at: www.medicago.org

Seq primer: (gta ata cga ctc act ata ggg c).

FEATURES
source
1..774
location/Qualifiers
/organism="Colletotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC10-23"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (curin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_id="DSCOT"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 26p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN
Query Match 36.6%; Score 113.6; DB 13; Length 774;
Best Local Similarity 73.4%; Pred. No. 2.2e-22;
Matches 204; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

D 38 ATCATCGAATCTTTGAACGCAATTTGGCGCCGCAAGATTTCTGGCGGCAATGCTGTCG 97
D 5 ATTATCGAATCTTTGAACGCAATTTGGCGCCGCAAGATTTCTGGCGGCAATGCTGTCG 64
Q 98 AGCGTCATTTCAACCTCAAGCCCCCGGGTTGTGTGGGATCGCAAGCCCTTCGCG 157
D 65 AGCGTCATTTCAACCTCAAGCACC-----GCTTGGCGTTGGGCTTCCAGCGCT 114
Q 158 CAAGCCGCGCCGCAATTTAATGCGGCTCTGCC-TGAGCTTCCATTGCGTAGTAATAA 216
D 115 GACGTGGGCGCTCAAGACAGTGGCGGAGCCTCGCGAGGCTCTTGGTAGTAACATA 174

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OY 217 ACCCTGCACTGTA--CGCGGCGGCGCAAGCCGTTAAACCCCACTTCT--GAATG 272
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DB 175 CCACCTGCCACCGGACCGGACGCACTCTCCGCTGAAACCCCAATTTTACAAG 234
OY 273 TTGACCTCGATCAGTAGAATATACCGCTGAACTTAA 310
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DB 235 TTGACCTCGATCAGTAGAATATACCGCTGAACTTAA 272

RESULT 15
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LOCUS EST61590 DSC7 Colletotrichum trifolii cDNA clone pDSC7-20, mRNA
DEFINITION
ACCESSION B0751027 GI:21906432
VERSION B0751027
KEYWORDS EST,
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
REFERENCE 1 (bases 1 to 743)
AUTHORS Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
          Cheung,F. and Fraser,C.M.
          ESTs from mycelia of Colletotrichum trifolii race 1
          Unpublished (2002)
          Other_ESTs: EST631589
          Contact: Deborah A. Samac
          Department of Plant Pathology
          University of Minnesota
          495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
          Tel: 612 625 1243
          Fax: 651 649 5058
          Email: debby@puccini.crl.umn.edu
          TIGR sequence name: MTSAB20TV More information is available at:
          www.medicago.org
          Seq primer: (gta ata cga ctc act ata ggg c).
          Location/Qualifiers
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              /db_xref="taxon:5466"
              /clone="pDSC7-20"
              /tissue_type="mycelia"
              /dev_stage="young, actively growing mycelia (3 days after
              inoculation) grown in liquid culture (cutin minimal medium
              containing 2%glucose)."
              /lab_host="DH5alpha"
              /clone_lib="DSC7"
              /note="Vector: pBluescript SK+, Site_1: EcoRI, Site_2:
              EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
              enriched RNA. The cDNA was ligated into Lambda gill from
              Stratagene and packaged using Gigapack packaging extracts.
              An aliquot of the amplified library was used to transduce
              E. coli Y1090 and phage DNA was purified from a liquid
              lysate. The cDNA inserts were gel purified after EcoRI
              digestion and ligated into pBluescript SK+. Aliquots of
              the ligation were used to transform E. coli DH5alpha which
              were plated onto medium with X-gal for selection of
              recombinants."

FEATURES
SOURCE
ORIGIN
Query Match 36.1%; Score 112; DB 13; Length 743;
Best Local Similarity 73.0%; Pred. No. 6.3e-22;
Matches 203; Conservative 0; Mismatches 60; Indels 15; Gaps 4;
OY 38 ATCATCGAATCTTTGAACGACATGCGCGCGCAATTTCTGGCGGCGCATGCTGTTCG 97
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DB 5 ATTTGGAATCTTTGAACGACATGCGCGCGCAATTTCTGGCGGCGCATGCTGTTCG 64
OY 98 AGCGTCATTTCAACCTTCAAGCACC-----GCTTGCGTGGGGCTTCCACGGCT 114
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DB 65 AGCGTCATTTCAACCTTCAAGCACC-----GCTTGCGTGGGGCTTCCACGGCT 114
OY 158 CAAGCCGCGCCCGAATCTAGTGGCGGTCTGCG-TGAGCTTCATTTGCGTAGTAGTAA 216
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DB 115 GACGTGGGCGCTTCAAGACAGTGGCGGACCTTCGCGGAGCCTCTTGGCGTAGTAACTA 174
OY 217 ACCCTGCACTGTA--CGCGGCGGCGCAAGCGTTAAACCCCACTTCT--GAATG 272
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DB 175 CCACCTGCCACCGGACCGGACGCACTCTGCGTAAACCCCAATTTTACAAG 234
OY 273 TTGACCTCGATCAGTAGAATATACCGCTGAACTTAA 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 TTGACCTCGATCAGTAGAATATACCGCTGAACTTAA 272

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 05:20:41 ; Search time 1575.63 Seconds

(without alignments)
8527.610 Million cell updates/sec

Title: US-10-046-955-7

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Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1164953

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

GenBank1:
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2: gb_hcg:*
3: gb_in:*
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11: gb_scs:*
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30: em_hcg_hum:*
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33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	6 AR206401	AR206401 Sequence
2	310	100.0	310	6 BD083592	BD083592 Nucleic a
3	310	100.0	310	8 AF117922	AF117922 Gdbereil
4	232	74.8	351	8 AF162903	AF162903 Fusarium
5	232	74.8	556	8 AF455422	AF455422 Gdbereil
6	232	74.8	556	8 AF455460	AF455460 Gdbereil
7	232	74.8	556	8 AF455460	AF455460 Gdbereil
8	232	74.8	556	8 AF455460	AF455460 Gdbereil
9	232	74.8	556	8 AF455460	AF455460 Gdbereil
10	232	74.8	556	8 AF455460	AF455460 Gdbereil
11	232	74.8	556	8 AF455460	AF455460 Gdbereil
12	232	74.8	556	8 AF455460	AF455460 Gdbereil
13	228	73.5	534	8 AF168094	AF168094 Sequence
14	228	73.5	534	8 AF168094	AF168094 Sequence
15	226	72.9	502	8 AF165873	AF165873 Gdbereil
16	216	69.7	521	8 AF165873	AF165873 Gdbereil
17	181	58.4	531	8 AF158303	AF158303 Fusarium
18	181	58.4	540	8 AF158304	AF158304 Fusarium
19	177	57.1	534	8 AF061670	AF061670 Fusarium
20	177	57.1	534	8 AF061670	AF061670 Fusarium
21	165	53.2	522	8 FC061678	FC061678 Fusarium
22	158	51.0	541	8 AF158307	AF158307 Fusarium
23	158	51.0	541	8 AF158309	AF158309 Fusarium
24	155	50.0	535	8 AF034573	AF034573 Fusarium
25	155	50.0	535	8 AF034573	AF034573 Fusarium
26	154	49.7	535	8 AF034572	AF034572 Fusarium
27	143	46.1	471	8 AF150468	AF150468 Nectria h
28	139	44.8	534	8 AF061692	AF061692 Fusarium
29	134	43.2	349	8 AF162897	AF162897 Fusarium
30	134	43.2	527	8 AF061687	AF061687 Fusarium
31	134	43.2	527	8 AF158312	AF158312 Fusarium
32	134	43.2	557	8 FNYG8RNA	FNYG8RNA Fusarium
33	131	42.3	534	8 AF034574	AF034574 Fusarium
34	130	41.9	421	8 AF430128	AF430128 Fusarium
35	130	41.9	421	8 AF430129	AF430129 Fusarium
36	130	41.9	533	8 AF034568	AF034568 Fusarium
37	130	41.9	533	8 AF034575	AF034575 Fusarium
38	130	41.9	540	8 AF158302	AF158302 Fusarium
39	130	41.9	575	8 AF261662	AF261662 Fusarium
40	118	38.1	532	8 AF034560	AF034560 Fusarium
41	118	38.1	543	8 AF034581	AF034581 Fusarium
42	118	38.1	1460	8 AF310976	AF310976 Fusarium
43	118	38.1	1460	8 AF310977	AF310977 Fusarium
44	117	37.7	538	8 AF061695	AF061695 Fusarium
45	117	37.7	1458	8 AF310981	AF310981 Fusarium

ALIGNMENTS

RESULT 1
LOCUS AR206401 310 bp
DEFINITION Sequence 7 from patent US 6372430.
ACCESSION AR206401
VERSION AR206401.1 GI:21504992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 310)
AUTHORS Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.Soo.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL Patent: US 6372430-A 7 16-APR-2002;

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Best Local Similarity	100.0%;	Pred. No. 2.7e-171;
Matches 310;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	AAATCGATTAAGTAAATGTAATTCGAAAATTCAGTAATCATCGAATCTTTGAAGCACA 60
DB	1	AAATCGAATTAAGTAAATGTAATTCGAAAATTCAGTAATCATCGAATCTTTGAAGCACA 60
QY	61	TTGGCCGCCCGCCAGTATTCTGCGGGGAGTCCCTGTTGAGCGGTCAATTTCAACCTTAAGCC 120
DB	61	TTGGCCGCCCGCCAGTATTCTGCGGGGAGTCCCTGTTGAGCGGTCAATTTCAACCTTAAGCC 120
QY	121	CCGGGGTTTGGTGGTGGGGATCGGGAAGCCCTTGCGGGAGCCGCCCGCAATCTAGTG 180
DB	121	CCGGGGTTTGGTGGTGGGGATCGGGAAGCCCTTGCGGGAGCCGCCCGCAATCTAGTG 180
QY	181	GGGCTCTCGCTGCACGCTTCATTTGGTGTAGTAAAAACCTTCGCACTGTATACGCGCGC 240
DB	181	GGGCTCTCGCTGCACGCTTCATTTGGTGTAGTAAAAACCTTCGCACTGTATACGCGCGC 240
QY	241	GGCCAGCGCGTTAAACCCCACTTCTGAATTTGAACCTCGGANTCAGTAGAATACCG 300
DB	241	GGCCAGCGCGTTAAACCCCACTTCTGAATTTGAACCTCGGANTCAGTAGAATACCG 300
QY	301	CTGAACCTTA 310
DB	301	CTGAACCTTA 310
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BD083592		
LOCUS		
DEFINITION	BD083592	310 bp DNA linear PAT 27-AUG-2002
ACCESSION	BD083592	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
VERSION	BD083592.1	GI:22629202
KEYWORDS	JP 2001525665-A/7.	
SOURCE	Gibberella fujikuroi	
ORGANISM	Gibberella fujikuroi	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocormocetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.	
AUTHORS	1 (bases 1 to 310)	
TITLE	Morrison,C.J., Reiss,E., Aidorevich,I. and Choi,J.S.	
JOURNAL	Nucleic acids for detecting Aspergillus species and other filamentous fungi	
COMMENT	Patent: JP 2001525665-A 7 11-DEC-2001;	
	THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE	
	OS Fusarium moniliforme	
	PN JP 2001525665-A/7	
	PD 11-DEC-2001	
	PF 01-MAY-1998 JP 1998548275	
	PR 02-MAY-1997 US 60/045400	
	PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO	
	CC CHOI	
	CC C1201/68	
	CC Strandedness: Single;	
	CC Topology: linear;	
	PH Key	
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	Location/Qualifiers	
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QY	61	TTGGCCCGCCAGATTCGTGGCGGCGCATGCCGTTCGAGCGCTCATTTCAACCCCTCAAGCC	120	
Db	61	TTGGCCCGCCAGATTCGTGGCGGCGCATGCCGTTCGAGCGCTCATTTCAACCCCTCAAGCC	120	
QY	121	CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTGCGGCAACCCGCCGCCGAATCTAGTG	180	
Db	121	CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTGCGGCAACCCGCCGCCGAATCTAGTG	180	
QY	181	GCGGCTTCGTGCGAGCTTCATTCGATGTAATAAACCCCTCGCAACTGTGTACGCGGCGC	240	
Db	181	GCGGCTTCGTGCGAGCTTCATTCGATGTAATAAACCCCTCGCAACTGTGTACGCGGCGC	240	
QY	241	GCGCAAGCCGTTAAACCCCACTTCTGAAATGTTGACCTCGGATCAGGTAGGAATACCCG	300	
Db	241	GCGCAAGCCGTTAAACCCCACTTCTGAAATGTTGACCTCGGATCAGGTAGGAATACCCG	300	
QY	301	CTGAACCTTAA 310		
Db	301	CTGAACCTTAA 310		

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LOCUS	
DEFINITION	Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF117922
VERSION	AF117922.1 GI:8570108
KEYWORDS	
SOURCE	
ORGANISM	Gibberella fujikuroi Gibberella fujikuroi Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex. 1 (bases 1 to 310) Choi,J.S., Westerman,J.M. and Morrison,C.J. Rapid differentiation of filamentous fungi using species-specific DNA probes Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998) 2 (bases 1 to 310) Choi,J.S., Westerman,J.M. and Morrison,C.J. Direct Submission Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
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rRNA	
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QY 208 AGTAGTAAACCCCTCGAAGCTGTACGGGGGGGCGGCAAGCCGTTAAACCCCAACTTCT 267
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 Db 454 AGTAGTAAACCCCTCGAAGCTGTACGGGGGGGCGGCAAGCCGTTAAACCCCAACTTCT 513
 |||||
 QY 268 GAATGTTGACCTCGATCAGTAGAATAACCCGCTGAACCTTAA 310
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 Db 514 GAATGTTGACCTCGATCAGTAGAATAACCCGCTGAACCTTAA 556
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 RESULT 6
 AF455460
 LOCUS
 DEFINITION
 556 bp DNA linear PLN 16-JUN-2003
 Gibberella fujikuroi isolate wb355 small subunit ribosomal RNA
 gene, partial sequence; internal transcribed spacer 1, 5.8S
 ribosomal RNA gene and internal transcribed spacer 2, complete
 sequence; and large subunit ribosomal RNA gene, partial sequence.
 AF455460
 ACCESSION
 VERSION
 KEYWORDS
 AF455460.1 GI:21666892
 SOURCE
 ORGANISM
 Gibberella fujikuroi (anamorph: Fusarium fujikuroi)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
 fujikuroi complex.
 1 (bases 1 to 556)
 Buzina, W., Braun, H., Freudenichus, K., Lackner, A. and
 Stammeberger, H.
 Fungal Biodiversity as found in nasal mucus
 Med. Mycol. 41 (2), 149-161 (2003)
 2 (bases 1 to 556)
 Buzina, W., Braun, H., Freudenichus, K., Lackner, A. and
 Stammeberger, H.
 Direct Submission
 Submitted (04-DEC-2001) Laboratory for Mycology and Molecular
 Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A
 8036, Austria
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 QY 28 AATTGATGATCATCGAATCTTTGAAGCAGATTGGCCGACGATTTCTGGCGGCA 87
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 Db 274 AATTGATGATCATCGAATCTTTGAAGCAGATTGGCCGACGATTTCTGGCGGCA 333
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 QY 88 TGCCGTGAGGGTCAATTTCAACCCCTCAGCCCGGGTTTGGTGGGATCGGCA 147
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 QY 148 GCCCTGCGGCAAGCCGCGCCGAAATCTAGTGGCGTCTCGCTGACGCTTCATTGCGT 207
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 QY 208 AGTAGTAAACCCCTCGAAGCTGTACGGGGGGGCGGCAAGCCGTTAAACCCCAACTTCT 267
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Db 454 AGTAGTAAACCCCTCGAAGCTGTACGGGGGGGCGGCAAGCCGTTAAACCCCAACTTCT 513
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 QY 268 GAATGTTGACCTCGATCAGTAGAATAACCCGCTGAACCTTAA 310
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 Db 514 GAATGTTGACCTCGATCAGTAGAATAACCCGCTGAACCTTAA 556
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 RESULT 7
 PFURRNA
 LOCUS
 DEFINITION
 558 bp DNA linear PLN 14-JUN-2001
 Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S
 rRNA gene (partial), internal transcribed spacer 1 (ITS1) and
 internal transcribed spacer 2 (ITS2).
 X94176.1 X93900
 X94176.1 GI:1122868
 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
 internal transcribed spacer 2; ITS1; ITS2.
 Gibberella fujikuroi (anamorph: Fusarium fujikuroi)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
 fujikuroi complex.
 1
 Maalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.
 Discordant groupings of Fusarium spp. from sections Biegans,
 IJseola and Diamina a based on ribosomal ITS1 and ITS2 sequences
 Mycologia 88, 361-368 (1996)
 2 (bases 1 to 558)
 Maalwijk, C.
 Direct Submission
 Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant
 Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS
 On Jun 15, 2001 this sequence version replaced gi:1103564.
 Overlaps with X78260.
 COMMENT
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 /db_xref="taxon:5127"
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 178..335
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 ORIGIN
 Query Match 74.8%; Score 232; DB 8; Length 558;
 Best Local Similarity 99.6%; Pred. No. 3,4e-125;
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 28 AATTGATGATCATCGAATCTTTGAAGCAGATTGGCCGACGATTTCTGGCGGCA 87
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 Db 256 AATTGATGATCATCGAATCTTTGAAGCAGATTGGCCGACGATTTCTGGCGGCA 315
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 QY 88 TGCCGTGAGGGTCAATTTCAACCCCTCAGCCCGGGTTTGGTGGGATCGGCA 147
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Db 316 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 375
Qy 148 GCCCTTGGGCAAGCGCGCCCGAAATCTAGTGGGGCTCGCTGACATTTCCATTGGGT 207
Db 376 GCCCTTGGGCAAGCGCGCCCGAAATCTAGTGGGGCTCGCTGACATTTCCATTGGGT 435
Qy 208 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 267
Db 436 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 495
Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310
Db 496 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 538

RESULT 8
PPORRNA 558 bp DNA linear PLN 14-JUN-2001
LOCUS Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S
DEFINITION rRNA gene (partial), internal transcribed spacer 1 (ITS1) and
internal transcribed spacer 2 (ITS2).
ACCESSION X94171.1 GI:1122873
VERSION X94171.1 X93904
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
internal transcribed spacer 2; ITS1, ITS2.
SOURCE Fusarium proliferatum
ORGANISM Fusarium proliferatum
REFERENCE 1
AUTHORS Waalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.
TITLE Discordant groupings of Fusarium spp. from sections Eilegans,
JOURNAL Liseola and Diamina a based on ribosomal ITS1 and ITS2 sequences
REFERENCE Myologia 88, 361-368 (1996)
AUTHORS Waalwijk, C.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Plant
COMMENT Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS
On Jun 15, 2001 this sequence version replaced gi:1103572.
OVERLAPS with X78260.
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/note="internal transcribed spacer 1, ITS1"
178..335
/gene="5.8 rRNA"
178..335
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/note="internal transcribed spacer 2, ITS2"
501..558
/gene="28S rRNA"
501..558
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Best Local Similarity 99.6%; Pred. No. 3.4e-125;

Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 28 AATTCAGTGAATCATTCGAATTTTGAACGACATTGGGCCCGCAATTTCTGGCGGCA 87
Db 256 AATTCAGTGAATCATTCGAATTTTGAACGACATTGGGCCCGCAATTTCTGGCGGCA 315
Qy 88 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 147
Db 316 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 375
Qy 148 GCCCTTGGGCAAGCGCGCCCGAAATCTAGTGGGGCTCGCTGACATTTCCATTGGGT 207
Db 376 GCCCTTGGGCAAGCGCGCCCGAAATCTAGTGGGGCTCGCTGACATTTCCATTGGGT 435
Qy 208 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 267
Db 436 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 495
Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310
Db 496 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 538

RESULT 9
AY237110 562 bp DNA linear PLN 09-APR-2003
LOCUS Fusarium sp. 03001 18S ribosomal RNA gene, partial sequence;
DEFINITION internal transcribed spacer 1, 5.8 ribosomal RNA gene and internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.
ACCESSION AY237110.1 GI:29691499
VERSION AY237110.1 GI:29691499
KEYWORDS Fusarium sp. 03001
SOURCE Fusarium sp. 03001
ORGANISM Fusarium sp. 03001
REFERENCE 1
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
TITLE Hypocreales; Hypocreales; mitosporic Hypocreales; Fusarium.
JOURNAL 1 (bases 1 to 562)
AUTHORS Alunian, M.R. and Heiang, T.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2003) Environmental Biology, University of
Guelph, Guelph, ON N1G 2W1, Canada
FEATURES
source location/Qualifiers
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/db_xref="taxon:227081"
<1..40
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41..186
/product="internal transcribed spacer 1"
187..345
/product="5.8 ribosomal RNA"
346..510
/product="internal transcribed spacer 2"
511..562
/product="28S ribosomal RNA"
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Query Match 74.8%; Score 232; DB 8; Length 562;
Best Local Similarity 99.6%; Pred. No. 3.4e-125;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 28 AATTCAGTGAATCATTCGAATTTTGAACGACATTGGGCCCGCAATTTCTGGCGGCA 87
Db 266 AATTCAGTGAATCATTCGAATTTTGAACGACATTGGGCCCGCAATTTCTGGCGGCA 325
Qy 88 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 147
Db 326 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 385
Qy 148 GCCCTTGGGCAAGCGCGCCCGAAATCTAGTGGGGCTCGCTGACATTTCCATTGGGT 207

JOURNAL Patent: US 6287800-A 1 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..2293
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 99.6%; Pred. No. 3.6e-123;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 87
Db 1999 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 2058
Qy 88 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 147
Db 2059 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 2118
Qy 148 GCCCTTGCGGCAAGCCGCGCCGAAATCTAGTGGCGGCTGCGTCGACGCTTCATTCGCT 207
Db 2119 GCCCTTGCGGCAAGCCGCGCCGAAATCTAGTGGCGGCTGCGTCGACGCTTCATTCGCT 2178
Qy 208 AGTAGTAAACCTTCGCAACTGTACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 267
Db 2179 AGTAGTAAACCTTCGCAACTGTACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 2238
Qy 268 GAATGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 310
Db 2239 GAATGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 2281

RESULT 13

LOCUS FPJ34557 534 bp DNA linear PLN 15-JUL-1998
DEFINITION Fusarium fujikuroi internal transcribed spacer RNA.
ACCESSION U34557
VERSION U34557.1 GI:1808928

KEYWORDS

SOURCE

ORGANISM

Gibberella fujikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
fujikuroi complex.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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PUBMED

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JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

1..534
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/mol_type="genomic DNA"
/strain="NRRL 13566"
/db_xref="taxon:5127"
1..534
/product="internal transcribed spacer"

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Best Local Similarity 99.6%; Pred. No. 7.9e-123;

Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 87
Db 256 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 315
Qy 88 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 147
Db 316 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 375
Qy 148 GCCCTTGCGGCAAGCCGCGCCGAAATCTAGTGGCGGCTGCGTCGACGCTTCATTCGCT 207
Db 376 GCCCTTGCGGCAAGCCGCGCCGAAATCTAGTGGCGGCTGCGTCGACGCTTCATTCGCT 435
Qy 208 AGTAGTAAACCTTCGCAACTGTACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 267
Db 436 AGTAGTAAACCTTCGCAACTGTACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 495
Qy 268 GAATGTTGACCTCGGATCAGTAGAATACCCGCTGAAC 306
Db 496 GAATGTTGACCTCGGATCAGTAGAATACCCGCTGAAC 534

RESULT 14
LOCUS FPJ34558 534 bp DNA linear PLN 15-JUL-1998
DEFINITION Fusarium proliferatum NRRL 22944 internal transcribed spacer RNA.
ACCESSION U34558
VERSION U34558.1 GI:1808934

KEYWORDS

SOURCE

ORGANISM

Fusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
fujikuroi complex.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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1..534
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/mol_type="genomic DNA"
/strain="NRRL 22944"
/db_xref="taxon:42674"
1..534
/product="internal transcribed spacer"

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Best Local Similarity 99.6%; Pred. No. 7.9e-123;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 87
Db 256 AATTCAGTAATCATCATGATCTTTGAAAGCAATTGCGCCGCAAGTATTCGCGGCA 315
Qy 88 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 147
Db 316 TGCCGTTCGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGGTTGGGGATCGGCA 375

QY 148 GCCCTTGGCGCAACCGCGCCCGGAATCTAGTGGCGGTCTCGCTGCAAGCTTCCATTGGCT 207
 Db 376 GCCCTTGGCGCAACCGCGCCCGGAATCTAGTGGCGGTCTCGCTGCAAGCTTCCATTGGCT 435
 QY 208 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCAACTTCT 267
 Db 436 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCAACTTCT 495
 QY 268 GAATGTTGACCTCGGATCAGTAGAATATACCCGCTGAAC 306
 Db 496 GAATGTTGACCTCGGATCAGTAGAATATACCCGCTGAAC 534

RESULT 15
 AF165873 502 bp DNA linear PLN 18-JUL-1999
 LOCUS
 DEFINITION
 Gibberella fujikuroi internal transcribed spacer 1, 5.8S ribosomal
 RNA gene and internal transcribed spacer 2, complete sequence; and
 28S ribosomal RNA gene, partial sequence.
 ACCESSION
 AF165873 GI:5524730
 VERSION
 AF165873.1
 KEYWORDS
 ORGANISM
 Gibberella fujikuroi
 Gibberella fujikuroi
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
 fujikuroi complex.
 REFERENCE
 1 (bases 1 to 502)
 Iwen, P.C., Henry, T. and Hinrichs, S.H.
 TITLE
 Sequence analysis of the internal transcribed spacer regions of
 Fusarium species most commonly associated with human invasive
 disease
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 502)
 Iwen, P.C., Henry, T. and Hinrichs, S.H.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (07-JUL-1999) Pathology and Microbiology, University of
 Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE
 JOURNAL
 68198-6495, USA

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 148..304
 /product="5.8S ribosomal RNA"
 305..470
 /product="internal transcribed spacer 2"
 471..502
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 rRNA
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 rRNA

ORIGIN
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 Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTGAGTGAATCATGATCTTTGAACGACATTTGCCCGCCAGATTCTGGCGGGCA 87
 Db 226 AATTGAGTGAATCATGATCTTTGAACGACATTTGCCCGCCAGATTCTGGCGGGCA 285
 QY 88 TGCCCTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTGGTGTGGGATCGGCA 147
 Db 286 TGCCCTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTGGTGTGGGATCGGCA 345
 QY 148 GCCCTTGGCGCAACCGCGCCCGGAATCTAGTGGCGGTCTCGCTGCAAGCTTCCATTGGCT 207

Db 346 GCCCTTGGCGCAACCGCGCCCGGAATCTAGTGGCGGTCTCGCTGCAAGCTTCCATTGGCT 405
 QY 208 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCAACTTCT 267
 Db 406 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCAACTTCT 465
 QY 268 GAATGTTGACCTCGGATCAGTAGAATATACCCGCTGA 304
 Db 466 GAATGTTGACCTCGGATCAGTAGAATATACCCGCTGA 502

Search completed: October 1, 2004, 09:56:24
 Job time : 1578.63 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:41:36 ; Search time 259.73 Seconds
(without alignments)
5070.430 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
Sequence: 1 aaatcgatgaatgaatgta.....ggaataccgcgtgaactaa 310

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 212409041 residues

Word size : 10

Total number of hits satisfying chosen parameters: 596607

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : N Geneseq_29Jan04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001s:*\n5: geneseqn2001bs:*\n6: geneseqn2002s:*\n7: geneseqn2003as:*\n8: geneseqn2003bs:*\n9: geneseqn2003cs:*\n10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	2 AAV70851	Aav70851 Internal
2	232	74.8	2293	4 AAS16211	Aas16211 Fungus ge
3	228	73.5	534	7 ACC50001	Acc50001 Internal
4	117	37.7	502	3 AAA61893	Aaa61893 Fusarium
5	99	31.9	647	6 ABV78700	Abv78700 C. crass
6	95	30.6	661	6 ABV78721	Abv78721 C. sinen
7	94	30.3	504	2 AAV70851	Aav70851 Internal
8	94	30.3	504	2 AAV62591	Aav62591 Fusarium
9	94	30.3	504	2 AAV59028	Aav59028 F. culmor
10	94	30.3	504	4 AAS08426	Aas08426 Internal
11	94	30.3	521	7 ACC50000	Acc50000 Internal
12	94	30.3	522	7 ACC49999	Acc49999 Internal
13	94	30.3	522	7 ACC50002	Acc50002 Internal
14	94	30.3	545	2 AAV62593	Aav62593 Fusarium
15	94	30.3	545	2 AAV59030	Aav59030 F. monili
16	94	30.3	546	2 AAV62596	Aav62596 Fusarium
17	94	30.3	546	2 AAV59007	Aav59007 F. poae
18	92	29.7	382	3 AAA72783	Aaa72783 5.8S rRNA
19	79	25.5	135	3 AAF10640	Aaf10640 Fusarium
20	79	25.5	319	2 AAV70850	Aav70850 Internal
21	67	21.6	389	3 AAZ92490	Aaz92490 Rhizocton
22	67	21.6	569	2 AAT65101	Aat65101 T. harzia
23	67	21.6	569	2 AAT65099	Aat65099 T. harzia

24	67	21.6	582	2 AAT65100	Aat65100 T. harzia
25	66	21.3	561	2 AAV59009	Aav59009 F. avenac
26	66	21.3	659	6 ABV78724	Abv78724 C. sinen
27	55	17.7	353	2 AAT05402	Aat05402 Fusarium
28	52	16.8	503	2 AAT05401	Aat05401 Fusarium
29	52	16.8	503	2 AAV62592	Aav62592 Fusarium
30	52	16.8	503	2 AAV59029	Aav59029 F. gramin
31	46	14.8	545	2 AAT05403	Aat05403 Microdoch
32	43	13.9	537	3 AAZ91725	Aaz91725 Roseellini
33	42	13.5	343	2 AAV70871	Aav70871 Internal
34	42	13.5	344	2 AAV70870	Aav70870 Internal
35	42	13.5	553	3 AAZ91726	Aaz91726 Roseellini
36	41	13.2	377	6 ABA94559	Ab94559 Truncated
37	41	13.2	377	6 ABA94564	Ab94564 Consensus
38	41	13.2	377	6 ABA94561	Ab94561 Truncated
39	41	13.2	377	6 ABA94560	Ab94560 Truncated
40	41	13.2	389	3 AAA72781	Aaa72781 5.8S rRNA
41	41	13.2	415	4 AAF75169	Aaf75169 Consensus
42	41	13.2	415	4 AAF75170	Aaf75170 Consensus
43	41	13.2	451	2 AAZ23436	Aaz23436 Internal
44	41	13.2	466	8 ADA27221	Ada27221 P. micros
45	41	13.2	515	8 ACA62941	Aca62941 P. glomer

ALIGNMENTS

RESULT 1	AAV70851 standard; DNA; 310 BP.
ID	AAV70851
XX	AAV70851;
AC	AAV70851;
XX	
DT	17-OCT-2003 (revised)
DT	26-FEB-1999 (first entry)
XX	
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX	
XX	Internal transcribed spacer 2, ITS2; probe; Aspergillus flavus; A. niger;
KW	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;
KW	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinillicoides f. circinillicoides; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Gibberella fujikuroi.
XX	
PN	WO9850584-A2.
XX	
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US008926.
XX	
PR	02-MAY-1997; 97US-0045400P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Morrison CJ, Reiss E, Aldorevich L, Choi JS;
XX	WPI; 1999-034737/03.
XX	
DR	New nucleic acid probes for filamentous fungi - for detecting e.g.
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT	species.
XX	
PS	Claim 1; Page 12; 45pp; English.
XX	
XX	The present sequence represents an internal transcribed spacer 2 (ITS2)
CC	and adjacent regions. Probes can be derived from the present sequence
CC	which are species-specific. The specification also describes ITS2
CC	sequence-derived probes for identifying a species selected from

```

CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinellioides F. circinellioides, Rhizopus oryzae, R.
CC microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia
CC corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph
CC of Scedosporium apiospermum), Penicillium notatum, or Sporochrix
CC schenckii. The probes can be used for differentiating filamentous fungal
CC species from each other and from other medically important fungi.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;
Query Match 100.0%; Score 310; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.5e-154;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATGCGATNAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 1 AAATGCGATNAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
QY 61 TTGGGCCCCCGCAGATTCTGGCGGCATGCTGTTGCAAGGTCATTTCACACCTCAAGCC 120
DB 61 TTGGGCCCCCGCAGATTCTGGCGGCATGCTGTTGCAAGGTCATTTCACACCTCAAGCC 120
QY 121 CCCGGGTTTGGTGTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
DB 121 CCCGGGTTTGGTGTGGGAGATCGGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180
QY 181 GCGGTCCTGCTGACGCTTCCTCATTTGCGTAGTAATAAACCTTCGCACTGTGACGCGCGC 240
DB 181 GCGGTCCTGCTGACGCTTCCTCATTTGCGTAGTAATAAACCTTCGCACTGTGACGCGCGC 240
QY 241 GGGCAAGCGGTTAAACCCCAACTTCGAAATGTTGACCTGGATCGAGTGAATACCCCG 300
DB 241 GGGCAAGCGGTTAAACCCCAACTTCGAAATGTTGACCTGGATCGAGTGAATACCCCG 300
QY 301 CTGAACCTTAA 310
DB 301 CTGAACCTTAA 310

RESULT 2
AAS16211 standard; DNA; 2293 BP.
XX
XX AAS16211;
XX
XX 29-JAN-2002 (first entry)
XX
XX Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
XX
XX Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1; ITS2;
XX 5.8S rRNA; LTB-1027; species differentiation; GA_4; GA_3; GA_7;
XX flowering; fruit cell elongation; apple; pear; grape; fruit;
XX russet control; fungus; ds.
XX
XX Gibberella fujikuroi.
XX
XX Key Location/Qualifiers
XX FT misc_feature 1..1174
XX FT /tag= a
XX FT /note= "18S rRNA gene"
XX FT 1775..1921
XX FT /tag= b
XX FT /note= "ITS1 region"
XX FT 1922..2078
XX FT /tag= c
XX FT /note= "5.8S rRNA gene"
XX FT 2079..2243
XX FT /tag= d
XX FT /note= "ITS2 region"
XX FT 2244..2293
XX FT /tag= e
XX FT misc_feature
XX FT

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FT /note= "28S rRNA gene"
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XX US6287800-B1.
XX
XX 11-SEP-2001.
XX
XX 23-AUG-2000; 2000US-00645073.
XX
XX 31-AUG-1999; 99US-0151770P.
XX
XX (GALT/) GALIAZZO J L.
XX (LEEM/) LEE M D.
XX
XX Gallazzo JL, Lee MD;
XX
XX WPI; 2001-662197/76.
XX
XX A new method for producing a mixture of gibberellins from Gibberella
XX fujikuroi results in high titers of GA4 and GA7 useful to promote
XX flowering and fruit growth in the fruit growing industry.
XX
XX Example 4; Col 9-12; 7pp; English.
XX
XX This sequence represents a genomic DNA sequence containing the 18S rRNA
XX gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
XX rRNA sequences from a mutant strain of Gibberella fujikuroi (LTB-1027) of
XX the invention. This region of DNA is highly variable and can be used for
XX species and strain differentiation. The LTB-1027 mutant produces a
XX mixture of gibberellins which is at least 70 % GA 4 and GA 7.
XX Gibberellins GA 4 and GA 7 promote flowering and fruit cell elongation.
XX and are used by growers of apples, pears and grapes to produce larger
XX fruits and earlier harvests. The mixture of GA_3, GA_4 and GA_7 achieved
XX using the method of this invention should be particularly useful in the
XX apple industry where GA_4 has been found more effective in russet control
XX and in promoting fruit set. This method produces GA_4 and GA_7 in much
XX higher titers than prior art methods
XX
XX Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;
XX
XX Query Match 74.8%; Score 232; DB 4; Length 2293;
XX Best Local Similarity 99.6%; Pred. No. 6.4e-113;
XX Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 28 AATTCAGTGAATCATCGAATCTTTGAAGCAAGTCCGCCGCTATTCTGGCGGCA 87
DB 1999 AATTCAGTGAATCATCGAATCTTTGAAGCAAGTCCGCCGCTATTCTGGCGGCA 2058
QY 88 TGCCTGTTGACGCTGTCATTTCAACCTCAAGCCCGGGTTGTGTGGGATCGGCA 147
DB 2059 TGCCTGTTGACGCTGTCATTTCAACCTCAAGCCCGGGTTGTGTGGGATCGGCA 2118
QY 148 GCCCTTGGCGCAAGCCGCCGGAATTTAGTGGGCTGTGCTGACGCTTCATTGGCT 207
DB 2119 GCCCTTGGCGCAAGCCGCCGGAATTTAGTGGGCTGTGCTGACGCTTCATTGGCT 2178
QY 208 AGTAGTAAACCCCTGCAACTGTATCGGCGCGGCAAGCGGTAAACCCCAACTCT 267
DB 2179 AGTAGTAAACCCCTGCAACTGTATCGGCGCGGCAAGCGGTAAACCCCAACTCT 2238
QY 268 GAATGTTGACCTCGATCAGGTAGTAATACCGCTGAACCTTA 310
DB 2239 GAATGTTGACCTCGATCAGGTAGTAATACCGCTGAACCTTA 2281

RESULT 3
ACCS0001 standard; DNA; 534 BP.
XX
XX ACCS0001;
XX
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #3.
XX
XX

```

XX Mitochondria; fungal pathogen; ds.
KW Faarium proliferatum.
XX WO2003027635-A2.
XX 03-APR-2003.
XX 19-SEP-2002; 2002WO-US030311.
XX 24-SEP-2001; 2001US-00961755.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Beck UJ, Barnett CJ;
XX MPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
XX of Fusarium spp.
XX
XX Claim 5; Page 38-39; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
SQ Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
Query Match 73.5%; Score 228; DB 7; Length 534;
Best Local Similarity 99.6%; Pred. No. 8.8e-11;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 28 AATTGAGTGAATCATGCAATCTTTGAACGACATTCGCCCGCAGTATTCTGGCGGCA 87
DB 256 AATTGAGTGAATCATGCAATCTTTGAACGACATTCGCCCGCAGTATTCTGGCGGCA 315
QY 88 TGCCGTTCGAGCGCTTCAACCTCAAGCCCGGGGTTGGTGGGATCGGCA 147
DB 316 TGCCGTTCGAGCGCTTCAACCTCAAGCCCGGGGTTGGTGGGATCGGCA 375
QY 148 GCCCTTGGCGAAGCGCGCCGGAATCTAGTGGCGGTCTGCTGCATTCATTTGGCT 207
DB 376 GCCCTTGGCGAAGCGCGCCGGAATCTAGTGGCGGTCTGCTGCATTCATTTGGCT 435
QY 208 AGTAGTAAACCCCTCGCACTGTGACGGGGGCGGCAAGCCGTTAAACCCCACTTCT 267
DB 436 AGTAGTAAACCCCTCGCACTGTGACGGGGGCGGCAAGCCGTTAAACCCCACTTCT 495
QY 268 GAATGTGACCTCGGATCAGTAGGAATACCCGCTGAAC 306
DB 496 GAATGTGACCTCGGATCAGTAGGAATACCCGCTGAAC 534

RESULT 4
AAA61893
ID AAA61893 standard; DNA; 502 BP.
XX
XX AAA61893;
XX
XX 15-SEP-2003 (revised)
DT 14-NOV-2000 (first entry)
XX
XX
DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
KW HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
KW acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;

KW symptomatic infection; asymptomatic infection; potential HIV exposure;
KW combination therapy; ds.
XX Fusarium sp; MF6381.
XX WO200036132-A1.
XX
XX 22-JUN-2000.
XX
XX 09-DEC-1999; 99WO-US029356.
XX
XX 14-DEC-1998; 98US-0112168P.
XX
XX (MERI) MERCK & CO INC.
XX
XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
XX Dombrowski AW;
XX MPI; 2000-431606/37.
XX
XX
XX New steroid compounds are HIV integrase inhibitors used for treating HIV
PT infection and AIDS.
XX
XX
XX Disclosure; Page 14; 113pp; English.
XX
XX The invention relates to novel steroid compounds derived from the African
CC soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of
CC HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381.
CC The invention also relates to a composition comprising a compound of the
CC invention in combination with an AIDS antiviral agent, an immunomodulator
CC and an antileukemic agent. The compounds of the invention may be used in
CC the inhibition of HIV integrase and in the prevention and treatment of
CC HIV infection. A wide range of state of HIV infection may be treated;
CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
CC both symptomatic and asymptomatic HIV infection; and actual or potential
CC exposure to HIV. The compounds may be used to isolate HIV integrase
CC mutants which are potentially useful as screening tools for antiviral
CC compounds. The compounds may also be used to establish or determine the
CC site at which other antivirals bind to HIV integrase (e.g., by
CC competitive inhibition). The present sequence represents the ribosomal
CC DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp.
CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
CC to standardise OS field)
XX
SQ Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match 37.7%; Score 117; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 7.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 AATTGAGTGAATCATGCAATCTTTGAACGACATTCGCCCGCAGTATTCTGGCGGCA 87
DB 223 AATTGAGTGAATCATGCAATCTTTGAACGACATTCGCCCGCAGTATTCTGGCGGCA 282
QY 88 TGCCGTTCGAGCGCTTCAACCTCAAGCCCGGGGTTGGTGGGATCGG 144
DB 283 TGCCGTTCGAGCGCTTCAACCTCAAGCCCGGGGTTGGTGGGATCGG 339

RESULT 5
ABV78700
ID ABV78700 standard; rRNA; 647 BP.
XX
XX ABV78700;
XX
XX 14-JAN-2003 (first entry)
DT
XX
XX C. crassispora rRNA sequence #2.
DE
XX Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
KW Cordyceps sinensis; ss.
XX
OS Cordyceps crassispora.

```
XX
PN JP2002204696-A.
XX
PD 23-JUL-2002.
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
PA (HEAL-) HEALTHWAY KK.
PA (KANE/) KANESHIRO N.
XX
DR WPI; 2002-639075/69.
XX
PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT of seeds of Cordyceps sinensis.
XX
PS 2; Page 12; 33pp; Japanese.
XX
CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. crassispora rRNA sequence of the
CC invention
XX
SQ Sequence 647 BP; 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;
XX
Query Match 31.9%; Score 99; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 AATTCAGTGAATCATGATCTTTGAAGCAGCATTTGGCGCCGCGAGATTCTGGCGGGCA 87
DB 272 AATTCAGTGAATCATGATCTTTGAAGCAGCATTTGGCGCCGCGAGATTCTGGCGGGCA 331
QY 88 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCCCGGG 126
DB 332 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCCCGGG 370
XX
RESULT 6
ABV78721
ID ABV78721 standard; rRNA; 661 BP.
XX
AC ABV78721;
XX
DT 14-JAN-2003 (first entry)
XX
DE C. sinensis rRNA sequence #20.
XX
KM Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
KM Cordyceps sinensis; ss.
XX
OS Cordyceps sinensis.
XX
PN JP2002204696-A.
XX
PD 23-JUL-2002.
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
PA (HEAL-) HEALTHWAY KK.
PA (KANE/) KANESHIRO N.
XX
DR WPI; 2002-639075/69.
XX
PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT of seeds of Cordyceps sinensis.
XX
PS 23; Page 24; 33pp; Japanese.
XX
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```
CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
CC invention
XX
SQ Sequence 661 BP; 176 A; 192 C; 168 G; 123 T; 0 U; 2 Other;
XX
Query Match 30.6%; Score 95; DB 6; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.8e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 AATTCAGTGAATCATGATCTTTGAAGCAGCATTTGGCGCCGCGAGATTCTGGCGGGCA 87
DB 296 AATTCAGTGAATCATGATCTTTGAAGCAGCATTTGGCGCCGCGAGATTCTGGCGGGCA 355
QY 88 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCC 122
DB 356 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCC 390
XX
RESULT 7
AAT05400
ID AAT05400 standard; DNA; 504 BP.
XX
AC AAT05400;
XX
DT 04-JUN-1996 (first entry)
XX
DE Fusarium culmorum internal transcribed spacer sequence.
XX
KM Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KM Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
KM Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
KM internal transcribed region; strain; capture; colourimetric assay;
KM isolate; development; population; random amplified polymorphic DNA; ss.
XX
OS Fusarium culmorum.
XX
PN MO9529260-A2.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US004712.
XX
PR 25-APR-1994; 94US-00233608.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ligon JM, Beck JU;
XX
DR WPI; 1995-383005/49.
XX
PT DNA encoding intervening transcribed sequence - used for detection of
PT plant fungal pathogens.
XX
PS Claim 1; Page 54-55; 65pp; English.
XX
CC A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,
CC Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR
CC amplification of sequences found in the internal transcribed region (ITS)
CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AA094359-93
CC and AAT05357-72. These primers are derived from the ITS sequences of
CC these fungi (AAT05394-T05404 and AA094398) and are strain specific. The
CC amplification products of the reactions using these primers can be used
CC with the capture primers AAT05378-93 in colourimetric assays. The primers
CC and ITS DNAs can be used for the detection of specific fungal pathogen
CC isolates and in monitoring disease development in plant populations
XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
Query Match 30.3%; Score 94; DB 2; Length 504;
```

Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTGAGTATCATTCGAAATCTTTGAAGCAGCATTTGCCGCCAGATTTCTGGCGGCA 87
DB 239 AATTGAGTATCATTCGAAATCTTTGAAGCAGCATTTGCCGCCAGATTTCTGGCGGCA 298

QY 88 TGCCGTTCGAGCGTCATTTCAACCTCAAGCCC 121
DB 299 TGCCGTTCGAGCGTCATTTCAACCTCAAGCCC 332

RESULT 8
AAV62591
ID AAV62591 standard; DNA; 504 BP.
XX
AC AAV62591;
XX
DT 17-DEC-1998 (first entry)
XX
DE Fusarium culmorum PCR amplified ITS region consensus DNA sequence.
XX
KW Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KW Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
KW PCR; nucleic acid detection; ss.
XX
OS Fusarium culmorum.
XX
FH Key Location/Qualifiers
FT misc_feature 1..12
FT /tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 13..161
FT /tag= b
FT /note= "ITS 1"
FT misc_feature 162..318
FT /tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 319..472
FT /tag= d
FT /note= "ITS 2"
FT misc_feature 473..504
FT /tag= e
FT /note= "5' end of large subunit rRNA gene"
FT
XX
XX US5814453-A.
XX
XX 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-00867480.
XX
XX 19-APR-1995; 95WO-US004712.
XX 15-OCT-1996; 96US-00722187.
XX
XX (NOVS) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
XX sequence - used for detecting fungal pathogens in plant tissue.
XX
XX Claim 2; Fig 3; 56pp; English.
XX
XX
XX This represents the consensus DNA sequence of the internal transcribed
XX spacer (ITS) region that was PCR amplified from Fusarium culmorum
XX isolates, R-5106, R-5126 and R-5146. The invention provides a DNA
XX molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX pathogen, where the DNA molecule consists of an ITS sequence selected
XX from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX moniliforme, Septoria avenae or Microdochium nivale. A method for

CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
CC avenaceum and M. nivale isolates is also provided. The method comprises
CC isolating DNA from a plant leaf infected with at least one of the above
CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
CC PCR using specific primers from within these sequences. The pathogen(s)
CC are detected by visualising the amplified part of the ITS sequence
XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
Query Match 30.3%; Score 94; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTGAGTATCATTCGAAATCTTTGAAGCAGCATTTGCCGCCAGATTTCTGGCGGCA 87
DB 239 AATTGAGTATCATTCGAAATCTTTGAAGCAGCATTTGCCGCCAGATTTCTGGCGGCA 298

QY 88 TGCCGTTCGAGCGTCATTTCAACCTCAAGCCC 121
DB 299 TGCCGTTCGAGCGTCATTTCAACCTCAAGCCC 332

RESULT 9
AAV59028
ID AAV59028 standard; DNA; 504 BP.
XX
AC AAV59028;
XX
XX 25-MAR-2003 (revised)
XX 06-JAN-1999 (first entry)
XX
DE F. culmorum internal transcribed spacer.
XX
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX fungal pathogen identification; infection identification; ss.
XX
OS Fusarium culmorum.
XX
FH Key Location/Qualifiers
FT misc_feature 13..161
FT /tag= a
FT /note= "ITS1"
FT misc_feature 319..472
FT /tag= b
FT /note= "ITS2"
FT
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a basis
XX for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.
XX
XX Disclosure; Col 21-22; 20pp; English.
XX
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification/detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing

CC the infection allows early, and more specific fungicidal treatment.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)

XX Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 30.3%; Score 94; DB 2; Length 504;
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 87

Db 239 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 298

Qy 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121

Db 299 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 332

RESULT 10

AA08426
 ID AA08426 standard; DNA; 504 BP.

AC AA08426;

XX 26-SEP-2001 (first entry)

DE Internal transcribed spacer, ITS, region #16.

XX Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;

KW Sharp eyespot; fungal pathotype identification; isolate 62215.

XX Fusarium culmorum.

XX WO200151653-A1.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-EP000172.

XX 11-JAN-2000; 2000US-00481293.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Beck JJ, Barnett CJ;

XX WPI; 2001-442154/47.

XX New internal transcribed spacer DNA sequences, useful for identifying
 PT fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring
 PT disease development in plant population.

XX Disclosure; Page 31; 35pp; English.

XX The sequence is an internal transcribed spacer (ITS) region from Fusarium
 CC culmorum, isolate 62215. The ITS DNA sequences are useful for detecting
 CC Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot;
 CC for monitoring disease development in plant population, and for providing
 CC detailed information on the development and spread of specific pathogen
 CC races over extended geographical areas. The DNA sequences are
 CC specifically used as primers in PCR-based analysis for the identification
 CC of fungal pathotypes

XX Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;

XX Query Match 30.3%; Score 94; DB 4; Length 504;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-39;

XX Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 87

Db 242 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 301

Qy 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121
 Db 302 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 335

RESULT 11

ACC50000
 ID ACC50000 standard; DNA; 521 BP.

AC ACC50000;

XX 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #2.

XX Mitochondria; fungal pathogen; ds.

XX Gibberella zeae.

XX WO2003027635-A2.

XX 03-APR-2003.

XX 19-SEP-2002; 2002WO-US030311.

XX 24-SEP-2001; 2001US-00961755.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Beck JJ, Barnett CJ;

XX WPI; 2003-363229/34.

XX Detecting a fungal pathogen, useful for monitoring disease development,
 PT comprises subjecting the DNA to PCR amplification using at least one
 PT primer having sequence identity with at least 10 contiguous nucleotides
 PT of Fusarium spp.

XX Claim 5; Page 38; 44pp; English.

XX This invention relates to the detection of a fungal pathogen comprising
 CC isolating DNA from a plant leaf infected with a pathogen. The methods and
 CC primers are useful for identifying fungal isolates of fungal pathogens
 CC and monitoring of disease development in plant populations. The present
 CC sequence represents an internal transcribed spacer RNA encoding sequence

XX Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

XX Query Match 30.3%; Score 94; DB 7; Length 521;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-39;

XX Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 87

Db 256 AATTGAGTGAATCATTCGATCTTTGAACGACATTCGCGCCGCGAGATTCTGGCGGCA 315

Qy 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121

Db 316 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 349

RESULT 12

ACC49999
 ID ACC49999 standard; DNA; 522 BP.

AC ACC49999;

XX 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence.

XX Mitochondria; fungal pathogen; ds.

XX

XX

XX

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OS Fusarium subglutinans.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX PF 19-SEP-2002; 2002WO-US030311.
XX
XX PR 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Beck JÜ, Barnett CJ;
XX
XX MPI, 2003-363229/34.
XX
XX DR
XX
XX PT Detecting a fungal pathogen, useful for monitoring disease development,
XX comprises subjecting the DNA to PCR amplification using at least one
XX primer having sequence identity with at least 10 contiguous nucleotides
XX of Fusarium spp.
XX
XX PS Claim 5; Page 38; 44pp; English.
XX
XX CC This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 94; DB 7; Length 522;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-39;
XX Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGATTGCGCCGCGCAGATTCTGCGGGCA 87
DB 256 AATTCAGTGAATCATTCGATCTTTGAAAGCAGATTGCGCCGCGCAGATTCTGCGGGCA 315
QY 88 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 121
DB 316 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 349
XX
XX RESULT 13
XX ACC50002
XX ID ACC50002 standard; DNA; 522 BP.
XX
XX AC ACC50002;
XX
XX DT 27-OCT-2003 (revised)
XX DT 14-JUL-2003 (first entry)
XX
XX DE Internal transcribed spacer RNA encoding sequence #4.
XX
XX KW Mitochondria; fungal pathogen; ds.
XX
XX OS Gibberella moniliformis.
XX
XX PN WO2003027635-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 19-SEP-2002; 2002WO-US030311.
XX
XX PR 24-SEP-2001; 2001US-00961755.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Beck JÜ, Barnett CJ;
XX
XX MPI, 2003-363229/34.
XX

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PT Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
XX PS Claim 5; Page 39; 44pp; English.
XX
XX CC This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence.
XX (Updated on 27-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 94; DB 7; Length 522;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-39;
XX Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGATTGCGCCGCGCAGATTCTGCGGGCA 87
DB 256 AATTCAGTGAATCATTCGATCTTTGAAAGCAGATTGCGCCGCGCAGATTCTGCGGGCA 315
QY 88 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 121
DB 316 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 349
XX
XX RESULT 14
XX AAV62593
XX ID AAV62593 standard; DNA; 545 BP.
XX
XX AC AAV62593;
XX
XX DT 17-OCT-2003 (revised)
XX DT 17-DEC-1998 (first entry)
XX
XX DE Fusarium moniliforme PCR amplified ITS region DNA sequence.
XX
XX KW Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
XX OS Gibberella fujikuroi.
XX
XX FH Key
XX FH misc_feature 1..30 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "3' end of small subunit rRNA gene"
XX FT misc_feature 31..178
XX FT /*tag= b
XX FT /note= "ITS 1"
XX FT misc_feature 179..335
XX FT /*tag= c
XX FT /note= "5.8S rRNA gene"
XX FT misc_feature 336..488
XX FT /*tag= d
XX FT /note= "ITS 2"
XX FT misc_feature 489..545
XX FT /*tag= e
XX FT /note= "5' end of large subunit rRNA gene"
XX
XX PN US5814453-A.
XX
XX PD 29-SEP-1998.
XX
XX PF 02-JUL-1997; 97US-00887480.
XX
XX PR 19-APR-1995; 95WO-US004712.
XX PR 15-OCT-1996; 96US-00722187.
XX

```

PA (NOVS) NOVARTIS FINANCE CORP.
 XX
 PI Beck JJ;
 XX
 DR WPI; 1998-541745/46.
 XX
 PT DNA isolated from fungal RNA, and its internal transcribed spacer
 PT sequence - used for detecting fungal pathogens in plant tissue.
 XX
 PS Claim 2; Fig 3; 56pp; English.
 XX
 CC This represents the DNA sequence of the internal transcribed spacer (ITS)
 CC region that was PCR amplified from *Fusarium moniliforme*. The invention
 CC provides a DNA molecule isolated from the ribosomal RNA gene region of a
 CC fungal pathogen, where the DNA molecule consists of an ITS sequence
 CC selected from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*,
 CC *Fusarium moniliforme*, *Septoria avenae* or *Microdochium nivale*. A method
 CC for detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*
 CC *avenaceum* and *M. nivale* isolates is also provided. The method comprises
 CC isolating DNA from a plant leaf infected with at least one of the above
 CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
 CC PCR using specific primers from within these sequences. The pathogen(s)
 CC are detected by visualising the amplified part of the ITS sequence.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SO Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;
 Query Match 30.3%; Score 94; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 AATTCAGTATCATGATCTTTGAACGACATTGGCGCCGCCAGTATTCTGGCGGCA 87
 DB 256 AATTCAGTATCATGATCTTTGAACGACATTGGCGCCGCCAGTATTCTGGCGGCA 315
 QY 88 TGCCTGTTCGAGCGTCATTTCACCTCAAGCCC 121
 DB 316 TGCCTGTTCGAGCGTCATTTCACCTCAAGCCC 349

RESULT 15
 AAV59030
 ID AAV59030 standard; DNA; 545 BP.
 XX
 AC AAV59030;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1999 (first entry)
 XX
 DE F. moniliforme internal transcribed spacer.
 XX
 KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
 KW fungal pathogen identification; infection identification; ss.
 XX
 OS *Gibberella fujikuroi*.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 31..178
 FT /*tag= a
 FT /note= "ITS1"
 FT misc_feature 336..488
 FT /*tag= b
 FT /note= "ITS2"
 XX
 PN US5827695-A.
 PD 27-OCT-1998.
 XX
 PF 04-AUG-1997; 97US-00905314.
 PR 04-AUG-1997; 97US-00905314.
 XX

PA (NOVS) NOVARTIS FINANCE CORP.
 XX
 PI Beck JJ;
 XX
 DR WPI; 1998-593995/50.
 XX
 PT Wheat pathogen internal transcribed spacer sequences - used as a basis
 PT for primers for the species-specific polymerase chain reaction detection
 PT of the pathogens.
 XX
 PS Disclosure; Col 23-26; 20pp; English.
 XX
 CC This sequence represents an internal transcribed spacer (ITS) sequence of
 CC the invention. The primer pairs, based on the ITS sequences, are used for
 CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
 CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*
 CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
 CC strains of fungi show different symptoms during infection, which may or
 CC may not be due to infection. Early identification of the strain causing
 CC the infection allows early, and more specific fungicidal treatment.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SO Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;
 Query Match 30.3%; Score 94; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 AATTCAGTATCATGATCTTTGAACGACATTGGCGCCGCCAGTATTCTGGCGGCA 87
 DB 256 AATTCAGTATCATGATCTTTGAACGACATTGGCGCCGCCAGTATTCTGGCGGCA 315
 QY 88 TGCCTGTTCGAGCGTCATTTCACCTCAAGCCC 121
 DB 316 TGCCTGTTCGAGCGTCATTTCACCTCAAGCCC 349

Search completed: October 1, 2004, 09:02:49
 Job time : 260.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:06:18 : Search time 51.256 Seconds
(without alignments)
3356.386 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
Sequence: 1 aaatcgataagtaattgta.....ggaatcccgctgaactta 310

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 10

Total number of hits satisfying chosen parameters: 85480

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

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5: /cgn2_6/ptodata/2/ina/PTUS_CONB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	4 US-09-423-233-7	Sequence 7, Appl1
2	232	74.8	2293	3 US-09-645-073-1	Sequence 1, Appl1
3	99	31.9	531	1 US-08-652-127C-7	Sequence 7, Appl1
4	99	31.9	581	1 US-08-652-127C-6	Sequence 6, Appl1
5	94	30.3	504	1 US-08-887-480-82	Sequence 82, Appl1
6	94	30.3	504	1 US-08-905-314A-19	Sequence 19, Appl1
7	94	30.3	504	2 US-08-722-187-82	Sequence 82, Appl1
8	94	30.3	504	4 US-09-481-293-32	Sequence 32, Appl1
9	94	30.3	504	5 PCT-US95-04712-82	Sequence 84, Appl1
10	94	30.3	545	1 US-08-887-480-84	Sequence 21, Appl1
11	94	30.3	545	1 US-08-905-314A-21	Sequence 84, Appl1
12	94	30.3	546	1 US-08-887-480-96	Sequence 96, Appl1
13	94	30.3	546	1 US-08-905-314A-22	Sequence 22, Appl1
14	92	29.7	594	1 US-08-652-127C-5	Sequence 5, Appl1
15	79	25.5	319	4 US-09-423-233-6	Sequence 6, Appl1
16	66	21.3	561	1 US-08-905-314A-24	Sequence 24, Appl1
17	55	17.7	353	2 US-08-722-187-84	Sequence 84, Appl1
18	55	17.7	353	2 PCT-US95-04712-84	Sequence 84, Appl1
19	55	17.7	583	1 US-08-652-127C-8	Sequence 8, Appl1
20	52	16.8	503	1 US-08-887-480-83	Sequence 83, Appl1
21	52	16.8	503	1 US-08-905-314A-20	Sequence 20, Appl1
22	52	16.8	503	2 US-08-722-187-83	Sequence 83, Appl1
23	52	16.8	503	2 PCT-US95-04712-83	Sequence 83, Appl1
24	46	14.8	545	2 US-08-722-187-85	Sequence 85, Appl1
25	46	14.8	545	2 PCT-US95-04712-85	Sequence 85, Appl1
26	42	13.5	343	4 US-09-423-233-27	Sequence 27, Appl1
27	42	13.5	344	4 US-09-423-233-26	Sequence 26, Appl1

28	41	13.2	415	4 US-09-635-747-39	Sequence 39, Appl1
29	41	13.2	415	4 US-09-635-747-40	Sequence 40, Appl1
30	41	13.2	451	3 US-09-037-990B-5	Sequence 1, Appl1
31	41	13.2	515	4 US-09-517-790-1	Sequence 1, Appl1
32	41	13.2	516	4 US-09-517-790-2	Sequence 2, Appl1
33	41	13.2	523	4 US-09-517-790-4	Sequence 4, Appl1
34	41	13.2	526	4 US-08-481-293-13	Sequence 33, Appl1
35	41	13.2	534	1 US-08-233-608-5	Sequence 5, Appl1
36	41	13.2	534	1 US-08-887-480-5	Sequence 5, Appl1
37	41	13.2	534	2 US-08-722-187-5	Sequence 5, Appl1
38	41	13.2	534	5 PCT-US95-04712-5	Sequence 5, Appl1
39	41	13.2	536	4 US-09-517-790-5	Sequence 5, Appl1
40	41	13.2	540	1 US-08-233-608-6	Sequence 6, Appl1
41	41	13.2	540	1 US-08-887-480-6	Sequence 6, Appl1
42	41	13.2	540	2 US-08-722-187-6	Sequence 6, Appl1
43	41	13.2	540	5 PCT-US95-04712-6	Sequence 6, Appl1
44	41	13.2	548	1 US-08-233-608-1	Sequence 1, Appl1
45	41	13.2	548	1 US-08-887-480-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-423-233-7
; Sequence 7, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2e+160;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB      1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60

QY      61 TTGGGCGCGCGAGTATTCGCGGCGCATGCTGTTGAGCGTCAATTCGAACCTCGAAGCC 120
DB      61 TTGGGCGCGCGAGTATTCGCGGCGCATGCTGTTGAGCGTCAATTCGAACCTCGAAGCC 120

QY      121 CCGGGTTTGTTGGGGAATTCGCGAAGCCCTTCGCGAAGCGGCGCCGGAATCTAGTG 180
DB      121 CCGGGTTTGTTGGGGAATTCGCGAAGCCCTTCGCGAAGCGGCGCCGGAATCTAGTG 180

QY      181 GCGGTCGCTGCGAGCTTCATTCGTAAGTAAGTAAGAAACCTTCGCAATGTAACGCGCGC 240
DB      181 GCGGTCGCTGCGAGCTTCATTCGTAAGTAAGTAAGAAACCTTCGCAATGTAACGCGCGC 240

QY      241 GCGGTCGCTGCGAGCTTCATTCGTAAGTAAGTAAGAAACCTTCGCAATGTAACGCGCGC 300
DB      241 GCGGTCGCTGCGAGCTTCATTCGTAAGTAAGTAAGAAACCTTCGCAATGTAACGCGCGC 300

QY      301 CTGAACCTTAA 310
DB      301 CTGAACCTTAA 310

RESULT 2
US-09-645-073-1
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; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titer of Gibberellins GA4 and GA7
; FILE REFERENCE: I02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
; US-09-645-073-1

Query Match 74.8%; Score 232; DB 3; Length 2293;
Best Local Similarity 99.6%; Pred. No. 1,2e-117;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 87
Db 1999 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 2058
Qy 88 TGCCGTGAGCGGTCAATTTCAACCCCTCAAGCCCGGTTGGTGTGGGGAATCGGCA 147
Db 2059 TGCCGTGAGCGGTCAATTTCAACCCCTCAAGCCCGGTTGGTGTGGGGAATCGGCA 2118
Qy 148 GCCCTGCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 207
Db 2119 GCCCTGCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2178
Qy 208 AGTAGTAAACCCCTCGCACTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 267
Db 2179 AGTAGTAAACCCCTCGCACTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2238
Qy 268 GAATGTTGACCTCGGATCGAGTAGGAATACCCGCTGAATTTAA 310
Db 2239 GAATGTTGACCTCGGATCGAGTAGGAATACCCGCTGAATTTAA 2281

RESULT 3
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-7

Query Match 31.9%; Score 99; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 87
Db 230 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 289
Qy 88 TGCCGTGAGCGGTCAATTTCAACCCCTCAAGCCCGCGG 126
Db 290 TGCCGTGAGCGGTCAATTTCAACCCCTCAAGCCCGCGG 328

RESULT 4
US-08-652-127C-6
; Sequence 6, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-6

Query Match 31.9%; Score 99; DB 1; Length 581;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 87
Db 280 AATTCAGTGAATCATGATCTTTGAACGACATTGGCCCGCCAGATTTCTGGCGGCA 339
Qy 88 TGCCGTGAGCGGTCAATTTCAACCCCTCAAGCCCGCGG 126

Db 340 TGCGTTGAGCGTCATTTCAACCTCAAGCCCGGG 378

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RESULT 5
US-08-887-480-82
; Sequence 82, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8689
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319..472
; OTHER INFORMATION: /note= "ITS 2"
; NAME/KEY: misc_feature
; LOCATION: 473..504
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-887-480-82
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Query Match 30.3%; Score 94; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAGCAGCATTTGGCCCGCAGATTCTGGCGGCA 87
DB 239 AATTCAGTGAATCATTCGATCTTTGAAGCAGCATTTGGCCCGCAGATTCTGGCGGCA 298
QY 88 TGCGTTGAGCGTCATTTCAACCTCAAGCCCGGG 121
DB 299 TGCGTTGAGCGTCATTTCAACCTCAAGCCCGGG 332

RESULT 6
US-08-905-314A-19
; Sequence 19, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8689
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
; NAME/KEY: misc_feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319..472
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OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match      30.3%; Score 94; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 87
DB 239 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 298
QY 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121
DB 299 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 332

RESULT 7
US-08-722-187-82
Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligon, James M
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722.187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fcu1m.con)"
US-08-722-187-82
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```
Query Match      30.3%; Score 94; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 87
DB 239 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 298
QY 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121
DB 299 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 332

RESULT 8
US-09-481-293-32
Sequence 32, Application US/09481293
Patent No. 6485907
GENERAL INFORMATION:
APPLICANT: Beck, James
APPLICANT: Barnett, Jason
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
FILE REFERENCE: PB/5-3113PI
CURRENT APPLICATION NUMBER: US/09/481,293
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 504
TYPE: DNA
ORGANISM: Fusarium culmorum
US-09-481-293-32
```

```
Query Match      30.3%; Score 94; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 87
DB 242 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCGCGCAGATTTGGCGGCA 301
QY 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121
DB 302 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 335

RESULT 9
PCT-US95-04712-82
Sequence 82, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
```

ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504 /note="DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fculm.con)"
PCT-US95-04712-82

Query Match 30.3%; Score 94; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 5,8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGACGACGACATTCGCCCGCCAGATTTCTGGCGGCA 87
DB 239 AATTCAGTGAATCATCGAATCTTTGACGACGACATTCGCCCGCCAGATTTCTGGCGGCA 298
QY 88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 121
DB 299 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 332

RESULT 10
US-08-887-480-84
Sequence 84, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: PCRPMO1
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note="5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-887-480-84

Query Match 30.3%; Score 94; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 5,7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGACGACGACATTCGCCCGCCAGATTTCTGGCGGCA 87
DB 256 AATTCAGTGAATCATCGAATCTTTGACGACGACATTCGCCCGCCAGATTTCTGGCGGCA 315
QY 88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 121
DB 316 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 349

RESULT 11
US-08-905-314A-21
Sequence 21, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium moniliforme
; INDIVIDUAL ISOLATE: 4551
; CLONE: pCRFMON1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..178
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 179..335
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 336..488
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 489..545
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-905-314A-21

Query Match          30.3%; Score 94; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCAGTATTTGGCGGCA 87
DB 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCAGTATTTGGCGGCA 315

QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 316 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 349

RESULT 12
US-08-887-480-96
; Sequence 96, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium poae
; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
; INDIVIDUAL ISOLATE: sequence)
; IMMEDIATE SOURCE:
; CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
; CLONE: pCRFpoaeT756(3-1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..180
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181..337
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 338..489
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 490..546
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-887-480-96

Query Match          30.3%; Score 94; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCAGTATTTGGCGGCA 87
DB 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCAGTATTTGGCGGCA 317

QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 318 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 351

RESULT 13
US-08-905-314A-22
; Sequence 22, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
```

APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 582769sartis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905.314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: PCRpoae1427(1-2), PCRpoaeT534(2-2), and
FEATURE:
CLONE: PCRpoaeT756(3-1)
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-22
Query Match 30.3%; Score 94; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 5,7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 AATTCAGTGAATCATTCGATTTTGAACGACATTCGCGCCGCGAGTATTTCTGCGGGCA 87
DB 258 AATTCAGTGAATCATTCGATTTTGAACGACATTCGCGCCGCGAGTATTTCTGCGGGCA 317

QY 88 TGCCTGTCGAGGTCATTTCAACCTCAAGCCC 121
DB 318 TGCCTGTCGAGGTCATTTCAACCTCAAGCCC 351
RESULT 14
US-08-652-127C-5
Sequence 5, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 594
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-5
Query Match 29.7%; Score 92; DB 1; Length 594;
Best Local Similarity 100.0%; Pred. No. 7.2e-41;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 AATTCAGTGAATCATTCGATTTTGAACGACATTCGCGCCGCGAGTATTTCTGCGGGCA 87
DB 285 AATTCAGTGAATCATTCGATTTTGAACGACATTCGCGCCGCGAGTATTTCTGCGGGCA 344
QY 88 TGCCTGTCGAGGTCATTTCAACCTCAAGC 119
DB 345 TGCCTGTCGAGGTCATTTCAACCTCAAGC 376
RESULT 15
US-09-423-233-6
Sequence 6, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423.233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 6
LENGTH: 319

TYPE: DNA
 ORGANISM: Fusarium solani
 US-09-423-233-6

Query Match 25.5%; Score 79; DB 4; Length 319;
 Best Local Similarity 100.0%; Pred. No. 9.7e-34;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	28	AATTGAGTGAATCATCTTTGAACGACATTGCGCCGCCAGTATTCTGGCGGCA	87
Db	30	AATTGAGTGAATCATCTTTGAACGACATTGCGCCGCCAGTATTCTGGCGGCA	89
QY	88	TGCTGTTCGAGCGTCATT	106
Db	90	TGCTGTTCGAGCGTCATT	108

Search completed: October 1, 2004, 11:12:57
 Job time : 52.256 secs


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Db      1 AATGCCAGTAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
Qy      61 TTGGCCCGCCGCAAGTATCTGGCGGCGCATGCTGTTTCAGCGCTCATTTCAACCTCAAGCC 120
Db      61 TTGGCCCGCCGCAAGTATCTGGCGGCGCATGCTGTTTCAGCGCTCATTTCAACCTCAAGCC 120
Qy      121 CCGCGGTTTGGTGTGGGGATCGCAAGCCCTTGGCGGCAAGCCGCGCGGCAAAATCTGTG 180
Db      121 CCGCGGTTTGGTGTGGGGATCGCAAGCCCTTGGCGGCAAGCCGCGCGGCAAAATCTGTG 180
Qy      181 GCGGCTCGCTGCACTTCATTCAGTAGTAAACCCCTCGCACTGTATCGCGCGC 240
Db      181 GCGGCTCGCTGCACTTCATTCAGTAGTAAACCCCTCGCACTGTATCGCGCGC 240
Qy      241 GGGCAAGCCGTTAAACCCCACTTGTGATTTGACTCGGATCAGTGAATATCCG 300
Db      241 GGGCAAGCCGTTAAACCCCACTTGTGATTTGACTCGGATCAGTGAATATCCG 300
Qy      301 CTGAACCTTAA 310
Db      301 CTGAACCTTAA 310

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RESULT 2

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US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

```

```

Query Match      73.5%; Score 228; DB 10; Length 534;
Best Local Similarity 99.6%; Pred. No. 1.3e-119;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      28 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 87
Db      256 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 315
Qy      88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTTGGTGTGGGATCGGCA 147
Db      316 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTTGGTGTGGGATCGGCA 375
Qy      148 GCGCTTGGGCAAGCCGCGCCGCAAAATCTAGTGGCGGTCTGCTGCAAGCTTCATTGCGT 207
Db      376 GCGCTTGGGCAAGCCGCGCCGCAAAATCTAGTGGCGGTCTGCTGCAAGCTTCATTGCGT 435
Qy      208 AGTAGTAAACCCCTCGCACTGTATCGCGGCGCGGCAACCCGTTAAACCCCACTTCT 267
Db      436 AGTAGTAAACCCCTCGCACTGTATCGCGGCGCGGCAACCCGTTAAACCCCACTTCT 495
Qy      268 GAATGTTGACCTCGATCAGTGAATATCCCGCTGAAC 306
Db      496 GAATGTTGACCTCGATCAGTGAATATCCCGCTGAAC 534

```

RESULT 3

```

US-09-961-755A-6
; Sequence 6, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6

```

```

Query Match      30.3%; Score 94; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 5e-43;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      28 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 87
Db      256 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 315
Qy      88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 121
Db      316 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 349

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RESULT 4

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US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

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```

Query Match      30.3%; Score 94; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 5e-43;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      28 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 87
Db      256 AATTCAGTGAATCATCGAATCTTTGAACGACATTGCGCCGCGCAGTATCTGGCGGCA 315
Qy      88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 121
Db      316 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 349

```

RESULT 5

```

US-09-961-755A-8
; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, Jim
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24

```

NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 522
TYPE: DNA
ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match 30.3%; Score 94; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 5e-43;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCGCA 87
DB 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCGCA 315
QY 88 TGCCGTTCGAGCGGTGATTTCAACCTCAAGCCC 121
DB 316 TGCCGTTCGAGCGGTGATTTCAACCTCAAGCCC 349

RESULT 6
US-10-046-955-6

Sequence 6, Application US/10046955
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aidorevich, Lilliana

APPLICANT: Choi, Jong Seo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-6

Query Match 25.5%; Score 79; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCGCA 87
DB 30 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCGCA 89
QY 88 TGCCGTTCGAGCGGTGATTTCAACCTCAAGCCC 106
DB 90 TGCCGTTCGAGCGGTGATTTCAACCTCAAGCCC 108

RESULT 7
US-10-046-955-27

Sequence 27, Application US/10046955
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aidorevich, Lilliana
APPLICANT: Choi, Jong Seo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 343
TYPE: DNA
ORGANISM: Scedosporium apiospermum
US-10-046-955-27

Query Match 13.5%; Score 42; DB 15; Length 343;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCG 69
DB 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCG 69

RESULT 8
US-10-046-955-26

Sequence 26, Application US/10046955
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aidorevich, Lilliana

APPLICANT: Choi, Jong Seo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 344
TYPE: DNA
ORGANISM: Scedosporium apiospermum
US-10-046-955-26

Query Match 13.5%; Score 42; DB 15; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCG 69
DB 29 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCGCCG 70

RESULT 9

US-09-961-663-14
 ; Sequence 14, Application US/09961663
 ; Patent No. US20020115084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
 ; FILE REFERENCE: PB/5-31382A
 ; CURRENT APPLICATION NUMBER: US/09/961,663
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: US 60/211902
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 377
 ; TYPE: DNA
 ; ORGANISM: Mycosphaerella sp.
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(377)
 ; OTHER INFORMATION: Truncated DNA sequence for the Internal
 ; OTHER INFORMATION: Transcribed Spacer of a fungus amplified from
 ; OTHER INFORMATION: banana sample "Capesterre-babin 2".
 US-09-961-663-14

Query Match 13.2%; Score 41; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68
 DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 10
 US-09-961-663-15
 ; Sequence 15, Application US/09961663
 ; Patent No. US20020115084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
 ; FILE REFERENCE: PB/5-31382A
 ; CURRENT APPLICATION NUMBER: US/09/961,663
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: US 60/211902
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 377
 ; TYPE: DNA
 ; ORGANISM: Mycosphaerella sp.
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(377)
 ; OTHER INFORMATION: Truncated DNA sequence for the Internal
 ; OTHER INFORMATION: Transcribed Spacer of fungus amplified from banana
 ; OTHER INFORMATION: sample "Matouba bas 3"
 US-09-961-663-15

Query Match 13.2%; Score 41; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68
 DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 11
 US-09-961-663-16
 ; Sequence 16, Application US/09961663
 ; Patent No. US20020115084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
 ; FILE REFERENCE: PB/5-31382A
 ; CURRENT APPLICATION NUMBER: US/09/961,663
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: US 60/211902
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 377
 ; TYPE: DNA
 ; ORGANISM: Mycosphaerella sp.
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(377)
 ; OTHER INFORMATION: Truncated DNA sequence for the Internal
 ; OTHER INFORMATION: Transcribed Spacer of a fungus amplified from
 ; OTHER INFORMATION: banana sample "Temoin Infest Forte"
 US-09-961-663-16

Query Match 13.2%; Score 41; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68
 DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 12
 US-09-961-663-19
 ; Sequence 19, Application US/09961663
 ; Patent No. US20020115084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnett, Jason
 ; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
 ; FILE REFERENCE: PB/5-31382A
 ; CURRENT APPLICATION NUMBER: US/09/961,663
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: US 60/211902
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 377
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Consensus
 ; OTHER INFORMATION: sequence of Mycosphaerella sp. ITS sequences shown
 ; OTHER INFORMATION: in SEQ ID NO:14-16.
 US-09-961-663-19

Query Match 13.2%; Score 41; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68
 DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 13

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US-10-356-320-1
; Sequence 1, Application US/10356320
; Publication No. US20040009573A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Ford, Eugene
; APPLICANT: James, Harper K.
; TITLE OF INVENTION: Pestalotiopsis Microsporia Isolates and Compounds Derived
; TITLE OF INVENTION: Therefrom
; FILE REFERENCE: A-72093 (470425-4)
; CURRENT APPLICATION NUMBER: US/10/356,320
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/352,254
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Pestalotiopsis sp. NG12-30
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301
; DATABASE ENTRY DATE: 2002-06-02
; RELEVANT RESIDUES: (1)..(466)
US-10-356-320-1

Query Match      13.2%; Score 41; DB 16; Length 466;
Best Local Similarity 100.0%; Pred. No. 9.7e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 68
DB      221 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 261

RESULT 14
US-09-961-663-17
; Sequence 17, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, James
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: PB/5-31382A
; CURRENT APPLICATION NUMBER: US/09/961,663
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/211902
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Mycosphaerella fijiensis
US-09-961-663-17

Query Match      13.2%; Score 41; DB 9; Length 534;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 68
DB      249 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 289

RESULT 15
US-09-961-663-18
; Sequence 18, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Beck, James
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; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: PB/5-31382A
; CURRENT APPLICATION NUMBER: US/09/961,663
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/211902
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Mycosphaerella musicola
US-09-961-663-18

Query Match      13.2%; Score 41; DB 9; Length 540;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 68
DB      258 AATTCAGTGAATCATCGAATCTTTGACGACATTTGGCGCC 298

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:04:24 Search time 2101.99 seconds
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Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
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8: em_hcc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	21.6	735	14	CF880267 tric081xc
2	67	21.6	739	14	CF870552 tric024xb
3	67	21.6	755	14	CF870665 tric024xj
4	67	21.6	796	14	CB900742 CB900742 tric024xb

5	67	21.6	808	14	CB900860 tric024xj
6	67	21.6	840	14	CB907036 tric081xc
7	45	14.5	704	13	B0751285 B0751285
8	45	14.5	725	13	B0752001 B0752001
9	45	14.5	743	13	B0751027 B0751027
10	45	14.5	745	13	B0751971 B0751971
11	45	14.5	758	13	B0751399 B0751399
12	45	14.5	774	13	B0752136 B0752136
13	45	14.5	806	13	B0751015 B0751015
14	45	14.5	806	13	B0751484 B0751484
15	45	14.5	994	13	B0752289 B0752289
16	44	14.2	169	12	BM870292 BM870292
17	42	13.5	560	14	CF944721 CF944721
18	42	13.5	780	14	CB903866 CB903866
19	42	13.5	780	14	CF874466 CF874466
20	39	12.6	366	12	B1850064 B1850064
21	39	12.6	376	13	B0752420 B0752420
22	39	12.6	431	14	CD034605 CD034605
23	39	12.6	769	14	CD456856 CD456856
24	39	12.6	989	14	CD456827 CD456827
25	36	11.6	150	12	BM361006 BM361006
26	36	11.6	150	12	BM361064 BM361064
27	36	11.6	157	12	BM361387 BM361387
28	36	11.6	157	12	BM361430 BM361430
29	36	11.6	194	13	B0751934 B0751934
30	35	11.3	214	10	BF251183 BF251183
31	35	11.3	320	28	AZ925653 AZ925653
32	35	11.3	360	28	AZ923094 AZ923094
33	35	11.3	384	28	BZ304161 BZ304161
34	35	11.3	392	28	AZ923588 AZ923588
35	35	11.3	407	28	AZ923857 AZ923857
36	35	11.3	424	28	AZ923253 AZ923253
37	35	11.3	436	28	AQ874616 AQ874616
38	35	11.3	436	28	AQ492096 AQ492096
39	35	11.3	440	28	AZ931033 AZ931033
40	35	11.3	448	28	AZ916873 AZ916873
41	35	11.3	453	28	AQ874719 AQ874719
42	35	11.3	454	29	CNS07850 CNS07850
43	35	11.3	456	28	AZ923320 AZ923320
44	35	11.3	458	28	BZ304060 BZ304060
45	35	11.3	462	28	AZ931784 AZ931784

ALIGNMENTS

RESULT 1
LOCUS tric081xc18.b2 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina CDNA clone tric081xc18, mRNA sequence.
ACCESSION CF880267
VERSION CF880267.1 GI:38134949
KEYWORDS EST.

SOURCE
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
AUTHORS Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and
Dean, R.A.

TITLE Analysis of the protein processing and secretion pathways in a
Trichoderma reesei EST dataset
JOURNAL Unpublished (2003)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: 1T-P1 primer.

FEATURES
source Location/Qualifiers
1.739
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QMe6"
/db_xref="taxon:51453"
/clone="tric024xb14"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: PREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 87
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77 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 136
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QY 88 TGCCTGT 94
|||
Db 137 TGCCTGT 143

RESULT 2
CF870552 739 bp mRNA linear EST 31-OCT-2003
LOCUS trico24xb14.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone trico24xb14, mRNA sequence.
VERSION CF870552
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.
REFERENCE 1 (bases 1 to 739)
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL Unpublished (2003)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
Location/Qualifiers
1.739
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QMe6"
/db_xref="taxon:51453"
/clone="trico24xb14"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: PREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 87
|||
Db 70 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 129
|||
QY 88 TGCCTGT 94
|||
Db 130 TGCCTGT 136

RESULT 3
CF870665 755 bp mRNA linear EST 31-OCT-2003
LOCUS trico24xb104.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone trico24xb104, mRNA sequence.
VERSION CF870665
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.
REFERENCE 1 (bases 1 to 755)
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset
JOURNAL Unpublished (2003)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: Tr-F1 primer.
Location/Qualifiers
1.755
/organism="Hypocrea jecorina"
/mol_type="mRNA"
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/db_xref="taxon:51453"
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/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: PREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 755;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 87
|||
Db 70 AATTGATGATCATCTTGAACGACATTGGCCCGCCAGTATTCTGGCGGCA 129
|||
QY 88 TGCCTGT 94
|||
Db 130 TGCCTGT 136

RESULT 4
CB900742 796 bp mRNA linear EST 02-JUL-2003
LOCUS trico24xb14 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone trico24xb14, mRNA sequence.
VERSION CB900742
KEYWORDS EST.
GI:30115400

SOURCE
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
1 (bases 1 to 796)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
JOURNAL MEDLINE
PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

FEATURES
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/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric024x14"
/dev_stage="mycelia"
/note="Vector: PREP3; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 796;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
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tric024x104 T.reesei mycelial culture, Version 3 apr11 Hypocrea
jecorina cDNA clone tric024x104, mRNA sequence.

ACCESSION
CB900860
CB900860.1 GI:30115518

VERSION
EST.

KEYWORDS
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

REFERENCE
AUTHORS
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
JOURNAL MEDLINE
PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 796;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
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tric024x104 T.reesei mycelial culture, Version 3 apr11 Hypocrea
jecorina cDNA clone tric024x104, mRNA sequence.

ACCESSION
CB900860
CB900860.1 GI:30115518

VERSION
EST.

KEYWORDS
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
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J. Biol. Chem. 278 (34), 31988-31997 (2003)

REFERENCE
AUTHORS
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
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PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 796;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
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LOCUS
CB900860 808 bp mRNA linear EST 02-JUL-2003
tric024x104 T.reesei mycelial culture, Version 3 apr11 Hypocrea
jecorina cDNA clone tric024x104, mRNA sequence.

ACCESSION
CB900860
CB900860.1 GI:30115518

VERSION
EST.

KEYWORDS
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

REFERENCE
AUTHORS
1 (bases 1 to 808)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
JOURNAL MEDLINE
PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

SOURCE
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
1 (bases 1 to 796)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
JOURNAL MEDLINE
PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
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tric081xc18 T.reesei mycelial culture, Version 3 apr11 Hypocrea
jecorina cDNA clone tric081xc18, mRNA sequence.

ACCESSION
CB907036
CB907036.1 GI:30121694

VERSION
EST.

KEYWORDS
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 840)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

REFERENCE
AUTHORS
1 (bases 1 to 840)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
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22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

ORIGIN
Query Match 21.6%; Score 67; DB 14; Length 808;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
CB907036 840 bp mRNA linear EST 02-JUL-2003
tric081xc18 T.reesei mycelial culture, Version 3 apr11 Hypocrea
jecorina cDNA clone tric081xc18, mRNA sequence.

ACCESSION
CB907036
CB907036.1 GI:30121694

VERSION
EST.

KEYWORDS
Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 840)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

REFERENCE
AUTHORS
1 (bases 1 to 840)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE
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PUBMED
22803314
12788920
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA

Query Match 21.6%; Score 67; DB 14; Length 840;
 Best Local Similarity 100.0%; Pred. No. 1.8e-24;
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 sequence.
 accession BQ752001
 version BQ752001.1
 keywords GI:21907406
 source EST.
 organism Colletotrichum trifolii
 reference Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
 Cheung,F. and Fraser,C.M.
 title ESTs from mycelia of Colletotrichum trifolii race 1
 journal Unpublished (2002)
 comment Other ESTs: EST632563
 contact: Deborah A. Samac
 department of Plant Pathology
 university of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 tel: 612 625 1243
 fax: 651 649 5058
 email: debby@pucini.crl.umn.edu
 tigr sequence name: MTSAD127V More information is available at:
 www.medicago.org
 seq primer: (gca ata cga ctc act ata ggg c).
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 /lab_host="D5alphi"
 /clone_lib="DSCOT"
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ORIGIN
 Query Match 14.5%; Score 45; DB 13; Length 704;
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Query Match 14.5%; Score 45; DB 13; Length 725;
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 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 sequence.
 accession BQ751027
 version BQ751027.1
 keywords GI:21907406
 source EST.
 organism Colletotrichum trifolii
 reference Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
 Cheung,F. and Fraser,C.M.
 title ESTs from mycelia of Colletotrichum trifolii race 1
 journal Unpublished (2002)
 comment Other ESTs: EST632563
 contact: Deborah A. Samac
 department of Plant Pathology
 university of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 tel: 612 625 1243
 fax: 651 649 5058
 email: debby@pucini.crl.umn.edu
 tigr sequence name: MTSAD122TV More information is available at:
 www.medicago.org
 seq primer: (gca ata cga ctc act ata ggg c).
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 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; Isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN
 Query Match 14.5%; Score 45; DB 13; Length 725;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
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 keywords
 EST.
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 Colletotrichum trifolii
 organism
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 reference
 1 (bases 1 to 743)
 Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Cheung, F., and Fraser, C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 unpublished (2002)
 title
 JOURNAL
 comment
 Other ESTs: EST615589
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debby@puccini.crl.umn.edu
 TIGR sequence name: MTSAB20TV More information is available at:
 www.medicago.org
 Seq primer: (gca ata cga ctc act ata ggg c).
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 /note="Vector: pBluescript SK+, Site 1: EcoRI, Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 743;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

42 ATTCTGGCGGCGATGCTGTTGAGCGTCATTTCACCTCAAGC 86

RESULT 10
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 accession B0751971
 version B0751971
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 source EST.
 organism Colletotrichum trifolii
 comment Colletotrichum trifolii
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae; mitosporic Phyllostachyaceae; Colletotrichum.

reference
 1 (bases 1 to 745)
 Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Cheung, F., and Fraser, C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 unpublished (2002)
 title
 JOURNAL
 comment
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debby@puccini.crl.umn.edu
 TIGR sequence name: MTSAB103TV More information is available at:
 www.medicago.org
 Seq primer: (gca ata cga ctc act ata ggg c).
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FEATURES

source

Query Match 14.5%; Score 45; DB 13; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
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ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
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Db

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 source EST.
 organism Colletotrichum trifolii
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 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae; mitosporic Phyllostachyaceae; Colletotrichum.
 reference
 1 (bases 1 to 758)
 Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Cheung, F., and Fraser, C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 unpublished (2002)
 title
 JOURNAL
 comment
 Other ESTs: EST631961
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debbys@pucini.crl.umn.edu
 TIGR sequence name: MTSAD95TV More information is available at:
 www.medicago.org
 Seq primer: (gta Aca Cga Ctc Act Aca 999 C).

FEATURES

source

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 /clone_lib="DSC7"
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ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 758;
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 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 KEYWORDS EST.
 SOURCE Colletotrichum trifolii
 ORGANISM Colletotrichum trifolii
 COMMENT Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae; mitosporic Phyllochoraceae; Colletotrichum.
 1 (bases 1 to 774)
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Frazer,C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 Unpublished (2002)
 Other ESTs: EST632698
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debbys@pucini.crl.umn.edu
 TIGR sequence name: MTSAD95TV More information is available at:
 www.medicago.org

FEATURES

source

1.774
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 ATTCTGGCGGCGATGCTGTTCGAGCGTCATTTCACCTCAAGC 119
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 Db 42 ATTCTGGCGGCGATGCTGTTCGAGCGTCATTTCACCTCAAGC 86

/mol_type="mRNA"
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 /clone="pDSC710-23"
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 /dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
 /lab_host="DH5alpha"
 /clone_lib="DSC7"
 /note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into Bluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

RESULT 13
 LOCUS B0751015 806 bp mRNA linear EST 18-JUL-2002
 DEFINITION EST631578 DSC7 Colletotrichum trifolii cDNA clone pDSC72-7, mRNA
 sequence.
 ACCESSION B0751015
 VERSION B0751015.1 GI:21906420
 KEYWORDS EST.
 SOURCE Colletotrichum trifolii
 ORGANISM Colletotrichum trifolii
 COMMENT Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae; mitosporic Phyllochoraceae; Colletotrichum.
 1 (bases 1 to 806)
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Frazer,C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 Unpublished (2002)
 Other ESTs: EST631577
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debbys@pucini.crl.umn.edu
 TIGR sequence name: MTSAB07TV More information is available at:
 www.medicago.org

FEATURES

source

1.806
 /organism="Colletotrichum trifolii"
 /mol_type="mRNA"
 /strain="race 1"
 /db_xref="taxon:5466"
 /clone="pDSC72-7"
 /tissue_type="mycelia"
 /dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
 /lab_host="DH5alpha"

/clone.lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 806;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 75 ATCTGGCGGCGATGCTGTTCGAGCGTCATTCAACCTCAAGC 119
|||||
43 ATTCTGGCGGCGATGCTGTTCGAGCGTCATTCAACCTCAAGC 87

RESULT 14
BQ751484 806 bp mRNA linear EST 18-JUL-2002
LOCUS BQ751484
DEFINITION BQ751484 DSCT Colletotrichum trifolii cDNA clone pDSCT5-48, mRNA
SEQUENCE.
ACCESSION BQ751484
VERSION BQ751484.1 GI:21906889
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 806)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,
Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other ESTs: EST632046
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAB48TV More information is available at:
www.medicago.org
Seq primer: (gtA ACA CGA CTC ACT ACA 999 C).

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

1. 806
/organism="Colletotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
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/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone.lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of

the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 806;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 75 ATCTGGCGGCGATGCTGTTCGAGCGTCATTCAACCTCAAGC 119
|||||
43 ATTCTGGCGGCGATGCTGTTCGAGCGTCATTCAACCTCAAGC 87

RESULT 15
BQ752289 994 bp mRNA linear EST 18-JUL-2002
LOCUS BQ752289
DEFINITION BQ752289 DSCT Colletotrichum trifolii cDNA clone pDSCT11-50, mRNA
SEQUENCE.
ACCESSION BQ752289
VERSION BQ752289.1 GI:21907694
KEYWORDS EST.
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 994)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,
Cheung, F. and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other ESTs: EST632851
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAK50TV More information is available at:
www.medicago.org
Seq primer: (gtA ACA CGA CTC ACT ACA 999 C).

FEATURES
source

1. 994
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/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCT11-50"
/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone.lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 994;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 146.608 Seconds

(without alignments)
5321.503 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgtcaatcgcgtccctc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sgs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sgs:*
28: em_un:*
29: em_vt:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
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37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6 AR206444	AR206444 Sequence
2	18	100.0	18	6 BD083635	BD083635 Nucleic a
3	18	100.0	335	8 AF162898	AF162898 Fusarium
4	18	100.0	335	8 AF162899	AF162899 Fusarium
5	18	100.0	336	8 AF162900	AF162900 Fusarium
6	18	100.0	328	8 AF339418	AF339418 Fusarium
7	18	100.0	426	8 AF383320	AF383320 Fusarium
8	18	100.0	430	8 AF502842	AF502842 Leaf lilt
9	18	100.0	441	8 AY387703	AY387703 Fusarium
10	18	100.0	445	8 AY380575	AY380575 Fusarium
11	18	100.0	445	8 AY387698	AY387698 Fusarium
12	18	100.0	445	8 AY387699	AY387699 Fusarium
13	18	100.0	445	8 AY387702	AY387702 Fusarium
14	18	100.0	445	8 AY387704	AY387704 Fusarium
15	18	100.0	445	8 AY387705	AY387705 Fusarium
16	18	100.0	447	8 AY387701	AY387701 Fusarium
17	18	100.0	455	8 FOU28159	U28159 Fusarium ox
18	18	100.0	455	8 FOU28161	U28161 Fusarium ox
19	18	100.0	456	8 AF440527	AF440527 Fusarium
20	18	100.0	456	8 AF440529	AF440529 Fusarium
21	18	100.0	456	8 AF440531	AF440531 Fusarium
22	18	100.0	456	8 AF440532	AF440532 Fusarium
23	18	100.0	456	8 AF440534	AF440534 Fusarium
24	18	100.0	456	8 AF440539	AF440539 Fusarium
25	18	100.0	456	8 AF440540	AF440540 Fusarium
26	18	100.0	456	8 AF440542	AF440542 Fusarium
27	18	100.0	456	8 AF440552	AF440552 Fusarium
28	18	100.0	456	8 AF440561	AF440561 Fusarium
29	18	100.0	456	8 AF440563	AF440563 Fusarium
30	18	100.0	457	8 AF440533	AF440533 Fusarium
31	18	100.0	457	8 AF440538	AF440538 Fusarium
32	18	100.0	457	8 AF440560	AF440560 Fusarium
33	18	100.0	457	8 AF440562	AF440562 Fusarium
34	18	100.0	458	8 AF055220	AF055220 Fusarium
35	18	100.0	460	8 AY259214	AY259214 Fusarium
36	18	100.0	497	8 AY243058	AY243058 Ascomycet
37	18	100.0	501	8 AY247553	AY247553 Fusarium
38	18	100.0	501	8 AY262831	AY262831 Fusarium
39	18	100.0	501	8 AY354386	AY354386 Fusarium
40	18	100.0	501	8 AY354388	AY354388 Fusarium
41	18	100.0	501	8 AY354389	AY354389 Fusarium
42	18	100.0	501	8 AY354390	AY354390 Fusarium
43	18	100.0	501	8 AY354393	AY354393 Fusarium
44	18	100.0	501	8 AY354396	AY354396 Fusarium
45	18	100.0	501	8 AY354397	AY354397 Fusarium

ALIGNMENTS

RESULT 1
LOCUS AR206444
DEFINITION Sequence 50 from patent US 6372430.
ACCESSION AR206444
VERSION AR206444.1 GI:21505047
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.Soo.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL Patent: US 6372430-A 50 16-APR-2002;

FEATURES	Location/Qualifiers
source	1..18 /organism="unknown"
ORIGIN	/mol_type="unassigned DNA"
Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 22;
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QY	1 CGTTAATTCGCGTTCCTC 18
Db	1 CGTTAATTCGCGTTCCTC 18
RESULT 2	
BD083635	18 bp DNA linear PAT 27-AUG-2002
LOCUS	
DEFINITION	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi.
ACCESSION	BD083635
VERSION	BD083635.1 GI:22629245
KEYWORDS	JP 2001525665-A/50.
SOURCE	Fusarium oxysporum
ORGANISM	Fusarium oxysporum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex. 1 (bases 1 to 18)
REFERENCE	Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S. Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi Patent: JP 2001525665-A 50 11-DEC-2001;
JOURNAL	THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
COMMENT	OS Fusarium oxysporum PN JP 2001525665-A/50 PD 11-DEC-2001 PF 01-MAY-1998 JP 1998548275 PR 02-MAY-1997 US 60/045400 PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO PI CHOI PC C12Q1/68 CC Strandedness: Single; CC Topology: Linear; FH key Location/Qualifiers.
FEATURES	Location/Qualifiers.
source	1..18 /organism="Fusarium oxysporum" /mol_type="genomic DNA" /db_xref="taxon:5507"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGTTAATTCGCGTTCCTC 18
Db	1 CGTTAATTCGCGTTCCTC 18
RESULT 3	
LOCUS	335 bp DNA linear PLN 15-NOV-2001
DEFINITION	Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.
ACCESSION	AF162898
VERSION	AF162898.1 GI:5690387

KEYWORDS	Fusarium oxysporum f. sp. conglutinans
SOURCE	Fusarium oxysporum f. sp. conglutinans
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
REFERENCE	1 (bases 1 to 335)
AUTHORS	Min,B.R.
TITLE	Direct Submission
JOURNAL	Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea .
FEATURES	Location/Qualifiers
source	1..335 /organism="Fusarium oxysporum f. sp. conglutinans" /mol_type="genomic DNA" /strain="MAFF 744001" /db_xref="taxon:100902" /note="forma specialis: conglutinans forma specialis: conglutinans" 1..128 /product="5.8S ribosomal RNA" 129..277 /product="internal transcribed spacer 2" 278..>335 /product="28S ribosomal RNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 8; Length 335;
Best Local Similarity	100.0%; Pred. NO. 24;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CGTTAATTCGGCTTCTC 18 Db 162 CGTAATTCCGCGTCTC 179
RESULT 4	
LOCUS	AF162899 335 bp DNA linear PLN 04-AUG-1999
DEFINITION	Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF162899
VERSION	AF162899.1 GI:5690388
KEYWORDS	.
SOURCE	Fusarium oxysporum f. sp. fragariae
ORGANISM	Fusarium oxysporum f. sp. fragariae
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
AUTHORS	1 (bases 1 to 335)
TITLE	Min,B.R.
JOURNAL	Direct Submission
FEATURES	Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
source	Location/Qualifiers
1..335	/organism="Fusarium oxysporum f. sp. fragariae" /mol_type="genomic DNA" /strain="MAFF 744009" /db_xref="taxon:100903" /note="forma specialis: fragariae forma specialis: fragariae" 1..128 /product="5.8S ribosomal RNA" 129..277 /product="internal transcribed spacer 2" 278..>335 /product="28S ribosomal RNA"
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Best Local Similarity	100.0%; Pred. NO. 24;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||

Db 162 CGTTAATTCGGCTTCCTC 179

RESULT 5
AF162900

LOCUS AF162900 336 bp DNA linear PLN 04-AUG-1999

DEFINITION Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF162900

VERSION AF162900.1 GI:5690389

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 336)
Min, B. R.
Direct Submission
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea

FEATURES
Location/Qualifiers
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forma specialis: raphani
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129..274
/product="internal transcribed spacer 2"
275..336
/product="28S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||

Db 163 CGTTAATTCGGCTTCCTC 180

RESULT 6
AF339418

LOCUS AF339418 338 bp DNA linear PLN 25-OCT-2002

DEFINITION Fusarium oxysporum strain FS-1 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF339418

VERSION AF339418.1 GI:24369714

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 338)
Tooley, P. W., Hatziloukas, E., Scott, D. L. Jr. and Carras, M. M.
Use of ligase chain reaction for detection of Phytophthora
infestans in potatoes
Unpublished
2 (bases 1 to 338)
Tooley, P. W., Hatziloukas, E., Scott, D. L. Jr. and Carras, M. M.
Direct Submission
Submitted (23-JAN-2001) Agricultural Research Service, U.S.

Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD
21702-5023, USA

FEATURES
Location/Qualifiers
1..338
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/mol_type="genomic DNA"
/strain="FS-1"
/db_xref="taxon:5507"
<1..338
/note="contains 5.8S ribosomal RNA, internal transcribed
spacer 2, and 28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 338;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||

Db 162 CGTTAATTCGGCTTCCTC 179

RESULT 7
AY383320

LOCUS AY383320 426 bp DNA linear PLN 05-OCT-2003

DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-1-1 internal
transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,
complete sequence; and internal transcribed spacer 2, partial
sequence.

ACCESSION AY383320

VERSION AY383320.1 GI:37142968

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum f. sp. vanillae
Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 426)
Wang, Y. Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X. Y.
Fusarium oxysporum f. sp. vanillae isolate DL-1-1 ITS1, 5.8S rDNA,
ITS 2 sequence
Unpublished
2 (bases 1 to 426)
Wang, Y. Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X. Y.
Direct Submission
Submitted (08-SEP-2003) Dept. Plant Pathology, Yunnan Agricultural
University, Long Tou Street, Kunming, Yunnan 650201, P. R. China

FEATURES
Location/Qualifiers
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/organism="Fusarium oxysporum f. sp. vanillae"
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/isolate="DL-1-1"
/db_xref="taxon:247126"
/note="forma specialis: vanillae"
<1..117
/product="internal transcribed spacer 1"
118..274
/product="5.8S ribosomal RNA"
275..426
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||

Db 309 CGTTAATTCGGCTTCCTC 326

RESULT 8
AF502842/c

LOCUS AF502842 430 bp DNA linear PLN 13-MAY-2002
 DEFINITION leaf litter ascomycete strain its331 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AF502842
 VERSION AF502842
 KEYWORDS
 SOURCE leaf litter ascomycete strain its331
 ORGANISM Eukaryota; Fungi; Ascomycota.
 REFERENCE 1 (bases 1 to 430)
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
 TITLE Biogeography of leaf litter fungi
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 430)
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
 FEATURES
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 1..430
 /organism="leaf litter ascomycete strain its331"
 /mol_type="genomic DNA"
 /strain="its331"
 /isolate="1000502849"
 /specific_host="Miconia te"
 /db_xref="taxon:194114"
 /country="Puerto Rico"
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 /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA and internal transcribed spacer 2"
 ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 430;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTTAATTCGGCTTCCTC 18
 Db 82 CGTTAATTCGGCTTCCTC 65
 RESULT 9
 LOCUS AY387703 441 bp DNA linear PLN 07-OCT-2003
 DEFINITION Fusarium oxysporum isolate DU-2-7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AY387703
 VERSION AY387703
 KEYWORDS
 SOURCE Fusarium oxysporum
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
 REFERENCE 1 (bases 1 to 441)
 AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.
 TITLE Fusarium oxysporum isolate DU-2-7 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished
 REFERENCE 2 (bases 1 to 441)
 AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
 FEATURES
 Location/Qualifiers

source
 1..441
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="DU-2-7"
 /db_xref="taxon:5507"
 <1..135
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 136..293
 /product="5.8S ribosomal RNA"
 294..>441
 /product="internal transcribed spacer 2"
 ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 441;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTTAATTCGGCTTCCTC 18
 Db 327 CGTTAATTCGGCTTCCTC 344
 RESULT 10
 LOCUS AY380575 445 bp DNA linear PLN 04-OCT-2003
 DEFINITION Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AY380575
 VERSION AY380575
 KEYWORDS
 SOURCE Fusarium oxysporum f. sp. vanillae
 ORGANISM Fusarium oxysporum f. sp. vanillae
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
 REFERENCE 1 (bases 1 to 445)
 AUTHORS Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.
 TITLE ITS1, 5.8S and ITS2 rDNA sequence from Fusarium oxysporum f. sp. vanillae Unpublished
 REFERENCE 2 (bases 1 to 445)
 AUTHORS Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples Republic of China
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 /organism="Fusarium oxysporum f. sp. vanillae"
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 /isolate="HK-5a-4"
 /db_xref="taxon:247126"
 /note="forma specialis: vanillae"
 <1..135
 /product="internal transcribed spacer 1"
 136..293
 /product="5.8S ribosomal RNA"
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 /product="internal transcribed spacer 2"
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 Query Match 100.0%; Score 18; DB 8; Length 445;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTTAATTCGGCTTCCTC 18
 Db 327 CGTTAATTCGGCTTCCTC 344

RESULT 11
LOCUS AY387698 445 bp DNA linear PLN 07-OCT-2003
DEFINITION Fusarium oxysporum f. sp. vanillae isolate ML-8-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387698
VERSION AY387698.1 GI:37362903
KEYWORDS Fusarium oxysporum f. sp. vanillae
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Fusarium oxysporum f. sp. vanillae
REFERENCE Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B. Molecular investigation of isolates of *Fusarium oxysporum* in relation to the control of root rot disease in vanilla plantifolia Andr.
TITLE Unpublished
JOURNAL 2 (bases 1 to 445)
REFERENCE Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B. Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
LOCATION/Qualifiers
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/organism="Fusarium oxysporum f. sp. vanillae"
/mol_type="genomic DNA"
/isolate="ML-8-1"
/db_xref="taxon:247126"
/notes="forma_specialis: vanillae"
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136..293
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/product="internal transcribed spacer 2"
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Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR
1 CGTTAATTCGGCTCCTC 18
|||||
327 CGTTAATTCGGCTCCTC 344
RESULT 12
LOCUS AY387699 445 bp DNA linear PLN 07-OCT-2003
DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387699
VERSION AY387699.1 GI:37362904
KEYWORDS Fusarium oxysporum f. sp. vanillae
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Fusarium oxysporum f. sp. vanillae
REFERENCE Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B. Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
LOCATION/Qualifiers
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source
1..445
/organism="Fusarium oxysporum f. sp. vanillae"
/mol_type="genomic DNA"
/isolate="ML-7-1"
/db_xref="taxon:5507"
<1..135
/product="internal transcribed spacer 1"
136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 2"
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Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR
1 CGTTAATTCGGCTCCTC 18
|||||
327 CGTTAATTCGGCTCCTC 344

transcribed spacer 2 sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
LOCATION/Qualifiers
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/isolate="DL-4b"
/db_xref="taxon:247126"
/notes="forma_specialis: vanillae"
<1..135
/product="internal transcribed spacer 1"
136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR
1 CGTTAATTCGGCTCCTC 18
|||||
327 CGTTAATTCGGCTCCTC 344
RESULT 13
LOCUS AY387702 445 bp DNA linear PLN 07-OCT-2003
DEFINITION Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387702
VERSION AY387702.1 GI:37362907
KEYWORDS Fusarium oxysporum
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
REFERENCE Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J. Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
LOCATION/Qualifiers
FEATURES
source
1..445
/organism="Fusarium oxysporum f. sp. vanillae"
/mol_type="genomic DNA"
/isolate="ML-7-1"
/db_xref="taxon:5507"
<1..135
/product="internal transcribed spacer 1"
136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR
1 CGTTAATTCGGCTCCTC 18
|||||
327 CGTTAATTCGGCTCCTC 344

Query Match 100.0%; Score 18; DB 8; Length 445;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTCCTC 18
 |||||
 327 CGTTAATTCGGCTCCTC 344

Db

RESULT 14
 AY387704
 LOCUS
 DEFINITION Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AY387704
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
 1 (bases 1 to 445)
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Jang, J.
 Direct Submission
 Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
 Location/Qualifiers
 1..445
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="ML-8-4"
 /db_xref="taxon:5507"
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 /product="internal transcribed spacer 1"
 136..293
 /product="5.8S ribosomal RNA"
 294..>445
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTCCTC 18
 |||||
 327 CGTTAATTCGGCTCCTC 344

Db

RESULT 15
 AY387705
 LOCUS
 DEFINITION Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AY387705
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;

REFERENCE 1 (bases 1 to 445)
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Chen, J.B.
 Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
 Unpublished
 2 (bases 1 to 445)
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Chen, J.B.
 Direct Submission
 Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
 Location/Qualifiers
 1..445
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="ML-5-2"
 /db_xref="taxon:5507"
 <1..135
 /product="internal transcribed spacer 1"
 136..293
 /product="5.8S ribosomal RNA"
 294..>445
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTCCTC 18
 |||||
 327 CGTTAATTCGGCTCCTC 344

Db

Search completed: October 1, 2004, 05:17:02
 Job time : 148.108 secs

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
 CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
 CC are species-specific, and can be used for identifying a species selected
 CC from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,
 CC *M. indicus*, *M. circinellus*, *Rhizoglyphus*, *Rhizopus oryzae*, *R.*
 CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*
 CC *corymbifera*, *Cunninghamella elegans*, *Pseudallesheria boydii* (teleomorph
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*
 CC *schenkii*. The probes can be used for differentiating filamentous fungal
 CC species from each other and from other medically important fungi
 XX

SQ Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 Db 1 CGTTAATTCGGCTTCCTC 18

RESULT 2
 ID AAA72783 standard; DNA; 382 BP.
 AC AAA72783;
 DT 13-DEC-2000 (first entry)
 XX 5.8s rRNA gene sequence.
 DE
 XX Black spot disease; brown spot disease; fungi; fruit vegetable;
 KM field crop; *Alternaria*; 5.8s rRNA; detection; ds.
 XX
 OS *Fusarium oxysporum*.
 XX WO200046397-A1.
 PN 10-AUG-2000.
 PD
 XX 24-JAN-2000; 2000WO-US001466.
 PF
 XX 02-FEB-1999; 99US-00241427.
 PR
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA (KASH/) KASHI Y.
 PI Kashi Y, Zur G, Sharf R, Hallerman E;
 XX WPI; 2000-499381/44.
 DR
 XX Nucleic acid based assay and kit for detection of *Alternaria*
 PT contamination in food products involves analyzing the sample of food
 PT product for nucleic acid sequences unique to *Alternaria*.
 XX
 PS Example; Fig 1; 47pp; English.
 XX The invention relates to a nucleic acid based method for the detection of
 CC *Alternaria* contamination in a food product. The method involves obtaining
 CC and analysing a food product sample for a nucleic acid sequence unique to
 CC *Alternaria*. Detectable levels of the nucleic acid sequence can be used as
 CC an indication of *Alternaria* contamination. Fungi from the genus
 CC *Alternaria* are ubiquitous saprophytes and are economically important
 CC pathogens affecting a wide range of plants. *Alternaria* are the causative
 CC agents of black or brown spot disease in many fruits, vegetables and
 CC field crops. The method is used for the detection of *Alternaria*
 CC contamination in food products. The present sequence represents the
 CC *Fusarium oxysporum* 5.8s rRNA gene, used in examples illustrating the
 CC invention
 XX

SQ Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 382;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 Db 287 CGTTAATTCGGCTTCCTC 304

RESULT 3
 ID ABQ37055 standard; DNA; 538 BP.
 AC ABQ37055;
 DT 12-JUL-2002 (first entry)
 XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 23646.
 DE
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KM drug; side effect; cancer; central nervous system; cardiovascular;
 KM gastrointestinal; respiratory system; single nucleotide polymorphism;
 KM SNP; cell differentiation; ds.
 XX
 OS *Homo sapiens*.
 XX WO200218632-A2.
 PN 07-MAR-2002.
 PD
 XX 01-SEP-2001; 2001WO-EP010074.
 PF
 XX 01-SEP-2000; 2000DE-01043826.
 PR 05-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 DR
 XX Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ5121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 XX
 SQ Sequence 538 BP; 256 A; 160 C; 61 G; 61 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 538;

Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCCTC 18
Db 105 GTTAATTCGCGTTCCTC 89

RESULT 4

ABQ37054
ID ABQ37054 standard; DNA, 538 BP.

ABQ37054;

12-JUN-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 23645.

Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.

Homo sapiens.

MO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826.

05-SEP-2000; 2000DE-01044543.

(EPIC-) EPIDENOMICS AG.

Olek A, Piepenbrock C, Berlin K, Guetig D;

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for
diagnosis and prognosis, comprises selective hybridization of amplicons
from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of
methylation of a particular cytosine in a motif 5'-CGG-3', present in a
genomic sample of DNA. The sample is treated chemically to convert
cytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridized to two classes, each with at least one member,
of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
degree of hybridization to both classes is determined from the label on
the amplicon. From the ratio of labels hybridized to the two classes of
oligomers, the degree of methylation is calculated. The method is used:
(i) for diagnosis and/or prognosis of side effects of therapeutic drugs
and of a wide range of diseases, e.g. cancer, disorders of the central
nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
particularly by detecting mutations or single nucleotide polymorphisms
(SNP's); and (ii) for differentiation of cell or tissue types and for
investigating cell differentiation. The method allows the methylation
status of many C residues to be determined simultaneously. ABQ3410-
ABQ54121 represent genomic DNA sequences used to illustrate the method
for determining the degree of cytosine methylation described in the
disclosure of the invention

Sequence 538 BP; 61 A; 61 C; 160 G; 256 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 538;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCCTC 18
Db 434 GTTAATTCGCGTTCCTC 450

RESULT 5

ACA13108/c
ID ACA13108 standard; DNA, 127 BP.

ACA13108;

27-OCT-2003 (revised)

19-JUN-2003 (first entry)

Prokaryotic essential gene antisense oligonucleotide #978.

Antisense; ss; prokaryotic essential gene; cell proliferation;
drug design.

Archaea.

MO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.

Claim 1; SEQ ID NO 978; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is one of the 6213

CC antisense sequences of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (updated on 27-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 127 BP; 42 A; 31 C; 22 G; 32 T; 0 U; 0 Other;
Query Match 83.3%; Score 15; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GTTAATTGCGGTTCC 16
Db 117 GTTAATTGCGGTTCC 103
RESULT 6
AAS48419/c
ID AAS48419 standard; DNA; 128 BP.
XX
AC AAS48419;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation inhibitory sequence #89.
XX
KM Antisense; ss; prokaryotic cellular proliferation; antibiotic;
XX antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
XX 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
XX 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
XX 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 1; SEQ ID NO 996; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC antibodies capable of binding to the expressed proteins, and to obtain
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence is an antisense oligonucleotide of the
CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 U; 0 Other;
Query Match 83.3%; Score 15; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GTTAATTGCGGTTCC 16
Db 118 GTTAATTGCGGTTCC 104
RESULT 7
AAS47978/c
ID AAS47978 standard; DNA; 250 BP.
XX
AC AAS47978;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation inhibitory sequence #548.
XX
KM Antisense; ss; prokaryotic cellular proliferation; antibiotic;
XX antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
XX 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
XX 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
XX 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 1; SEQ ID NO 555; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence is an antisense oligonucleotide of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation or screening for homologous molecules for rational
 CC drug discovery programs; or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC XX

SO Sequence 1467 BP; 464 A; 268 C; 311 G; 424 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 7; Length 1467;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATTGCGCTCC 16
 |||||
 Db 1027 GTTAATTGCGCTCC 1041

RESULT 10
 AAX13271
 ID AAX13271 standard; DNA; 9212 BP.

XX AAX13271;

DT 19-MAR-1999 (first entry)

XX Enterococcus faecalis genome contig SEQ ID NO:334.

DE Enterococcus faecalis; contig; detection; Enterococcal infection;

XX Enterococcus faecalis; computer readable medium; ds.

KM Enterococcus faecalis.

XX OS

PN MO9850555-A2.

PD 12-NOV-1998.

XX 04-MAY-1998; 98WO-US008985.

PR 06-MAY-1997; 97US-0044031P.

PR 16-MAY-1997; 97US-004655P.

PR 14-NOV-1997; 97US-0066009P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Kunsch CA, Dillon PJ, Barash S;

XX WPI; 1999-045171/04.

DR New isolated Enterococcus faecalis polynucleotides and polypeptides -

PT used to develop products for the detection of Enterococcus and for use in

XX vaccines for prevention or attenuation of Enterococcus infection.

XX Claim 1; Page 1436-1441; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it

CC 962 nucleotide sequences isolated from the Enterococcus faecalis genome.

CC AAX12938 to AAX13919 represent these nucleotide sequences which are
 CC primary nucleotide sequences, also known as contigs. The computer-based
 CC system can identify fragments of the Enterococcus faecalis genome with
 CC commercial importance. The products can be used to detect the presence of
 CC Enterococcus faecalis in samples. They can also be used for diagnosing
 CC Enterococcal infection in an animal and monitoring progression of
 CC disease, and for identifying agents which can be used to modulate the
 CC growth or pathogenicity of Enterococcus faecalis, or another related
 CC organism, in vivo or in vitro. In particular the polypeptides encoded by
 CC the Enterococcus faecalis nucleotide sequences can be used in vaccines to
 CC prevent or attenuate an Enterococcal infection
 CC XX

SO Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 0 U; 13 Other;
 Query Match 83.3%; Score 15; DB 2; Length 9212;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATTGCGCTCC 16
 |||||
 Db 4989 GTTAATTGCGCTCC 5003

RESULT 11
 ABS99066
 ID ABS99066 standard; DNA; 9212 BP.

XX ABS99066;

AC 18-DEC-2002 (first entry)

DE Enterococcus faecalis contig sequence #334.

XX Computer readable medium; Enterococcus faecalis; microbe; growth;

KM pathogenicity; vaccine; resistance; Enterococcal infection; commercial;

KM therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;

KM biochip technology; antibacterial; modulator of nucleic acid expression;

KM contig; ds.

XX Enterococcus faecalis.

XX US2002120116-A1.

PN 29-AUG-2002.

XX 04-MAY-1998; 98US-00070927.

PR 04-MAY-1998; 98US-00070927.

XX (KUNS/) KUNSCH C A.

PA (DILL/) DILLON P J.

PA (BARA/) BARASH S.

XX Kunsch CA, Dillon PJ, Barash S;

PI WPI; 2002-750065/81.

DR Computer readable medium having recorded on it a Enterococcus faecalis

XX nucleotide sequence useful for detecting diseases related to Enterococcus

PT infections in animals.

XX Claim 1; Page; 119pp; English.

XX The present invention relates to a new computer readable medium with an

CC Enterococcus faecalis nucleotide sequence. The invention is useful to

CC diagnose the presence of E. faecalis in a sample or determining the

CC presence of a specific microbe in a sample. The invention is also useful

CC for modulating the growth or pathogenicity of E. faecalis, in a vaccine to

CC confer resistance to Enterococcal infection, for commercial, therapeutic

CC and industrial purposes, and for fermenting a particular sugar source or

CC to produce a particular metabolite. The invention is useful for detecting

CC diseases related to Enterococcus infections in animals, and for detecting

CC E. faecalis using biochip technology. The present nucleic acid sequence

CC represents an *Enterococcus faecalis* contig DNA sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov>

XX Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 0 U; 13 Other;

Query Match 83.3%; Score 15; DB 6; Length 9212;

Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4989 GTTATTTCGCGTTC 5003

RESULT 12
 ADC92275/C
 ID ADC92275 standard; DNA; 207 BP.

AC ADC92275;

DT 01-JAN-2004 (first entry)

DE E. faecium DNA sequence SEQ ID 1902.

KM ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
 KM abdominal-pelvic infection.

OS Enterococcus faecium.

PN US6583275-B1.

PD 24-JUN-2003.

PE 30-JUN-1998; 98US-00107532.

PR 02-JUL-1997; 97US-0051571P.

PA 14-MAY-1998; 98US-0085598P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

DR WPI; 2003-799836/75.

DR P-PSDB; ADC95929.

PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an
 PT *Enterococcus faecium* polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.

XX Example 1; SEQ ID NO 1902; 243bp; English.

CC The invention relates to an isolated nucleic acid derived from
 CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from E. faecium bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of *Candida albicans* -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating *Enterococcus faecium* infections. The present sequence represents
 CC one if the disclosed E. faecium nucleic acids.

SQ Sequence 207 BP; 68 A; 36 C; 47 G; 55 T; 0 U; 1 Other;

Query Match 82.2%; Score 14.8; DB 9; Length 207;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 84 CGTATTCTCTTCTC 67

RESULT 13
 ABO14482
 ID ABO14482 standard; DNA; 554 BP.

AC ABO14482;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1073.

KM Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KM drug; side effect; cancer; central nervous system; cardiovascular;
 KM gastrointestinal; respiratory system; single nucleotide polymorphism;
 KM SNP; cell differentiation; de.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PE 01-SEP-2001; 2001WO-EP010074.

PR 01-SEP-2000; 2000DE-01043826.

PR 05-SEP-2000; 2000DE-01044543.

PA (EPIC-) EPICENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABO13410-
 CC ABO54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

SQ Sequence 554 BP; 76 A; 67 C; 169 G; 242 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 554;

Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
113 CGTTAATTCGCGTTCCTC 130
Db

RESULT 14
ABQ14483/C
ID ABQ14483 standard; DNA; 554 BP.
XX
AC ABQ14483;
XX

DT 12-JUL-2002 (first entry)
XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1074.
XX

KM Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KM drug; side effect; cancer; central nervous system; cardiovascular;
KM gastrointestinal; respiratory system; single nucleotide polymorphism;
KM SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX

PN W0200218632-A2.
XX

PD 07-MAR-2002.
XX

PF 01-SEP-2001; 2001WO-EP010074.
XX

PR 01-SEP-2000; 2000DE-01043825.
XX

PR 05-SEP-2000; 2000DE-01044543.
XX

PA (EBIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX

DR WPI; 2002-371829/40.
XX

PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX

PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, respiratory systems etc.,
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX

XX Sequence 554 BP; 242 A; 169 C; 67 G; 76 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 554;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
442 CGTTAATTCGCGTTCCTC 425
Db

RESULT 15
AAS05503
ID AAS05503 standard; DNA; 650 BP.
XX
AC AAS05503;
XX

DT 07-SEP-2001 (first entry)
XX

DE Mammalian vestibular system geotactic behaviour modulator gene #103.
XX

KM Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;
KM graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds;
KM Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;
KM trauma; infection of the middle ear; ototoxic agent exposure.
XX

OS Drosophila melanogaster.
XX

PN W0200140519-A2.
XX

PD 07-JUN-2001.
XX

PF 01-DEC-2000; 2000MO-US032639.
XX

PR 02-DEC-1999; 99US-0168579P.
XX

PR 26-SEP-2000; 2000US-00669751.
XX

PA (NEUR-) NEUROSCIENCES RES FOUND INC.
XX

PI Greenspan RJ;
XX

DR WPI; 2001-356159/37.
XX

PT New isolated nucleic acid having mammalian vestibular system-modulating
PT activity useful in the treatment of disorders such as motion sickness and
PT vertigo.
XX

PS Claim 59; Page 126; 179pp; English.
XX

CC The sequences shown in AAS05401-AAS05661 represent DNA with mammalian
CC vestibular system-modulating activity. The DNA sequences can be used in a
CC method whereby a first and second strain of an invertebrate is obtained,
CC and both are subjected to conditions in which the strains exhibit
CC different geotactic behaviour. Genes that are differentially expressed in
CC the first strain relative to the second strain are then identified.
CC Mammalian genes having substantially the same nucleic acid sequence as
CC these modulate the mammalian vestibular system. Compounds containing
CC these genes are used to decrease the symptoms of graviperceptive
CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's
CC disease, acoustic neuroma, multiple sclerosis, syphilis, trauma,
CC infection of the middle ear, exposure to ototoxic agents and epilepsy
XX

XX Sequence 650 BP; 182 A; 181 C; 167 G; 120 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 5; Length 650;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
69 CGTTAATTCGCGTTCCTC 86
Db

Search completed: October 1, 2004, 03:41:16
Job time : 37.9347 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds
(without alignments)
1683.989 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaattcgcgttcctc 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCUTS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	15	83.3	615	US-09-134-000C-314	Sequence 314, Ap
3	14.8	82.2	207	US-09-107-532A-1902	Sequence 1902, Ap
4	14.8	82.2	650	US-09-669-751-103	Sequence 103, Ap
5	14.8	82.2	2457	US-09-134-000C-2950	Sequence 2950, Ap
6	14.4	80.0	963	US-09-134-001C-1367	Sequence 1367, Ap
7	14	77.8	3208	US-07-972-791-3	Sequence 3, Appl
8	14	77.8	3345	US-07-972-791-7	Sequence 7, Appl
9	14	77.8	3347	US-07-972-791-5	Sequence 5, Appl
10	14	77.8	3347	US-07-972-791-2	Sequence 2, Appl
11	14	77.8	3347	US-07-972-791-8	Sequence 8, Appl
12	14	77.8	3361	US-07-972-791-6	Sequence 6, Appl
13	14	77.8	3361	US-07-972-791-6	Sequence 6, Appl
14	14	77.8	702	US-09-543-681A-4125	Sequence 4125, Ap
15	13.8	76.7	1356	US-09-328-352-1886	Sequence 1886, Ap
16	13.8	76.7	1386	US-09-134-001C-984	Sequence 984, Ap
17	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
18	13.8	76.7	5679	US-09-598-421-10	Sequence 10, Appl
19	13.8	76.7	6723	US-08-844-274-13	Sequence 13, Appl
20	13.8	76.7	6723	US-08-844-274-14	Sequence 14, Appl
21	13.8	76.7	6723	US-09-598-421-13	Sequence 13, Appl
22	13.8	76.7	6723	US-09-598-421-14	Sequence 14, Appl
23	13.8	76.7	7560	US-08-844-274-20	Sequence 20, Appl
24	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl
25	13.8	76.7	9704	US-09-814-951A-3	Sequence 1, Appl
26	13.8	76.7	9717	US-09-251-645-1	Sequence 1, Appl
27	13.8	76.7	12666	US-08-961-527-137	Sequence 137, App

c 28	13.8	76.7	49795	4	US-09-453-702B-60	Sequence 60, Appl
c 29	13.6	75.6	3378	1	US-07-972-791-1	Sequence 1, Appl
c 30	13.4	74.4	549	4	US-09-328-352-1243	Sequence 3283, Ap
c 31	13.4	74.4	720	4	US-09-134-000C-1003	Sequence 1003, Ap
c 32	13.4	74.4	1293	4	US-09-489-039A-409	Sequence 409, Ap
c 33	13.4	74.4	1122	4	US-09-833-381-1392	Sequence 1392, Ap
c 34	13.4	74.4	2430	4	US-09-620-312D-176	Sequence 176, Ap
c 35	13.4	74.4	2967	4	US-09-185-501B-112	Sequence 112, Ap
c 36	13.4	74.4	10144	4	US-10-204-708-94	Sequence 94, Appl
c 37	13.2	73.3	23	3	US-09-139-617-10	Sequence 10, Appl
c 38	13.2	73.3	23	4	US-09-561-741A-10	Sequence 10, Appl
c 39	13.2	73.3	23	4	US-09-558-795-10	Sequence 10, Appl
c 40	13.2	73.3	305	4	US-09-489-039A-11	Sequence 11, Appl
c 41	13.2	73.3	465	4	US-09-489-039A-1305	Sequence 1305, Ap
c 42	13.2	73.3	471	3	US-09-181-183-1	Sequence 1, Appl
c 43	13.2	73.3	471	4	US-09-280-040-1	Sequence 1, Appl
c 44	13.2	73.3	471	4	US-09-277-700-1	Sequence 1, Appl
c 45	13.2	73.3	471	4	US-09-874-585D-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-423-233-50
Sequence 50, Application US/0942233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341mp
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium oxysporum
US-09-423-233-50

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1
CGTTAATTCCGCTTCCTC 18
DB 1 CGTTAATTCCGCTTCCTC 18

RESULT 2
US-09-134-000C-314
Sequence 314, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 314
LENGTH: 615
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-314

Query Match 83.3%; Score 15; DB 4; Length 615;

Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 16
Db 172 GTTAATTCGCGTTC 186

RESULT 3

US-09-107-532A-1902/c
; Sequence 1902, Application US/09107532A
; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESSES:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Artniello, Pamela Daneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1902:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...207

SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

US-09-107-532A-1902

Query Match 82.2%; Score 14.8; DB 4; Length 207;

Best Local Similarity 88.9%; Pred. No. 44;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18

Db 84 CGTTAATTCGCGTTC 67

RESULT 4

US-09-669-751-103

; Sequence 103, Application US/09669751

Patent No. 6551575

GENERAL INFORMATION:

APPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for

TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to

TITLE OF INVENTION: Balance and the Perception of Gravity

FILE REFERENCE: P-NI 3864

CURRENT APPLICATION NUMBER: US/09/669,751

CURRENT FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 60/168,579

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 261

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 103

LENGTH: 650

TYPE: DNA

ORGANISM: Drosophila

US-09-669-751-103

Query Match 82.2%; Score 14.8; DB 4; Length 650;

Best Local Similarity 88.9%; Pred. No. 48;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18

Db 69 CGTTAATTCGCGTTC 86

RESULT 5

US-09-134-000C-2950/c

; Sequence 2950, Application US/09134000C

Patent No. 6617155

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2950

LENGTH: 2457

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-2950

Query Match 82.2%; Score 14.8; DB 4; Length 2457;

Best Local Similarity 88.9%; Pred. No. 54;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18

Db 963 CGTTAATTCGCGTTC 946

RESULT 6

US-09-134-001C-1367/c

; Sequence 1367, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1367
LENGTH: 963
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1367

Query Match 80.0%; Score 14.4; DB 4; Length 963;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TTAATTCGCGTTCCTC 18
Db 640 TTAATTCGCGTTCCTC 625

RESULT 7
US-07-972-791-3/c
Sequence 3, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3208 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 1 (S2308)
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTC 15
Db 1488 GTTAATTCGCGTTC 1475

RESULT 8
US-07-972-791-7/c
Sequence 7, Application US/07972791

Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3345 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella melitensis
STRAIN: biovar 1
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTC 15
Db 1487 GTTAATTCGCGTTC 1474

RESULT 9
US-07-972-791-5/c
Sequence 5, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3346 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella neotomae
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTATTGCGGTC 15
DB 1488 GTTATTGCGGTC 1475

RESULT 10
US-07-972-791-2/c
Sequence 2, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMARELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus

STRAIN: biovar 5
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTATTGCGGTC 15
DB 1488 GTTATTGCGGTC 1475

RESULT 11
US-07-972-791-8/c
Sequence 8, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMARELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella suis
STRAIN: biovar 1
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTATTGCGGTC 15
DB 1488 GTTATTGCGGTC 1475

RESULT 12
US-07-972-791-6/c
Sequence 6, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.


```

; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PRAVEL, GAMBRELL, HEMITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,791
; FILING DATE: 19921106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; TELEX: 792026
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3361 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Brucella ovis
; US-07-972-791-6

Query Match          77.8%; Score 14; DB 1; Length 3361;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTC 15
      |||||
Db      1503 GTTAATTCGCGTTC 1490

RESULT 13
5310649-1/c
; Patent No. 5310649
; APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, Gary L.
; TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS
; OF BRUCELLA
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/527,017
; FILING DATE: 22-MAY-1990
; SEQ ID NO: 1;
; LENGTH: 3434
5310649-1

Query Match          77.8%; Score 14; DB 6; Length 3434;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTC 15
      |||||
Db      1692 GTTAATTCGCGTTC 1679

RESULT 14
US-09-543-681A-4125/c
; Sequence 4125, Application US/09543681A
; Patent No. 6605709
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; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4125
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4125

Query Match          76.7%; Score 13.8; DB 4; Length 702;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCCTC 18
      |||||
Db      44 GTTAATTCGCGATCCTC 28

RESULT 15
US-09-328-352-1886
; Sequence 1886, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1886
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1886

Query Match          76.7%; Score 13.8; DB 4; Length 1356;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCCTC 18
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Db      600 GTTAATTCGCGTTCCTC 616

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 73.304 Seconds

(without alignments)
1244.847 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaattcggttcctc 18

Scoring table: IDENTITY NUC

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Minimum DB seq length: 0

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Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-10-046-955-50	Sequence 50, Appl
2	15.4	85.6	4461	US-10-437-963-83618	Sequence 9613, A
3	15	83.3	127	US-10-282-122A-978	Sequence 978, App
4	15	83.3	128	US-09-815-242-996	Sequence 996, App
5	15	83.3	250	US-09-815-242-555	Sequence 555, App
6	15	83.3	250	US-10-282-122A-531	Sequence 531, App
7	15	83.3	1467	US-10-282-122A-6332	Sequence 6332, App
8	15	83.3	9212	US-09-070-927A-334	Sequence 334, App
9	14.8	82.2	262	US-09-535-459-1371	Sequence 1371, App
10	14.8	82.2	438	US-10-424-599-43896	Sequence 43896, A
11	14.8	82.2	585	US-10-437-963-81762	Sequence 81762, A
12	14.8	82.2	585	US-10-255-536-103	Sequence 103, App
13	14.8	82.2	3135	US-10-282-122A-20853	Sequence 20853, A
14	14.8	82.2	3138	US-09-815-242-6520	Sequence 6520, App

15	14.8	82.2	2731748	17	US-10-297-465A-1	Sequence 1, Appl
16	14.4	80.0	65	15	US-10-032-585-259	Sequence 259, App
17	14.4	80.0	230	13	US-10-085-783A-247	Sequence 247, App
18	14.4	80.0	230	16	US-10-242-535A-247	Sequence 247, App
19	14.4	80.0	306	9	US-09-974-300-6603	Sequence 6603, App
20	14.4	80.0	559	15	US-10-029-386-7594	Sequence 7594, App
21	14.4	80.0	651	13	US-10-027-632-266929	Sequence 266929, App
22	14.4	80.0	651	16	US-10-027-632-266929	Sequence 266929, App
23	14.4	80.0	914	16	US-10-369-493-35000	Sequence 35000, A
24	14.4	80.0	948	13	US-10-424-599-78398	Sequence 78398, A
25	14.4	80.0	1520	13	US-10-424-599-78398	Sequence 78398, A
26	14.4	80.0	6711	15	US-10-341-200-42	Sequence 42, Appl
27	14.4	80.0	8440	15	US-10-341-200-19	Sequence 19, Appl
28	14.4	80.0	1163020	16	US-10-398-221-10	Sequence 10, Appl
29	14.4	80.0	3011208	16	US-10-398-221-2058	Sequence 2058, App
30	14	77.8	926	13	US-10-424-599-59512	Sequence 59512, A
31	14	77.8	1496	13	US-10-424-599-59514	Sequence 59514, A
32	14	77.8	1585	17	US-10-437-963-93652	Sequence 93652, A
33	14	77.8	1773	17	US-10-437-963-93609	Sequence 93609, A
34	14	77.8	1806	17	US-10-437-963-93471	Sequence 93471, A
35	14	77.8	2102	17	US-10-437-963-93615	Sequence 93615, A
36	14	77.8	2455	17	US-10-437-963-93584	Sequence 93584, A
37	14	77.8	2569	16	US-10-369-493-36500	Sequence 36500, A
38	14	77.8	5917	17	US-10-437-963-93655	Sequence 93655, A
39	14	77.8	13627	17	US-10-433-793-6	Sequence 6, Appl
40	13.8	76.7	285	12	US-09-987-899-201	Sequence 201, App
41	13.8	76.7	346	12	US-10-424-599-93085	Sequence 93085, A
42	13.8	76.7	407	12	US-09-987-899-182	Sequence 182, App
43	13.8	76.7	418	12	US-09-987-899-160	Sequence 160, App
44	13.8	76.7	432	12	US-09-987-899-168	Sequence 168, App
45	13.8	76.7	432	12	US-09-987-899-169	Sequence 169, App

ALIGNMENTS

RESULT 1
US-10-046-955-50
; Sequence 50, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilianna
; APPLICANT: Choi, Jong Soo
; TITLE OR INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
; US-10-046-955-50
Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0

Db 1 CGTTAATTCGGCTTCCTC 18

RESULT 2

US-10-437-963-93618/c

Sequence 93618, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbaruk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 93618

LENGTH: 4461

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_91986C.1

US-10-437-963-93618

Query Match 85.6%; Score 15.4; DB 17; Length 4461;

Best Local Similarity 94.1%; Pred. No. 2.9e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTCCTC 18

Db 1209 GTTAATTCACGTTCTC 1193

RESULT 3

US-10-282-122A-978/c

Sequence 978, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 978

LENGTH: 127

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-10-282-122A-978

Query Match 83.3%; Score 15; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 16

Db 117 GTTAATTCGGCTTC 103

RESULT 4

US-09-815-242-996/c

Sequence 996, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FaecSeq for Windows Version 4.0

SEQ ID NO 996

LENGTH: 128

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-815-242-996

Query Match 83.3%; Score 15; DB 9; Length 128;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 16

Db 118 GTTAATTCGGCTTC 104

```
RESULT 5
US-09-815-242-555/c
; Sequence 555, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykend, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-555

Query Match      83.3%; Score 15; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCC 16
        |||||
Db      54 GTTAATTCGCGTTCC 40

RESULT 6
US-10-282-122A-531/c
; Sequence 531, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykend, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
```

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; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 531
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-531

Query Match      83.3%; Score 15; DB 13; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCC 16
        |||||
Db      54 GTTAATTCGCGTTCC 40

RESULT 7
US-10-282-122A-6332
; Sequence 6332, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykend, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6332
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-10-282-122A-6332

Query Match      83.3%; Score 15; DB 13; Length 1467;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTC 16
Db      1027 GTTAATTCGCGTTC 1041

RESULT 8
US-09-070-927A-334
; Sequence 334, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;          Patrick J. Dillon
;          Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; INFORMATION FOR SEQ ID NO: 334:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 334:
US-09-070-927A-334

Query Match      83.3%; Score 15; DB 9; Length 9212;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6332
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-10-282-122A-6332

Query Match      83.3%; Score 15; DB 13; Length 1467;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTC 16
Db      1027 GTTAATTCGCGTTC 1041

RESULT 9
US-09-535-459-1371/C
; Sequence 1371, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1371
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m1sc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371

Query Match      82.2%; Score 14.8; DB 10; Length 262;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCCTC 18
Db      102 CGTTAATTCGCGTTCCTC 85

RESULT 10
US-10-424-599-43896
; Sequence 43896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43896
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139637C.1
US-10-424-599-43896

Query Match      82.2%; Score 14.8; DB 13; Length 438;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCCTC 18
Db      297 CGTTAATTCGCGTTCATC 314
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RESULT 11
US-10-437-963-81762
; Sequence 81762, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81762
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81256C.1
US-10-437-963-81762

Query Match      82.2% Score 14.8; DB 17; Length 585;
Best Local Similarity 88.9%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGTTAATTCGGCTTCCTC 18
      |||||
Db      230 CGTTCAATTCGGCTTCAC 247

RESULT 12
US-10-255-536-103
; Sequence 103, Application US/10255536
; Publication No. US20030087807A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/10/255,536
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/669,751
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-10-255-536-103

Query Match      82.2% Score 14.8; DB 15; Length 650;
Best Local Similarity 88.9%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGTTAATTCGGCTTCCTC 18
      |||||
Db      69 CGTTCAATTCGGCTTCCTC 86

RESULT 13
US-10-282-122A-20853/c

; Sequence 20853, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20853
; LENGTH: 3135
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20853

Query Match      82.2% Score 14.8; DB 13; Length 3135;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGTTAATTCGGCTTCCTC 18
      |||||
Db      1644 CGTTAATTCGGCTTCCTC 1627

RESULT 14
US-09-815-242-6520/c
; Sequence 6520, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
```

```
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6520
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3138)
US-09-815-242-6520
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Query Match      82.2%; Score 14.8; DB 9; Length 3138;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY      1 CGTTAATTCGGCTTCCTC 18
      ||||| ||||| |||||
Db      1644 CGTTAATTCGGCTTCCTC 1627
```

```
RESULT 15
US-10-297-465A-1
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medeiros, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of Xylella fastidiosa and Uses Thereof
; FILE REFERENCE: PAPER 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1
```

```
Query Match      82.2%; Score 14.8; DB 17; Length 2731748;
Best Local Similarity 88.9%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 CGTTAATTCGGCTTCCTC 18
      ||||| ||||| |||||
Db      2184289 CGTTAATTCGGCTTCCTC 2184306
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Search completed: October 1, 2004, 08:53:55
Job time : 83.304 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 252 Seconds

(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-50

Sequence: 1 cgttaatcgcttcctc 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrc:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_dhg:*
27: em_gss_vr1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.4	91.1	667	13	BQ483402
C 2	15.4	85.6	262	28	A2359925 1M0103B02
C 3	15.4	85.6	277	28	BH452985 BOHGA607F
C 4	15.4	85.6	402	29	CG858920 ZMMBAC026

C 5	15.4	85.6	493	28	A2498171
C 6	15.4	85.6	499	28	BH144783
C 7	15.4	85.6	588	28	BZ508556
C 8	15.4	85.6	740	29	AG042918
C 9	15.4	85.6	902	29	CG810640
C 10	15.4	85.6	902	14	CA278228
C 11	15.4	85.6	908	13	BX434865
C 12	15.4	85.6	921	14	CK288913
C 13	15.4	85.6	968	14	CK286745
C 14	15.4	85.6	1000	12	BP512280
C 15	15.4	85.6	1278	12	BM543811
C 16	15	83.3	311	10	AM833312
C 17	15	83.3	543	12	BI881942
C 18	15	83.3	547	14	CB406133
C 19	15	83.3	563	14	CB406132
C 20	15	83.3	636	10	BE557132
C 21	15	83.3	728	12	BG723264
C 22	15	83.3	870	14	CK200815
C 23	15	83.3	1057	29	AG081712
C 24	14.8	82.2	140	14	CB066245
C 25	14.8	82.2	187	12	BM616169
C 26	14.8	82.2	206	28	AZ991070
C 27	14.8	82.2	206	28	AZ991080
C 28	14.8	82.2	282	14	CB066239
C 29	14.8	82.2	303	9	AA785231
C 30	14.8	82.2	338	9	AJ502973
C 31	14.8	82.2	359	9	AL714174
C 32	14.8	82.2	388	10	BF490378
C 33	14.8	82.2	398	10	BE995152
C 34	14.8	82.2	400	28	BH701453
C 35	14.8	82.2	411	9	AI869164
C 36	14.8	82.2	417	14	CB767429
C 37	14.8	82.2	426	9	AI212546
C 38	14.8	82.2	430	9	AI946050
C 39	14.8	82.2	443	14	CB339034
C 40	14.8	82.2	448	28	AQ945783
C 41	14.8	82.2	457	12	BM130898
C 42	14.8	82.2	463	12	BM130858
C 43	14.8	82.2	464	9	AA941852
C 44	14.8	82.2	475	14	CA408218
C 45	14.8	82.2	481	12	BM130610

ALIGNMENTS

RESULT 1
BQ483402/c
LOCUS
DEFINITION
WHR3508_B09 D182S wheat unstressed root cDNA library
Triticum aestivum cDNA clone WHR3508_B09_D18, mRNA sequence.

ACCESSION
BQ483402
VERSION
BQ483402.1 GI:21319338

KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)

REFERENCE
Anderson, O.D., Chao, S., Close, T.J., Crossman, C., Fenton, R.D.,
Lazo, G.R., Nguyen, H.T., Rauech, C.J., Wilson, C., Woo, J., and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Unstressed root cDNA library
Unpublished (2002)

JOURNAL
COMMENT
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

Contact: Olin Anderson
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES

SOURCE

Location/Qualifiers

1. .667
/organism="Triticum aestivum"
/mol_type="rRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WB3508_B09_D18"
/tissue_type="Roots"
/dev_stage="Full tillering"
/lab_host="E. coli SOLR"
/clone_lib="Wheat unstrressed root cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants
were grown until full tillering stage and root tissue was
collected at Texas Tech University (Zhang, HT Nguyen
Lab). Total RNA and poly(A) RNA were prepared, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript SK(-) phagemids in the T1
Close lab (Close, Pencon) at the University of
California, Riverside. Colony plating, plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN

Query Match 91.1%; Score 16.4; DB 13; Length 667;
Best Local Similarity 94.4%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCTTCCTC 18
|||||

Db 243 GGTAAATTCGCTTCCTC 226
|||||

RESULT 2 262 bp DNA linear GSS 02-OCT-2000
AZ359925
LOCUS 1M0103B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0103B02 F, genomic survey sequence.
ACCESSION AZ359925
VERSION 1
KEYWORDS GI:10473625
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0103 row: B column: 02
Seq primer: GGTGTGAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 262.
Location/Qualifiers

FEATURES

SOURCE

1. .262
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 262;
Best Local Similarity 94.1%; Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCTTCCTC 18
|||||

Db 214 GTTAATTCGCTTCCTC 198
|||||

RESULT 3 277 bp DNA linear GSS 12-DEC-2001
BH452985
LOCUS BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, genomic
DEFINITION survey sequence.
ACCESSION BH452985
VERSION 1
KEYWORDS GI:1763696
SOURCE GSS.
ORGANISM Brassica oleracea
Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 277)
Town, C.D., Van Aken, S., Utehrack, T., Koo, H. and Frazer, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHGA60TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.
Location/Qualifiers

FEATURES

SOURCE

1. .277
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHGA60"
/clone_lib="BOHG"
/note="Vector: pHOSt1, Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 277;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17
 |||||
 Db 94 CGTTAATTCGCGTTCT 78

RESULT 4
 CG858920 402 bp DNA linear GSS 19-NOV-2003
 LOCUS ZMMBBC0267L01f ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone

DEFINITION ZMMBBC0267L01 5', genomic survey sequence.
 CG858920

ACCESSION CG858920.1 GI:38431633
 VERSION GSS.
 KEYWORDS Zea mays subsp. mays (maize)
 SOURCE Zea mays subsp. mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 clade; Panicoideae; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 Sequencing of the maize genome at PCR (2003c)
 Unpublished (2003)

REFERENCE 1
 AUTHORS Bharti,A.K.
 TITLE Contact: Bharti,A.K.
 JOURNAL Dr. Joachim Messing's lab
 COMMENT The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: T7
 Class: BAC ends
 High quality sequence start: 110.

FEATURES
 source
 Location/Qualifiers
 1..402
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:578"
 /clone="ZMMBBC0267L01"
 /lab_host="E. coli DH10B"
 /clone_lib="ZMMBBC (EcoRI)"
 /note="Vector: pTABBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 29; Length 402;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17
 |||||
 Db 69 CGTTAATTCGCGTTCT 85

RESULT 5
 AZ498171 493 bp DNA linear GSS 05-OCT-2000
 LOCUS AZ498171
 DEFINITION IM0335P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0335P13 F, genomic survey sequence.
 AZ498171
 ACCESSION AZ498171.1 GI:10675786
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 493)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D. Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL Contact: Robert B. Weis
 COMMENT University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0335 row: P column: 13
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 493.

FEATURES
 source
 Location/Qualifiers
 1..493
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0335P13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42ny: Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1) a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 493;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCTC 18
 |||||
 Db 383 GTTAATTCGCGTTCTC 367

RESULT 6
 BH144783 499 bp DNA linear GSS 16-AUG-2001
 LOCUS BH144783
 DEFINITION TDGE091TH CTGG Lycopersicon esculentum genomic clone CTG030P13,
 genomic survey sequence.
 BH144783
 ACCESSION BH144783.1 GI:15200046
 VERSION GSS.
 KEYWORDS Lycopersicon esculentum (tomato)
 SOURCE Lycopersicon esculentum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1
AUTHORS van der Hoeven, R., Sun, R., Cho, J., Uterback, T., Roming, C. and Tanksley, S.
TITLE Tomato Demethylated Genomic DNA Sequences
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13P-R
Class: Shotgun.

FEATURES
source
1. .499
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultiivar="B6203"
/db_xref="taxon:4081"
/clone="CTG30P13"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/clone_lib="CTCG"
/note="Vector: Bluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into PBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."

ORIGIN
Query Match 85.6%; Score 15.4; DB 28; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTATTCGCGTTCTC 18
|||||
116 GTTATTCGCGTTCTC 132

RESULT 7
LOCUS BZ508556 588 bp DNA linear GSS 16-DEC-2002
DEFINITION BONSH38TF BO_1.6_2_KB.tot Brassica oleracea genomic clone BONSH38.
ACCESSION BZ508556
VERSION BZ508556.1 GI:27031477
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 588)
Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BONSH38TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
1. .588
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONSH38"
/clone_lib="BO_1.6_2_KB.tot"
/note="Vector: pBOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pBOS1 using BstXI linkers"

ORIGIN
Query Match 85.6%; Score 15.4; DB 28; Length 588;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTATTCGCGTTCT 17
|||||
445 CGTATTCGCGTTCT 429

RESULT 8
LOCUS AG042918 740 bp DNA linear GSS 01-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-021B05.R, genomic survey sequence.
ACCESSION AG042918
VERSION AG042918.1 GI:16571643
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
2 (bases 1 to 740)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimbases@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .740
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-021B05.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 85.6%; Score 15.4; DB 29; Length 740;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTATTCGCGTTCTC 18
|||||
Db 614 GTTATTCGCGTTCTC 630

RESULT 9
LOCUS CG810640
DEFINITION FSA082TF largeinsertGenomicLibrary Fusarium virguliforme genomic clone KMFW4N19, genomic survey sequence.
ACCESSION CG810640
VERSION CG810640
KEYWORDS GSS.
SOURCE Fusarium virguliforme
ORGANISM Fusarium virguliforme
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
AUTHORS Meksem,K., Ishihara,H., Koo,H., Shultz,J., Ali,S., Iqbal,J., Lightfoot,D.A. and Town,C.D.
TITLE End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: FSA082TR
Contact: Chris Town and K. Meksem
The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 618 453 3103 and 301-838-3523
Fax: 618 453-7457 and 301-838-0208
Email: meksem@siu.edu; cdtown@tigr.org (URL: <http://Fusariumvirguliforme.siu.edu>)
Seq primer: TGTAAACGACGCCAGT
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..819
/organism="Fusarium virguliforme"
/mol_type="genomic DNA"
/cultivar="Monticello"
/db_xref="taxon:232082"
/clone="KMFW4N19"
/clone_id="LargeinsertGenomicLibrary"
/note="Organ: Hyphae; Vector: PINDICOBACS; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector PINDICOBACS and electro-transformed into DH10B cells."

ORIGIN
Query Match 85.6%; Score 15.4; DB 29; Length 819;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTAAATTCGGCTTCCT 17
|||||
Db 322 GTTCAATTCGGCTTCCT 338

RESULT 10
CA278228/c
LOCUS CA278228
DEFINITION CA278228 902 bp mRNA linear EST 26-SEP-2003 SCFSD2037A01.g SD2 Saccharum officinarum cDNA clone SCFSD2037A01 5', mRNA sequence.
ACCESSION CA278228
VERSION CA278228
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 902)

AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCSEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: partruda@unicamp.br
Clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcap.unesp.br>
Plate: 037 row: A column: 01
Seq primer: T7 Promoter Primer.

FEATURES
source
Location/Qualifiers
1..902
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCFSD2037A01"
/lab_host="DH10B"
/clone_id="SD2"
/note="Organ: Developing seeds (small insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI. An unidirectional cDNA library generated from [developing seeds (small insert library)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a Sephrose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucsest.lad.ic.unicamp.br/public>

ORIGIN
Query Match 85.6%; Score 15.4; DB 14; Length 902;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GTTAAATTCGGCTTCCTC 18
|||||
Db 542 GTTAAATTCGGCTTCCTC 526

RESULT 11
BX434865
LOCUS BX434865
DEFINITION BX434865 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DP012YH19 3-PRIME, mRNA sequence.
ACCESSION BX434865
VERSION BX434865
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 7207.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK03AB03NM1&cluster=7207.r>. Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAK03AB03NM1.

FEATURES
SOURCE

Location/Qualifiers
1. .908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF012YH19"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 85.6%; Score 15.4; DB 13; Length 908;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTAAATTCGCGTTCTT 17
|||||
1 CCTAATTCGCGTTCTT 775

Db 759 CCTAATTCGCGTTCTT 775

RESULT 12
LOCUS CK288913 921 bp mRNA linear EST 15-DEC-2003
DEFINITION EST751635 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NMBX06 5' end, mRNA sequence.

ACCESSION CK288913
VERSION CK288913.1 GI:39866895
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 921)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskawicz,B., Jin,H. and Baker,B.
Skaskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST751636
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers

FEATURES
SOURCE

1. .921
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NMBX06"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 921;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTAAATTCGCGTTCTT 18
|||||
208 GTTCAATTCGCGTTCTT 224

Db 208 GTTCAATTCGCGTTCTT 224

RESULT 13
LOCUS CK286745 968 bp mRNA linear EST 15-DEC-2003
DEFINITION EST749467 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NMBX430 5' end, mRNA sequence.

ACCESSION CK286745
VERSION CK286745.1 GI:39862605
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 968)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers

FEATURES
SOURCE

1. .968
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NMBX430"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 968;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTAAATTCGCGTTCTT 18
|||||
200 GTTCAATTCGCGTTCTT 216

Db 200 GTTCAATTCGCGTTCTT 216

RESULT 14
LOCUS BP512280/c 1000 bp mRNA linear EST 16-SEP-2003
DEFINITION BP512280 Hydra magnipapillata cDNA library Hydra magnipapillata

```

ACCESSION      BPS12280
VERSION        BPS12280.1  GI:34778413
KEYWORDS
SOURCE
ORGANISM       Hydra magnipapillata
                Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                Hydroidea; Hydra.
REFERENCE      1 (bases 1 to 1000)
                Hayakawa,S., Hwang,J.S., Nishimiya-Fujisawa,C., Ogura,A., Ikeo,K.,
                Fujisawa,T. and Gojobori,T.
TITLE          Hydra EST project
JOURNAL        Unpublished (2003)
COMMENT        Contact: Jung Shan Hwang
                Center for Information Biology and DNA Data Bank of Japan
                National Institute of Genetics
                111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-55-981-6847(ex.6898)
                Fax: 81-55-981-6848
                Email: jhwang@lab.nig.ac.jp, URL:http://www.cdb.nig.ac.jp.
FEATURES
  source
    1..1000
    /organism="Hydra magnipapillata"
    /mol_type="mRNA"
    /strain="105"
    /db_xref="taxon:6085"
    /clone="hmp_05882"
    /tissue_type="whole body"
    /dev_stage="adult budding stage"
    /clone_idb="Hydra magnipapillata cDNA library"

ORIGIN
Query Match      85.6%; Score 15.4; DB 12; Length 1000;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCCT 17
        |||||
        419 CGTTAATTCGCGTTCCT 403

RESULT 15
BMS43811      1278 bp      mRNA      linear      EST 20-FEB-2002
LOCUS         BMS43811
DEFINITION    AGENCOURT_6492104 NIH_MGC_125 Homo sapiens cDNA IMAGE:5589146
                5', mRNA sequence.
ACCESSION     BMS43811
VERSION       BMS43811.1  GI:18774526
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1278)
                NIH-MGC http://mgi.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
                unpublished (1999)
JOURNAL
COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cga@db-remail.nih.gov
                Tissue Procurement: Invitrogen
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNLN at:
                http://image.llnl.gov
                Plate: LHAM12361 row: 9 column: 03
                High quality sequence start: 8
                High quality sequence stop: 548.
                Location/Qualifiers
                1..1278
                /organism="Homo sapiens"
                /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="IMAGE:5589146"
/lab_host="DH10B"
/clone_idb="NIH_MGC_125"
/organism="Hydra magnipapillata"
/site="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
/site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 Kb, insert size range 1-3.5 Kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN
Query Match      85.6%; Score 15.4; DB 12; Length 1278;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCCT 17
        |||||
        794 CGTTAATTCGCGTTCCT 810

Search completed: October 1, 2004, 08:01:51
Job time : 260.333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 13:33:17 ; Search time 1409 Seconds
(without alignments)
604.127 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18
Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY NUC
Gapop 10-0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits: 4526729 seqs, 23644849745 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 100%
Maximum Match 100%
Listing first 5000 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hcg: 3: gb_in: 4: gb_on: 5: gb_ov: 6: gb_pat: 7: gb_pl: 8: gb_pr: 9: gb_ro: 10: gb_ro: 11: gb_sgs: 12: gb_sy: 13: gb_un: 14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	AR206444	AR206444 Sequence
2	18	100.0	18	BD083635	BD083635 Nucleic a
3	18	100.0	335	AF162898	AF162898 Fusarium
4	18	100.0	335	AF162899	AF162899 Fusarium
5	18	100.0	336	AF162900	AF162900 Fusarium
6	18	100.0	338	AF339418	AF339418 Fusarium
7	18	100.0	426	AF502842	AF502842 Leaf 11ct
8	18	100.0	430	AF502842	AF502842 Leaf 11ct
9	18	100.0	441	AY387703	AY387703 Fusarium
10	18	100.0	441	AY387703	AY387703 Fusarium
11	18	100.0	445	AY387698	AY387698 Fusarium
12	18	100.0	445	AY387699	AY387699 Fusarium
13	18	100.0	445	AY387702	AY387702 Fusarium
14	18	100.0	445	AY387704	AY387704 Fusarium
15	18	100.0	445	AY387705	AY387705 Fusarium
16	18	100.0	447	AY667482	AY667482 Fusarium
17	18	100.0	447	AY667484	AY667484 Fusarium
18	18	100.0	447	AY667490	AY667490 Fusarium
19	18	100.0	447	AY387701	AY387701 Fusarium

20	18	100.0	455	8	FOU28159	U28159 Fusarium ox
21	18	100.0	455	8	FOU28161	U28161 Fusarium ox
22	18	100.0	456	8	AF440527	AF440527 Fusarium
23	18	100.0	456	8	AF440529	AF440529 Fusarium
24	18	100.0	456	8	AF440531	AF440531 Fusarium
25	18	100.0	456	8	AF440532	AF440532 Fusarium
26	18	100.0	456	8	AF440534	AF440534 Fusarium
27	18	100.0	456	8	AF440539	AF440539 Fusarium
28	18	100.0	456	8	AF440540	AF440540 Fusarium
29	18	100.0	456	8	AF440542	AF440542 Fusarium
30	18	100.0	456	8	AF440552	AF440552 Fusarium
31	18	100.0	456	8	AF440561	AF440561 Fusarium
32	18	100.0	456	8	AF440563	AF440563 Fusarium
33	18	100.0	457	8	AF440533	AF440533 Fusarium
34	18	100.0	457	8	AF440538	AF440538 Fusarium
35	18	100.0	457	8	AF440560	AF440560 Fusarium
36	18	100.0	457	8	AF440562	AF440562 Fusarium
37	18	100.0	458	8	AF055220	AF055220 Fusarium
38	18	100.0	460	8	AY259214	AY259214 Fusarium
39	18	100.0	456	8	AY208788	AY208788 Fusarium
40	18	100.0	497	8	AY243058	AY243058 Ascomycet
41	18	100.0	501	8	AY247553	AY247553 Fusarium
42	18	100.0	501	8	AY262831	AY262831 Fusarium
43	18	100.0	501	8	AY354386	AY354386 Fusarium
44	18	100.0	501	8	AY354388	AY354388 Fusarium
45	18	100.0	501	8	AY354389	AY354389 Fusarium
46	18	100.0	501	8	AY354390	AY354390 Fusarium
47	18	100.0	501	8	AY354393	AY354393 Fusarium
48	18	100.0	501	8	AY354396	AY354396 Fusarium
49	18	100.0	501	8	AY354397	AY354397 Fusarium
50	18	100.0	501	8	AY354398	AY354398 Fusarium
51	18	100.0	501	8	AY354399	AY354399 Fusarium
52	18	100.0	506	8	AF069310	AF069310 Fusarium
53	18	100.0	506	8	AY127697	AY127697 Fusarium
54	18	100.0	506	8	AY127698	AY127698 Fusarium
55	18	100.0	506	8	AY127699	AY127699 Fusarium
56	18	100.0	515	8	AY555719	AY555719 Fusarium
57	18	100.0	520	8	FOU34566	U34566 Fusarium ox
58	18	100.0	521	8	AF176656	AF176656 Fusarium
59	18	100.0	523	8	AF502841	AF502841 Leaf 11ct
60	18	100.0	531	8	FOY24876	FOY24876 Fusarium
61	18	100.0	544	8	FOY24876	FOY24876 Fusarium
62	18	100.0	545	8	FOY24876	FOY24876 Fusarium
63	18	100.0	546	8	FOY24876	FOY24876 Fusarium
64	18	100.0	546	8	FOY24876	FOY24876 Fusarium
65	18	100.0	552	8	AY147369	AY147369 Fusarium
66	18	100.0	552	8	AY462580	AY462580 Fusarium
67	18	100.0	555	8	AY462579	AY462579 Fusarium
68	18	100.0	616	8	AF322074	AF322074 Fusarium
69	18	100.0	616	8	AF322075	AF322075 Fusarium
70	18	100.0	616	8	AF322076	AF322076 Fusarium
71	18	100.0	636	8	AF443071	AF443071 Fusarium
72	18	100.0	655	8	AF669120	AF669120 Fusarium
73	18	100.0	666	8	AY667489	AY667489 Fusarium
74	18	100.0	671	8	AY669122	AY669122 Fusarium
75	18	100.0	678	8	AY669125	AY669125 Fusarium
76	18	100.0	1134	8	AY188919	AY188919 Fusarium
77	18	100.0	1471	8	FO588RNA	Y07991 F. oxysporum

ALIGNMENTS

RESULT 1
AR206444
DEFINITION Sequence 50 from patent US 6372430.
ACCESSION AR206444
VERSION AR206444.1
KEYWORDS GI:21505047
SOURCE Unknown.
ORGANISM Unknown.
Unclasseified.

linear PAT 20-JUN-2002

REFERENCE 1 (bases 1 to 18)
AUTHORS Moritsun,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL Patent: US 6372430-A 50 16-APR-2002;
FEATURES
source
1.18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18
|||||
1 CGTTAATTCGCGTTCTC 18

Db 1 CGTTAATTCGCGTTCTC 18

RESULT 2
BD083635 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD083635
DEFINITION Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION BD083635
VERSION BD083635.1 GI:22629245
KEYWORDS JP 2001525665-A/50.
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 18)
Moritsun,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL Patent: JP 2001525665-A 50 11-DEC-2001.
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
COMMENT OS Fusarium oxysporum
PV JP 2001525665-A/50
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
PI CHOI
PC C1201/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key location/Qualifiers.
1.18 location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:5507"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18
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1 CGTTAATTCGCGTTCTC 18

Db 1 CGTTAATTCGCGTTCTC 18

RESULT 3
AF162898 335 bp DNA linear PLN 15-NOV-2001
LOCUS AF162898

DEFINITION Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF162898
VERSION AF162898.1 GI:5690387
KEYWORDS
SOURCE Fusarium oxysporum f. sp. conglutinans
ORGANISM Fusarium oxysporum f. sp. conglutinans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 335)
Min,B.R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Biology, SangMyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
source
1.335 location/Qualifiers
/organism="Fusarium oxysporum f. sp. conglutinans"
/mol_type="genomic DNA"
/strain="MAFF 744001"
/db_xref="taxon:100902"
/note="forma specialis: conglutinans"
forma_specialis: conglutinans
<1.128
/product="5.8S ribosomal RNA"
129..277
/product="internal transcribed spacer 2"
278..>335
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18
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162 CGTTAATTCGCGTTCTC 179

Db 162 CGTTAATTCGCGTTCTC 179

RESULT 4
AF162899 335 bp DNA linear PLN 04-AUG-1999
LOCUS AF162899
DEFINITION Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF162899
VERSION AF162899.1 GI:5690388
KEYWORDS
SOURCE Fusarium oxysporum f. sp. fragariae
ORGANISM Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 335)
Min,B.R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Biology, SangMyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
source
1.335 location/Qualifiers
/organism="Fusarium oxysporum f. sp. fragariae"
/mol_type="genomic DNA"
/strain="MAFF 744009"
/db_xref="taxon:100903"
/note="forma specialis: fragariae"
forma_specialis: fragariae
<1.128
/product="5.8S ribosomal RNA"
129..277
/product="internal transcribed spacer 2"
278..>335
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18
|||||
1 CGTTAATTCGCGTTCTC 18

Db 1 CGTTAATTCGCGTTCTC 18

RESULT 3
AF162898 335 bp DNA linear PLN 15-NOV-2001
LOCUS AF162898

ORIGIN /product="28S ribosomal RNA"

Query Match 100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
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Db 162 CGTTAATTCGCGTTCCTC 179

RESULT 5
AF162900 336 bp DNA linear PLN 04-AUG-1999
LOCUS Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial
DEFINITION sequence; internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION AF162900.1 GI:5690389
VERSION
KEYWORDS
SOURCE Fusarium oxysporum f. sp. raphani
ORGANISM Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 336)
AUTHORS Min, B.R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea
LOCATION/Qualifiers
source 1. .336
/organism="Fusarium oxysporum f. sp. raphani"
/mol_type="genomic DNA"
/db_xref="taxon:96318"
/note="forma specialis: raphani"
forma specialis: raphani"
<1. .128
/product="5.8S ribosomal RNA"
129. .274
/product="internal transcribed spacer 2"
275. .>336
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 336;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 163 CGTTAATTCGCGTTCCTC 180

RESULT 6
AF339418 338 bp DNA linear PLN 25-OCT-2002
LOCUS Fusarium oxysporum strain FS-1 5.8S ribosomal RNA gene, partial
DEFINITION sequence; internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION AF339418
VERSION AF339418.1 GI:24369714
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 338)
AUTHORS Toolley, P.W., Hatziloukas, E., Scott, D.L. Jr. and Carras, M.M.
TITLE Use of ligase chain reaction for detection of Phytophthora
infestans in potatoes

JOURNAL Unpublished
2 (bases 1 to 338)
AUTHORS Toolley, P.W., Hatziloukas, E., Scott, D.L. Jr. and Carras, M.M.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2001) Agricultural Research Service, U.S.
Department of Agriculture, 1301 Diltto Ave., Ft. Detrick, MD
21702-5023, USA
LOCATION/Qualifiers
source 1. .338
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="FS-1"
/db_xref="taxon:5507"
<1. .>338
/note="contains 5.8S ribosomal RNA, internal transcribed
spacer 2, and 28S ribosomal RNA"

misc_RNA

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 338;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 162 CGTTAATTCGCGTTCCTC 179

RESULT 7
AY383320 426 bp DNA linear PLN 05-OCT-2003
LOCUS Fusarium oxysporum f. sp. vanillae isolate DU-1-1 internal
DEFINITION transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,
complete sequence; and internal transcribed spacer 2, partial
sequence.
ACCESSION AY383320.1 GI:37142968
VERSION
KEYWORDS
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Fusarium oxysporum f. sp. vanillae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 426)
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X.Y.
TITLE Fusarium oxysporum f. sp. vanillae isolate DU-1-1 ITS1, 5.8S rDNA,
ITS 2 sequence
JOURNAL Unpublished
2 (bases 1 to 426)
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X.Y.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2003) Dept. Plant Pathology, Yunnan Agricultural
University, Long You Street, Kunming, Yunnan 650201, P.R. China
LOCATION/Qualifiers
source 1. .426
/organism="Fusarium oxysporum f. sp. vanillae"
/mol_type="genomic DNA"
/isolate="DU-1-1"
/db_xref="taxon:247126"
/note="forma specialis: vanillae"
<1. .117
/product="internal transcribed spacer 1"
118. .274
/product="5.8S ribosomal RNA"
275. .>426
/product="internal transcribed spacer 2"

misc_RNA

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||

Db 309 CGTTAATTCGCGTTCCTC 326

RESULT 8
AF502842/c 430 bp DNA linear PLN 13-MAY-2002
LOCUS
DEFINITION Leaf litter ascomycete strain its31 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF502842 GI:20531649
VERSION AF502842.1
KEYWORDS leaf litter ascomycete strain its31
SOURCE leaf litter ascomycete strain its31
ORGANISM Eukaryota; Fungi; Ascomycota.

REFERENCE
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
TITLE Biogeography of leaf litter fungi
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 430)
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
FEATURES
source
1..430
/organism="leaf litter ascomycete strain its31"
/mol_type="genomic DNA"
/strain="its31"
/isolate="1000502849"
/specific_host="Miconia te"
/db_xref="taxon:194114"
/country="Puerto Rico"
<1..>430
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA and internal transcribed spacer 2"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 430;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
82 CGTTAATTCGCGTTCCTC 65

RESULT 9
AY387703 441 bp DNA linear PLN 07-OCT-2003
LOCUS
DEFINITION Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AY387703 GI:37362908
VERSION AY387703.1
KEYWORDS Fusarium oxysporum
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 441)
1 (bases 1 to 441)
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.
Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished
2 (bases 1 to 441)
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.

REFERENCE
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.
TITLE Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 441)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.

TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
FEATURES
source
1..441
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="DL-2-7"
/db_xref="taxon:5507"
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136..293
/product="5.8S ribosomal RNA"
294..>441
/product="internal transcribed spacer 2"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 441;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
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327 CGTTAATTCGCGTTCCTC 344

RESULT 10
AY380575 445 bp DNA linear PLN 04-OCT-2003
LOCUS
DEFINITION Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AY380575 GI:37039595
VERSION AY380575.1
KEYWORDS Fusarium oxysporum f. sp. vanillae
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 445)
1 (bases 1 to 445)
Ruan,X.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.
ITS1 5.8S and ITS2 rDNA sequence from Fusarium oxysporum f. sp. vanillae Unpublished
2 (bases 1 to 445)
Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples Republic of China
FEATURES
source
1..445
/organism="Fusarium oxysporum f. sp. vanillae"
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/note="forma_specialis: vanillae"
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294..>445
/product="internal transcribed spacer 2"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCTTCCTC 18
|||||
Db 327 CGTTAATTCGCTTCCTC 344

RESULT 11
AY387698 445 bp DNA linear PLN 07-OCT-2003
LOCUS AY387698
DEFINITION Fusarium oxysporum f. sp. vanillae isolate ML-8-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
VERSION AY387698
KEYWORDS AY387698.1 GI:37362903
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Liao,B.
TITLE Molecular investigation of isolates of Fusarium oxysporum in relation to the control of root rot disease in vanilla planifolia Andr
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Liao,B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
FEATURES
source location/Qualifiers
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/organism="Fusarium oxysporum f. sp. vanillae"
/mol_type="genomic DNA"
/isolate="ML-8-1"
/db_xref="taxon:247126"
/note="forma_specialis: vanillae"
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136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 2"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCTTCCTC 18
|||||
Db 327 CGTTAATTCGCTTCCTC 344

RESULT 12
AY387699 445 bp DNA linear PLN 07-OCT-2003
LOCUS AY387699
DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
VERSION AY387699
KEYWORDS AY387699.1 GI:37362904
SOURCE Fusarium oxysporum f. sp. vanillae
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Liao,B.
TITLE Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Liao,B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
FEATURES
source location/Qualifiers
1..445
/organism="Fusarium oxysporum f. sp. vanillae"
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/isolate="DL-4b"
/db_xref="taxon:247126"
/note="forma_specialis: vanillae"

misc_RNA
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/product="internal transcribed spacer 1"
136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 2"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCTTCCTC 18
|||||
Db 327 CGTTAATTCGCTTCCTC 344

RESULT 13
AY387702 445 bp DNA linear PLN 07-OCT-2003
LOCUS AY387702
DEFINITION Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387702
VERSION AY387702.1 GI:37362907
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Yang,J.
TITLE Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Yang,J.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
FEATURES
source location/Qualifiers
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/organism="Fusarium oxysporum"
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/isolate="ML-7-1"
/db_xref="taxon:5507"
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/product="internal transcribed spacer 1"

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/product="5.8S ribosomal RNA"
misc_rna 294..>445
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ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 14
AY387704 445 bp DNA linear PLN 07-OCT-2003
LOCUS
DEFINITION Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387704
VERSION
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.
Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished
2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.
Direct Submission
Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
Location/Qualifiers
1..445
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="ML-8-4"
/db_xref="taxon:5507"

FEATURES
source
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/mol_type="genomic DNA"
/isolate="ML-8-4"
/db_xref="taxon:5507"

rnRNA 136..293
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misc_rna 294..>445
/product="internal transcribed spacer 1"
rRNA
/product="5.8S ribosomal RNA"
misc_rna 294..>445
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 15
AY387705 445 bp DNA linear PLN 07-OCT-2003
LOCUS
DEFINITION Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY387705
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 445)
Liu, B., Zhu, Y.Y., Ling, Y.Z. and Cao, Y.
Direct Submission
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003, P. R. China
Location/Qualifiers
1..447
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-117"
/specific_host="pease plant"
/db_xref="taxon:5507"

FEATURES
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/mol_type="genomic DNA"
/isolate="12-117"
/specific_host="pease plant"
/db_xref="taxon:5507"

rnRNA 139..296
/product="5.8S ribosomal RNA"

KEYWORDS
SOURCE
ORGANISM
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Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Chen, J.B.
Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished
2 (bases 1 to 445)
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Chen, J.B.
Direct Submission
Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
Location/Qualifiers
1..445
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="ML-5-2"
/db_xref="taxon:5507"

misc_rna
136..293
/product="5.8S ribosomal RNA"
294..>445
/product="internal transcribed spacer 1"

rnRNA
136..293
/product="5.8S ribosomal RNA"

misc_rna
294..>445
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 16
AY667482 447 bp DNA linear PLN 20-JUL-2004
LOCUS
DEFINITION Fusarium oxysporum isolate 12-117 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY667482
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 447)
Liu, B., Zhu, Y.Y., Ling, Y.Z. and Cao, Y.
Direct Submission
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003, P. R. China
Location/Qualifiers
1..447
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-117"
/specific_host="pease plant"
/db_xref="taxon:5507"

misc_rna
139..296
/product="5.8S ribosomal RNA"

misc_RNA 297..>447
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
330 CGTTAATTCGCGTTCCTC 347
RESULT 17
AY667484 447 bp DNA linear PLN 20-JUL-2004
LOCUS Fusarium oxysporum isolate 12-132 internal transcribed spacer 1,
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and
internal transcribed spacer 2, partial sequence.
ACCESSION AY667484 GI:50313399
VERSION
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 447)
REFERENCE Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.
AUTHORS Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
JOURNAL Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,
P. R. China
FEATURES
source 1..447
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-132"
/specific_host="melon plant"
/db_xref="taxon:5507"
<1..138
/product="internal transcribed spacer 1"
139..296
/product="5.8S ribosomal RNA"
297..>447
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
330 CGTTAATTCGCGTTCCTC 347
RESULT 18
AY667490 447 bp DNA linear PLN 20-JUL-2004
LOCUS Fusarium oxysporum isolate 12-136 internal transcribed spacer 1,
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and
internal transcribed spacer 2, partial sequence.
ACCESSION AY667490 GI:50313405
VERSION
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 447)
REFERENCE Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,
P.R. China
FEATURES
source Location/Qualifiers
1..447
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-136"
/specific_host="watermelon plant"
/db_xref="taxon:5507"
<1..138
/product="internal transcribed spacer 1"
139..296
/product="5.8S ribosomal RNA"
297..>447
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
330 CGTTAATTCGCGTTCCTC 347
RESULT 19
AY387701 447 bp DNA linear PLN 07-OCT-2003
LOCUS Fusarium oxysporum isolate WJD-2-2 internal transcribed spacer 1,
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and
internal transcribed spacer 2, partial sequence.
ACCESSION AY387701 GI:37362906
VERSION
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 447)
REFERENCE Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.
AUTHORS and Kong, Q.
TITLE Fusarium oxysporum isolate WJD-2-2 internal transcribed spacer 1,
JOURNAL 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
REFERENCE Unpublished
2 (bases 1 to 447)
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of
Plant Protection, Yunnan Agricultural University, Long You Street,
Kunming, Yunnan 650201, P. R. China
FEATURES
source Location/Qualifiers
1..447
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="WJD-2-2"
/db_xref="taxon:5507"
<1..119
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120..277
/product="5.8S ribosomal RNA"
278..>447
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATTCGCTTC 18
 Db 311 CGTTAATTCGCTTC 328

RESULT 20

LOCUS FOU28159 455 bp DNA linear PLN 08-JUN-1995
 DEFINITION Fusarium oxysporum strain DAOM 213391 internal transcribed spacer region ITS1, 5.8S ribosomal RNA gene, and internal transcribed spacer region ITS2. Includes the 5.8S gene.

ACCESSION U28159.1 GI:852527
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1 (bases 1 to 455)

REFERENCE 1
 AUTHORS Duggal, A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-1995) Artie Duggal, Forestry, University of Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada
 FEATURES
 SOURCE 1..455

/organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /strain="DAOM 213391"
 /db_xref="taxon:5507"

/note="The fungus was determined by Selfert K.A. and was isolated from wilted carnations from Kenya by Tewari J.P."

1..147
 /note="Internal transcribed spacer region; ITS1"

148..304
 /product="5.8S ribosomal RNA"

305..455

/note="Internal transcribed spacer region; ITS2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 455;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATTCGCTTC 18
 Db 338 CGTTAATTCGCTTC 355

RESULT 21
 FOU28161 455 bp DNA linear PLN 08-JUN-1995
 LOCUS
 DEFINITION Fusarium oxysporum strain CBS 171.31 internal transcribed spacer region ITS1, 5.8S ribosomal RNA gene, and internal transcribed spacer region ITS2. Includes the 5.8S gene.

ACCESSION U28161.1 GI:852529
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1 (bases 1 to 455)

REFERENCE 1
 AUTHORS Duggal, A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-1995) Artie Duggal, Forestry, University of Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada
 FEATURES
 SOURCE 1..455

/organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /strain="CBS 171.31"

/db_xref="taxon:5507"
 /note="The fungus was isolated and identified by Wollenweber H.W. from Pinus sp. from Germany"

1..147
 /note="Internal transcribed spacer region; ITS1"

148..304
 /product="5.8S ribosomal RNA"

305..455
 /note="Internal transcribed spacer region; ITS2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 455;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATTCGCTTC 18
 Db 338 CGTTAATTCGCTTC 355

RESULT 22
 AF440527 456 bp DNA linear PLN 24-SEP-2003
 LOCUS
 DEFINITION Fusarium oxysporum isolate 14RK-11 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

ACCESSION AF440527 GI:18034395
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1 (bases 1 to 456)

1 (bases 1 to 456)
 /note="Internal transcribed spacer region; ITS1"

148..304
 /product="5.8S ribosomal RNA"

305..456
 /product="Internal transcribed spacer 2"

/organism="Fusarium oxysporum"

/mol_type="genomic DNA"

/isolate="14RK-11"

/db_xref="taxon:5507"

1..147
 /product="Internal transcribed spacer 1"

148..305
 /product="5.8S ribosomal RNA"

306..456
 /product="Internal transcribed spacer 2"

/organism="Fusarium oxysporum"

/mol_type="genomic DNA"

/isolate="14RK-11"

/db_xref="taxon:5507"

1..147
 /product="Internal transcribed spacer 1"

148..305
 /product="5.8S ribosomal RNA"

306..456
 /product="Internal transcribed spacer 2"

/organism="Fusarium oxysporum"

/mol_type="genomic DNA"

/isolate="14RK-11"

/db_xref="taxon:5507"

1..147
 /product="Internal transcribed spacer 1"

148..305
 /product="5.8S ribosomal RNA"

306..456
 /product="Internal transcribed spacer 2"

/organism="Fusarium oxysporum"

complete sequence.

ACCESSION AF440529
VERSION AF440529.1 GI:18034397
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

1 (bases 1 to 456)
Baoy,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.
Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Baoy,J.R., Fravel,D.R. and Lazarovits,G.
Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
1. .456
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="73RK-14"
/db_xref="taxon:5507"
1. .147
/product="internal transcribed spacer 1"
148. .305
/product="5.8S ribosomal RNA"
306. .456
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCTC 18
|||||
Db 339 CGTTAATTCGCGTTCTC 356

RESULT 24
AF440531 456 bp DNA linear PLN 24-SEP-2003
LOCUS
DEFINITION
Fusarium oxysporum isolate 44RK-35 internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

1 (bases 1 to 456)
Baoy,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.
Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Baoy,J.R., Fravel,D.R. and Lazarovits,G.
Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
1. .456
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="44RK-35"

/db_xref="taxon:5507"
1. .147
/product="internal transcribed spacer 1"
148. .305
/product="5.8S ribosomal RNA"
306. .456
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCTC 18
|||||
Db 339 CGTTAATTCGCGTTCTC 356

RESULT 25
AF440532 456 bp DNA linear PLN 24-SEP-2003
LOCUS
DEFINITION
Fusarium oxysporum isolate 73RK-1 internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

1 (bases 1 to 456)
Baoy,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.
Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants
Can. J. Bot. 80 (3), 271-279 (2002)
2 (bases 1 to 456)
Baoy,J.R., Fravel,D.R. and Lazarovits,G.
Direct Submission
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
Location/Qualifiers
1. .456
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="73RK-1"
/db_xref="taxon:5507"
1. .147
/product="internal transcribed spacer 1"
148. .305
/product="5.8S ribosomal RNA"
306. .456
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCTC 18
|||||
Db 339 CGTTAATTCGCGTTCTC 356

RESULT 26
AF440534 456 bp DNA linear PLN 24-SEP-2003
LOCUS
DEFINITION
Fusarium oxysporum isolate AL22 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

```

VERSION      AF440534.1  GI:180344402
KEYWORDS
SOURCE       Fusarium oxysporum
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
              Fusarium oxysporum complex.
REFERENCE    Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
AUTHORS      Berkum,P.
TITLE        Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
              from tomato plants
JOURNAL      Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE    2 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Direct Submission
JOURNAL      Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
              Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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  misc_RNA
    306..456
    /product="internal transcribed spacer 2"
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
1 CGTTAATTCGCGTTCCTC 18
|||||
Db
339 CGTTAATTCGCGTTCCTC 356

RESULT 27
AF440539      456 bp      DNA      linear      PLN 24-SEP-2003
LOCUS         Fusarium oxysporum isolate DEH1 internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION     AF440539
VERSION       AF440539.1  GI:180344407
KEYWORDS
SOURCE       Fusarium oxysporum
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
              Fusarium oxysporum complex.
REFERENCE    1 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
              Berkum,P.
TITLE        Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
              from tomato plants
JOURNAL      Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE    2 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Direct Submission
JOURNAL      Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
              Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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    /isolate="DEH1"
    /db_xref="taxon:5507"
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  rRNA
    148..305
    /product="5.8S ribosomal RNA"
  misc_RNA
    306..456
    /product="internal transcribed spacer 2"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
1 CGTTAATTCGCGTTCCTC 18
|||||
Db
339 CGTTAATTCGCGTTCCTC 356

RESULT 29
AF440542      456 bp      DNA      linear      PLN 24-SEP-2003
LOCUS         Fusarium oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION     AF440542
VERSION       AF440542.1  GI:180344410
KEYWORDS

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RNA
148..305
/product="5.8S ribosomal RNA"
misc_RNA
306..456
/product="internal transcribed spacer 2"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
1 CGTTAATTCGCGTTCCTC 18
|||||
Db
339 CGTTAATTCGCGTTCCTC 356

RESULT 28
AF440540      456 bp      DNA      linear      PLN 24-SEP-2003
LOCUS         Fusarium oxysporum isolate DEH2 internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION     AF440540
VERSION       AF440540.1  GI:180344408
KEYWORDS
SOURCE       Fusarium oxysporum
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
              Fusarium oxysporum complex.
REFERENCE    1 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
              Berkum,P.
TITLE        Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
              from tomato plants
JOURNAL      Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE    2 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Direct Submission
JOURNAL      Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
              Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
  source
    1..456
    /organism="Fusarium oxysporum"
    /mol_type="genomic DNA"
    /isolate="DEH2"
    /db_xref="taxon:5507"
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    1..147
    /product="internal transcribed spacer 1"
  rRNA
    148..305
    /product="5.8S ribosomal RNA"
  misc_RNA
    306..456
    /product="internal transcribed spacer 2"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
1 CGTTAATTCGCGTTCCTC 18
|||||
Db
339 CGTTAATTCGCGTTCCTC 356

RESULT 29
AF440542      456 bp      DNA      linear      PLN 24-SEP-2003
LOCUS         Fusarium oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION     AF440542
VERSION       AF440542.1  GI:180344410
KEYWORDS

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SOURCE
ORGANISM Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
Berkum,P.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
source
1. .456
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="P047"
/db_xref="taxon:5507"
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1. .147
/product="internal transcribed spacer 1"
rRNA 148. .305
/product="5.8S ribosomal RNA"
306. .456
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTAATTCGGCTTCCTC 18
|||||
339 CGTTAATTCGGCTTCCTC 356
Db

RESULT 30
AF440552 456 bp DNA linear PLN 24-SEP-2003
LOCUS Fusarium oxysporum isolate IAT internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440552
VERSION AF440552.1 GI:18034420
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
Berkum,P.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
source
1. .456
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="P047"
/db_xref="taxon:5507"
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1. .147
/product="internal transcribed spacer 1"
rRNA 148. .305
/product="5.8S ribosomal RNA"
306. .456
/product="internal transcribed spacer 2"
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Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTAATTCGGCTTCCTC 18
|||||
339 CGTTAATTCGGCTTCCTC 356
Db

RESULT 32
AF440563 456 bp DNA linear PLN 24-SEP-2003
LOCUS Fusarium oxysporum isolate SA70 internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440563
VERSION AF440563.1 GI:18034431
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum

SOURCE
ORGANISM Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van
Berkum,P.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)
REFERENCE
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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1. .456
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/mol_type="genomic DNA"
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/db_xref="taxon:5507"
misc_RNA
1. .147
/product="internal transcribed spacer 1"
rRNA 148. .305
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306. .456
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTAATTCGGCTTCCTC 18
|||||
339 CGTTAATTCGGCTTCCTC 356
Db

RESULT 32
AF440563 456 bp DNA linear PLN 24-SEP-2003
LOCUS Fusarium oxysporum isolate P01 internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440563
VERSION AF440563.1 GI:18034431
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

1 (bases 1 to 456)
 Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

TITLE
 Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants

JOURNAL
 Can. J. Bot. 80 (3), 271-279 (2002)

REFERENCE
 2 (bases 1 to 456)
 Bao,J.R., Fravel,D.R. and Lazarovits,G.

AUTHORS
 Direct Submission

JOURNAL
 Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 1..456
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="SA70"
 /db_xref="taxon:5507"
 1..147
 /product="internal transcribed spacer 1"
 148..305
 /product="5.8S ribosomal RNA"
 306..456
 /product="internal transcribed spacer 2"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. NO. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 CGTTAATTCGCGTTCCTC 18
 |||||
 339 CGTTAATTCGCGTTCCTC 356

Db

RESULT 33
 AF440533 457 bp DNA linear PLN 24-SEP-2003
 LOCUS
 Fusarium oxysporum isolate AU01 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.
 AF440533
 AF440533.1 GI:18034401

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE
 1 (bases 1 to 457)
 Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

AUTHORS
 Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants

JOURNAL
 Can. J. Bot. 80 (3), 271-279 (2002)

REFERENCE
 2 (bases 1 to 457)
 Bao,J.R., Fravel,D.R. and Lazarovits,G.

AUTHORS
 Direct Submission

JOURNAL
 Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 1..457
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="AU01"
 /db_xref="taxon:5507"
 1..148
 /product="internal transcribed spacer 1"
 149..306
 /product="5.8S ribosomal RNA"
 307..457

/product="internal transcribed spacer 2"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 457;
 Best Local Similarity 100.0%; Pred. NO. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 CGTTAATTCGCGTTCCTC 18
 |||||
 340 CGTTAATTCGCGTTCCTC 357

Db

RESULT 34
 AF440538 457 bp DNA linear PLN 24-SEP-2003
 LOCUS
 Fusarium oxysporum isolate CS-20 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.
 AF440538
 AF440538.1 GI:18034406

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE
 1 (bases 1 to 457)
 Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

AUTHORS
 Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants

JOURNAL
 Can. J. Bot. 80 (3), 271-279 (2002)

REFERENCE
 2 (bases 1 to 457)
 Bao,J.R., Fravel,D.R. and Lazarovits,G.

AUTHORS
 Direct Submission

JOURNAL
 Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /isolate="CS-20"
 /db_xref="taxon:5507"
 1..147
 /product="internal transcribed spacer 1"
 148..305
 /product="5.8S ribosomal RNA"
 306..457
 /product="internal transcribed spacer 2"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 457;
 Best Local Similarity 100.0%; Pred. NO. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 CGTTAATTCGCGTTCCTC 18
 |||||
 339 CGTTAATTCGCGTTCCTC 356

Db

RESULT 35
 AF440560 457 bp DNA linear PLN 24-SEP-2003
 LOCUS
 Fusarium oxysporum isolate Litom internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.
 AF440560
 AF440560.1 GI:18034428

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;

REFERENCE 1 (bases 1 to 457)
 AUTHORS Bo,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkmun,P.
 TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants
 JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)
 REFERENCE 2 (bases 1 to 457)
 AUTHORS Bo,J.R., Fravel,D.R. and Lazarovits,G.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 1..457
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 /mol_type="genomic DNA"
 /isolate="PE13"
 /db_xref="taxon:5507"
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 1..457
 /product="internal transcribed spacer 1"
 rRNA
 149..306
 /product="5.8S ribosomal RNA"
 misc_RNA
 307..457
 /product="internal transcribed spacer 2"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 457;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
 |||
 Db 340 CGTTAATTCGGCTTCCTC 357

RESULT 36
 AF440562 457 bp DNA linear PLN 24-SEP-2003
 LOCUS *Fusarium oxysporum* isolate PE13 internal transcribed spacer 1, 5.8S
 DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
 sequence.
 ACCESSION AF440562
 VERSION AF440562
 KEYWORDS AF440562.1 GI:18034430
 SOURCE *Fusarium oxysporum*
 ORGANISM *Fusarium oxysporum*
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*;
Fusarium oxysporum complex.
 REFERENCE 1 (bases 1 to 457)
 AUTHORS Bo,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkmun,P.
 TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants
 JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)
 REFERENCE 2 (bases 1 to 457)
 AUTHORS Bo,J.R., Fravel,D.R. and Lazarovits,G.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
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 /db_xref="taxon:5507"
 misc_RNA
 1..148
 /product="internal transcribed spacer 1"
 rRNA
 149..306
 /product="5.8S ribosomal RNA"
 misc_RNA
 307..457
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 457;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
 |||
 Db 340 CGTTAATTCGGCTTCCTC 357

RESULT 37
 AF055220 458 bp DNA linear PLN 29-JUN-2000
 LOCUS *Fusarium oxysporum* strain FO 18S ribosomal RNA gene, partial
 DEFINITION sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA
 gene, complete sequence; and internal transcribed spacer 2, partial
 sequence.
 ACCESSION AF055220
 VERSION AF055220
 KEYWORDS AF055220.1 GI:3047288
 SOURCE *Fusarium oxysporum*
 ORGANISM *Fusarium oxysporum*
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*;
Fusarium oxysporum complex.
 REFERENCE 1 (bases 1 to 458)
 AUTHORS Dodd,S.L., Crowhurst,R.N., Rodrigo,A.G., Samuels,G.J., Hill,R.A.
 and Stewart,A.
 TITLE Examination of Trichoderma phylogenies derived from ribosomal DNA
 sequence data
 JOURNAL Mycol. Res. 104, 23-34 (2000)
 REFERENCE 2 (bases 1 to 458)
 AUTHORS Dodd,Wilson,S.L., Crowhurst,R.N., Rodrigo,A.G. and Stewart,A.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-1998) Soil, Plant and Ecological Science
 Division, Lincoln University, P.O. Box 84, Canterbury, New Zealand
 COMMENT On Apr 16, 1998 this sequence version replaced gi:3025822.
 FEATURES
 source
 1..458
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /strain="FO"
 /db_xref="taxon:5507"
 /note="pathogen of squash vegetable"
 rRNA
 <1..6
 /product="18S ribosomal RNA"
 misc_RNA
 7..153
 /product="internal transcribed spacer 1"
 rRNA
 154..311
 /product="5.8S ribosomal RNA"
 misc_RNA
 312..458
 /product="internal transcribed spacer 2"
 /note="ITS-2"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 458;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
 |||
 Db 345 CGTTAATTCGGCTTCCTC 362

RESULT 38
 AY259214 460 bp DNA linear PLN 28-APR-2003
 LOCUS *Fusarium oxysporum* f. sp. vasinfectum 18S ribosomal RNA gene,
 DEFINITION partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
 gene and internal transcribed spacer 2, complete sequence; and 28S
 ribosomal RNA gene, partial sequence.
 ACCESSION AY259214

```

VERSION      AY259214.1  GI:30171326
KEYWORDS
SOURCE       Fusarium oxysporum f. sp. vasinfectum
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
              Fusarium oxysporum complex.
REFERENCE    1 (bases 1 to 460)
AUTHORS     Abd-Elisalam,K.A.
TITLE        ITS sequence regions in Fov
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 460)
AUTHORS     Abd-Elisalam,K.A.
TITLE        Direct Submission
JOURNAL      Submitted (20-MAR-2003) Molecular Markers Lab., Plant Pathology
              Research Institute, 9-Gmaa St., Giza, 002 12619, Egypt
FEATURES
  source     1..460
              /organism="Fusarium oxysporum f. sp. vasinfectum"
              /mol_type="genomic DNA"
              /db_xref="taxon:61374"
              /note="forma_specialis: vasinfectum"
  rRNA       <1..120
              /product="18S ribosomal RNA"
  misc_RNA   121..240
              /product="internal transcribed spacer 1"
              241..320
              /product="5.8S ribosomal RNA"
              321..400
              /product="internal transcribed spacer 2"
              401..>460
              /product="28S ribosomal RNA"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 460;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
    |||
Db 343 CGTTAATTCGCGTTCCTC 360

RESULT 39
AY208788      496 bp      DNA      linear      PLN 30-JUL-2004
LOCUS         Fusarium oxysporum isolate Po23, internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION     AY208788
VERSION       AY208788.2  GI:40385898
KEYWORDS
SOURCE       Fusarium oxysporum
ORGANISM     Fusarium oxysporum
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
              Fusarium oxysporum complex.
REFERENCE    1 (bases 1 to 496)
AUTHORS     Gure,A., Wahlstrom,K. and Stenlid,J.
TITLE        Diversity of Fungi Associated with Seeds of Tropical Forest Trees:
              Podocarpus falcatus and Prunus africana
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 496)
AUTHORS     Gure,A. and Stenlid,J.
TITLE        Direct Submission
JOURNAL      Submitted (30-DEC-2002) Forest Mycology & Pathology, Swedish
              University of Agricultural Sciences, Ulls vag 26A, Uppsala, Uppland
              750 07, Sweden
REFERENCE    3 (bases 1 to 496)
AUTHORS     Gure,A. and Stenlid,J.
TITLE        Direct Submission
JOURNAL      Submitted (30-DEC-2003) Forest Mycology & Pathology, Swedish
              University of Agricultural Sciences, Ulls vag 26A, Uppsala, Uppland

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REMARK       750 07, Sweden
COMMENT      Sequence update by submitter
              On Dec 30, 2003 this sequence version replaced gi:28932934.
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              /db_xref="taxon:5507"
  misc_RNA   1..496
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              ribosomal RNA, and internal transcribed spacer 2"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
    |||
Db 357 CGTTAATTCGCGTTCCTC 374

RESULT 40
AY243058      497 bp      DNA      linear      PLN 14-APR-2003
LOCUS         Ascomycete sp. Dunel7 internal transcribed spacer 1, partial
DEFINITION    sequence; 5.8S ribosomal RNA gene, complete sequence; and internal
              transcribed spacer 2, partial sequence.
ACCESSION     AY243058
VERSION       AY243058.1  GI:29826153
KEYWORDS
SOURCE       ascomycete sp. Dunel7
ORGANISM     ascomycete sp. Dunel7
              Eukaryota; Fungi; Ascomycota.
REFERENCE    1 (bases 1 to 497)
AUTHORS     Beckstead,J. and Parker,I.M.
TITLE        Invasiveness of Ammophila arenaria: Release from soil-borne
              pathogens?
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 497)
AUTHORS     Gambetta,G., Gilbert,G.S. and Parker,I.M.
TITLE        Direct Submission
JOURNAL      Submitted (24-FEB-2003) Ecology and Evolutionary Biology,
              University of California, Santa Cruz, 1156 High St., EWS, Santa
              Cruz, CA 95064, USA
FEATURES
  source     1..497
              /organism="ascomycete sp. Dunel7"
              /mol_type="genomic DNA"
              /strain="Dunel7"
              /isolation_source="plants grown in greenhouse in
              unsterilized soil collected from Dune Beach, Half Moon
              Bay, California"
              /specific_host="Ammophila arenaria"
              /db_xref="taxon:227272"
  misc_RNA   <1..128
              /product="internal transcribed spacer 1"
              129..278
              /product="5.8S ribosomal RNA"
              279..>497
              /product="internal transcribed spacer 2"
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 497;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
    |||
Db 320 CGTTAATTCGCGTTCCTC 337

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RESULT 41
AY247553/c 501 bp DNA linear PLN 27-APR-2003
LOCUS
DEFINITION Fusarium oxysporum f. sp. vasinfectum isolate BANGD12/B2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AY247553.1 GI:30143797
VERSION
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 501)
Thornon,C.R., Groenhof,A.C., Forrest,R., Lamotte,R. and Talbot,N.J.
REFERENCE A one-step, immuno-chromatographic lateral flow device for the detection and quantification of Rhizoctonia solani in soil
TITLE Unpublished
2 (bases 1 to 501)
Thornon,C.R., Groenhof,A.C., Forrest,R., Lamotte,R. and Talbot,N.J.
REFERENCE Direct Submission
AUTHORS Submitted (03-MAR-2003) Biological Sciences, University of Exeter, Perry Road, Exeter, Devon EX4 4QG, England
JOURNAL
TITL Location/Qualifiers
FEATURES
SOURCE
1. 501
/organism="Fusarium oxysporum f. sp. vasinfectum"
/mol_type="genomic DNA"
/isolate="BANGD12/B2"
/db_xref="taxon:61374"
/note="forma_specialis: vasinfectum"
complement(1..501)
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2"

misc_RNA
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 119 CGTTAATTCGCGTTCCTC 102
|||||

RESULT 42
AY262831 501 bp DNA linear PLN 04-MAY-2003
LOCUS
DEFINITION Fusarium oxysporum f. sp. vasinfectum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AY262831
VERSION
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 501)
Abd-Elisalam,K.A.
REFERENCE Molecular diagnostic of Fusarium oxysporum f. sp. vasinfectum
AUTHORS Unpublished
JOURNAL
TITL 2 (bases 1 to 501)
Abd-Elisalam,K.A.
REFERENCE Direct Submission
AUTHORS Submitted (27-MAR-2003) Molecular Markers Lab., Plant Pathology Research Institute, 9-Gmaa St., 002 12619, Egypt
JOURNAL
TITL Location/Qualifiers
FEATURES

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1. 501
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/mol_type="genomic DNA"
/db_xref="taxon:61374"
/note="forma_specialis: vasinfectum"
rRNA
1. 115
/product="18S ribosomal RNA"
116..205
/product="internal transcribed spacer 1"
206..310
/product="5.8S ribosomal RNA"
311..420
/product="internal transcribed spacer 2"
421..501
/product="28S ribosomal RNA"

misc_RNA
rRNA
misc_RNA
rRNA
misc_RNA
rRNA

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 349 CGTTAATTCGCGTTCCTC 366
|||||

RESULT 43
AY354386 501 bp DNA linear PLN 15-SEP-2003
LOCUS
DEFINITION Fusarium oxysporum f. sp. radialis-lycopersici 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AY354386
VERSION
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. radialis-lycopersici
Fusarium oxysporum f. sp. radialis-lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 501)
Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
REFERENCE Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs
AUTHORS Span,J. Agric. Res. 1 (3) (2003) in press
2 (bases 1 to 501)
Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
REFERENCE Direct Submission
AUTHORS Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain
JOURNAL
TITL Location/Qualifiers
FEATURES
SOURCE
1. 501
/organism="Fusarium oxysporum f. sp. radialis-lycopersici"
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/country="Spain"
/note="forma_specialis: radialis-lycopersici"
1. 28
/product="18S ribosomal RNA"
29..175
/product="internal transcribed spacer 1"
176..333
/product="5.8S ribosomal RNA"
334..484
/product="internal transcribed spacer 2"
485..501
/product="28S ribosomal RNA"

Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 44
 AY354388
 LOCUS
 DEFINITION
 501 bp DNA linear PLN 15-SEP-2003
 Fusarium oxysporum f. sp. dianthi 18S ribosomal RNA gene, partial
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene
 and internal transcribed spacer 2, complete sequence; and 28S
 ribosomal RNA gene, partial sequence.

ACCESSION
 VERSION
 KEYWORDS
 ORGANISM
 AY354388
 AY354388.1 GI:34559393
 Fusarium oxysporum f. sp. dianthi
 Fusarium oxysporum f. sp. dianthi
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Genetic relationships among seven specialized forms of Fusarium
 oxysporum determined by DNA sequencing of the ITS region and AFLPs
 Span. J. Agric. Res. 1 (3) (2003) In press

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Direct Submission
 Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca
 (Murcia) 30150, Spain

FEATURES
 source
 location/Qualifiers
 1..501
 /organism="Fusarium oxysporum f. sp. dianthi"
 /mol_type="genomic DNA"
 /strain="Sur-10"
 /specific_host="carnation"
 /db_xref="taxon:42551"
 /country="Spain"
 /note="forma_specialis: dianthi"
 <1..28
 /product="18S ribosomal RNA"
 29..175
 /product="internal transcribed spacer 1"
 176..333
 /product="5.8S ribosomal RNA"
 334..484
 /product="internal transcribed spacer 2"
 485..>501
 /product="28S ribosomal RNA"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 45
 AY354389
 LOCUS
 DEFINITION
 501 bp DNA linear PLN 15-SEP-2003
 Fusarium oxysporum f. sp. dianthi 18S ribosomal RNA gene, partial
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene
 and internal transcribed spacer 2, complete sequence; and 28S

ribosomal RNA gene, partial sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AY354389
 AY354389.1 GI:34559394
 Fusarium oxysporum f. sp. dianthi
 Fusarium oxysporum f. sp. dianthi
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Genetic relationships among seven specialized forms of Fusarium
 oxysporum determined by DNA sequencing of the ITS region and AFLPs
 Span. J. Agric. Res. 1 (3) (2003) In press

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Direct Submission
 Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca
 (Murcia) 30150, Spain

FEATURES
 source
 location/Qualifiers
 1..501
 /organism="Fusarium oxysporum f. sp. dianthi"
 /mol_type="genomic DNA"
 /strain="Gsa-2"
 /specific_host="carnation"
 /db_xref="taxon:42551"
 /country="Spain"
 /note="forma_specialis: dianthi"
 <1..28
 /product="18S ribosomal RNA"
 29..175
 /product="internal transcribed spacer 1"
 176..333
 /product="5.8S ribosomal RNA"
 334..484
 /product="internal transcribed spacer 2"
 485..>501
 /product="28S ribosomal RNA"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 46
 AY354390
 LOCUS
 DEFINITION
 501 bp DNA linear PLN 15-SEP-2003
 Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene
 and internal transcribed spacer 2, complete sequence; and 28S
 ribosomal RNA gene, partial sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AY354390
 AY354390.1 GI:34559395
 Fusarium oxysporum f. sp. melonis
 Fusarium oxysporum f. sp. melonis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Genetic relationships among seven specialized forms of Fusarium
 oxysporum determined by DNA sequencing of the ITS region and AFLPs
 Span. J. Agric. Res. 1 (3) (2003) In press

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and
 Cifuentes,D.
 Direct Submission
 Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca
 (Murcia) 30150, Spain

AUTHORS Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain
FEATURES Location/Qualifiers
 1..501
 /organism="Fusarium oxysporum f. sp. melonis"
 /mol_type="genomic DNA"
 /strain="ATCC 28858"
 /specific_host="muskmelon"
 /db_xref="ATCC:28858"
 /db_xref="taxon:61369"
 /country="France"
 /note="forma_specialis: melonis"
 <1..28
 /product="18S ribosomal RNA"
 29..175
 /product="internal transcribed spacer 1"
 176..333
 /product="5.8S ribosomal RNA"
 334..484
 /product="internal transcribed spacer 2"
 485..501
 /product="28S ribosomal RNA"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 367 CGTTAATTCGGCTTCCTC 384

RESULT 47
LOCUS AY354393 501 bp DNA linear PLN 15-SEP-2003
DEFINITION Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AY354393
VERSION AY354393.1 GI:34559398
KEYWORDS Fusarium oxysporum f. sp. melonis
SOURCE Fusarium oxysporum f. sp. melonis
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 501)
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
TITLE Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs
JOURNAL Span. J. Agric. Res. 1 (3) (2003) In press
REFERENCE 2 (bases 1 to 501)
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain
FEATURES Location/Qualifiers
 1..501
 /organism="Fusarium oxysporum f. sp. melonis"
 /mol_type="genomic DNA"
 /strain="Fon 28"
 /specific_host="muskmelon"
 /db_xref="taxon:61369"
 /country="Spain"
 /note="forma_specialis: melonis"
 <1..28

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 367 CGTTAATTCGGCTTCCTC 384

misc_RNA /product="18S ribosomal RNA"
 29..175
 /product="internal transcribed spacer 1"
 176..333
 /product="5.8S ribosomal RNA"
 334..484
 /product="internal transcribed spacer 2"
 485..501
 /product="28S ribosomal RNA"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 367 CGTTAATTCGGCTTCCTC 384

RESULT 48
LOCUS AY354396 501 bp DNA linear PLN 15-SEP-2003
DEFINITION Fusarium oxysporum f. nivaeum strain Fon 1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AY354396
VERSION AY354396.1 GI:34559401
KEYWORDS Fusarium oxysporum f. nivaeum
SOURCE Fusarium oxysporum f. nivaeum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 501)
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
TITLE Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs
JOURNAL Span. J. Agric. Res. 1 (3) (2003) In press
REFERENCE 2 (bases 1 to 501)
 Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain
FEATURES Location/Qualifiers
 1..501
 /organism="Fusarium oxysporum f. nivaeum"
 /mol_type="genomic DNA"
 /strain="Fon 1"
 /specific_host="watermelon"
 /db_xref="taxon:120297"
 /country="Spain"
 /note="forma: nivaeum"
 <1..28
 /product="18S ribosomal RNA"
 29..175
 /product="internal transcribed spacer 1"
 176..333
 /product="5.8S ribosomal RNA"
 334..484
 /product="internal transcribed spacer 2"
 485..501
 /product="28S ribosomal RNA"

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 501;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 367 CGTTAATTCGGCTTCCTC 384

Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 49
AY354397
LOCUS
DEFINITION

AY354397 501 bp DNA linear PLN 15-SEP-2003
Fusarium oxysporum f. niveum strain Fon 7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY354397.1 GI:34559402
Fusarium oxysporum f. niveum
Fusarium oxysporum f. niveum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE
AUTHORS

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs 2 (bases 1 to 501)
Span. J. Agric. Res. 1 (3) (2003) In press

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Direct Submission
Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia)

FEATURES
source

1. 501
/organism="Fusarium oxysporum f. niveum"
/mol_type="genomic DNA"
/strain="Fon 7"
/specific_host="watermelon"
/db_xref="taxon:120297"
/country="Spain"
/note="forma: 'niveum'
<1. .28
/product="18S ribosomal RNA"
29. .175
/product="internal transcribed spacer 1"
176. .333
/product="5.8S ribosomal RNA"
334. .484
/product="internal transcribed spacer 2"
485. .>501
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 50
AY354398
LOCUS
DEFINITION

AY354398 501 bp DNA linear PLN 15-SEP-2003
Fusarium oxysporum f. sp. lagenariae 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY354398.1 GI:34559403
Fusarium oxysporum f. sp. lagenariae
Fusarium oxysporum f. sp. lagenariae

REFERENCE
AUTHORS

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs 2 (bases 1 to 501)
Span. J. Agric. Res. 1 (3) (2003) In press

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Direct Submission
Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia)

FEATURES
source

1. 501
/organism="Fusarium oxysporum f. sp. lagenariae"
/mol_type="genomic DNA"
/strain="ATCC 18143"
/db_xref="ATCC:18143"
/db_xref="taxon:120295"
/country="Japan"
/note="forma: 'lagenaria'
<1. .28
/product="18S ribosomal RNA"
29. .175
/product="internal transcribed spacer 1"
176. .333
/product="5.8S ribosomal RNA"
334. .484
/product="internal transcribed spacer 2"
485. .>501
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 51
AY354399
LOCUS
DEFINITION

AY354399 501 bp DNA linear PLN 15-SEP-2003
Fusarium oxysporum f. sp. juiffiae 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY354399.1 GI:34559404
Fusarium oxysporum f. sp. juiffiae
Fusarium oxysporum f. sp. juiffiae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE
AUTHORS

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs 2 (bases 1 to 501)
Span. J. Agric. Res. 1 (3) (2003) In press

Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.
Direct Submission
Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia)

FEATURES
Location/Qualifiers

source

1. 501
/organism="Fusarium oxysporum f. sp. Jaffae"
/mol_type="genomic DNA"
/strain="ATCC 28860"
/db_xref="ATCC:28860"
/db_xref="taxon:243110"
/country="Japan"
/note="forma_specialis: Jaffae"
1. 28
/product="18S ribosomal RNA"
29. 175
/product="internal transcribed spacer 1"
176. 333
/product="5.8S ribosomal RNA"
334. 484
/product="internal transcribed spacer 2"
485. 501
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATCGCGTTCCTC 18
|||||
Db 367 CGTTAATCGCGTTCCTC 384

RESULT 52
AF069310 506 bp rRNA linear PLN 08-JUN-1999
LOCUS
DEFINITION
Fusarium oxysporum internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
AF069310
AF069310.1 GI:5006327

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 506)
Paavanan-Huhtala,S., Hyvonen,J., Bulat,S.A. and Yli-Mattila,T.
RAPD-PCR, isozyme, rDNA RFLP and rDNA sequence analyses in identification of Finnish Fusarium oxysporum isolates
Mycol. Res. 103 (5), 625-634 (1999)
2 (bases 1 to 506)
Yli-Mattila,T. and Paavanan-Huhtala,S.
Direct Submission
Submitted (31-MAY-1998) Lab. of Plant Physiology and Molecular Biology, Dept. of Biology, Univ. of Turku, Turku 20014, Finland
Location/Qualifiers
1. 506
/organism="Fusarium oxysporum"
/mol_type="rRNA"
/strain="91138"
/db_xref="taxon:5507"
/country="Finland:Espoo"
/note="Isolated from barley root in 1986"
1. 138
/product="internal transcribed spacer 1"
/note="ITS1"
139. 296
/product="5.8S ribosomal RNA"
297. 446
/product="internal transcribed spacer 2"
/note="ITS2"
447. 506
/product="28S ribosomal RNA"

ORIGIN

misc_RNA
rRNA
misc_RNA
rRNA

Query Match 100.0%; Score 18; DB 8; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATCGCGTTCCTC 18
|||||
Db 330 CGTTAATCGCGTTCCTC 347

RESULT 53
AY127697 506 bp DNA linear PLN 14-AUG-2002
LOCUS
DEFINITION
Fusarium oxysporum 40-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
AY127697
AY127697.1 GI:22252968

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 506)
Becerra-Lopez Lavalie,L.A.
Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in *Gossypium hirsutum* L.
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building A12, Sydney, NSW, Australia, in press
2 (bases 1 to 506)
Becerra-Lopez Lavalie,L.A., Saleeba,J.A. and Lyon,B.R.
Molecular identification and classification of fungi isolated from stem tissue of cotton (*Gossypium hirsutum* L)
Unpublished
3 (bases 1 to 506)
Becerra-Lopez Lavalie,L.A., Saleeba,J.A. and Lyon,B.R.
Direct Submission
Submitted (27-JUN-2002) School of Biological Sciences, The University of Sydney, Macleay Building A12, Science Road, NSW 2006, Australia
Location/Qualifiers
1. 506
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="40-1"
/specific_host="Gossypium hirsutum"
/db_xref="taxon:5507"
/country="Australia"
1. 20
/product="18S ribosomal RNA"
21. 158
/product="internal transcribed spacer 1"
159. 316
/product="5.8S ribosomal RNA"
317. 468
/product="internal transcribed spacer 2"
469. 506
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTAATCGCGTTCCTC 18
|||||
Db 350 CGTTAATCGCGTTCCTC 367

RESULT 54
AY127698 506 bp DNA linear PLN 14-AUG-2002
LOCUS

DEFINITION Fusarium oxysporum 48-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AY127698

VERSION AY127698.1 GI:22252969

KEYWORDS Fusarium oxysporum

SOURCE Fusarium oxysporum

ORGANISM Fusarium oxysporum

REFERENCE 1 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A.
Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in *Gossypium hirsutum* L
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building A12, Sydney, NSW, Australia, In press

REFERENCE 2 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A., Saleeba, J.A. and Lyon, B.R.
Molecular identification and classification of fungi isolated from stem tissue of cotton (*Gossypium hirsutum* L)
Unpublished

JOURNAL 3 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A., Saleeba, J.A. and Lyon, B.R.
Direct Submission
Submitted (27-JUN-2002) School of Biological Sciences, The University of Sydney, Macleay Building A12, Science Road, NSW 2006, Australia

FEATURES
source
1..506
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="48-2"
/specific_host="Gossypium hirsutum"
/db_xref="taxon:5507"
/country="Australia"
<1..20
/product="18S ribosomal RNA"
21..158
/product="internal transcribed spacer 1"
159..316
/product="5.8S ribosomal RNA"
317..468
/product="internal transcribed spacer 2"
469..>506
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18
|||||
350 CGTTAATTCGGCTTCCTC 367

DB

RESULT 55
AY127699 506 bp DNA linear PLN 14-AUG-2002

LOCUS Fusarium oxysporum 49-2 18S ribosomal RNA gene, partial sequence;
DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.

ACCESSION AY127699

VERSION AY127699.1 GI:22252970

KEYWORDS Fusarium oxysporum

SOURCE Fusarium oxysporum

ORGANISM Fusarium oxysporum

REFERENCE 1 (bases 1 to 515)
Becerra-Lopez Lavalley, L.A., Saleeba, J.A. and Lyon, B.R.
Direct Submission
Submitted (24-FEB-2004) Antioxidants Research Lab, Korea Research
Institute of Bioscience and Biotechnology, Yuseong-gu, Daejeon,
Chungnam 305-333, South Korea
Location/Qualifiers

REFERENCE 1 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A.
Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in *Gossypium hirsutum* L
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building A12, Sydney, NSW, Australia, In press

REFERENCE 2 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A., Saleeba, J.A. and Lyon, B.R.
Molecular identification and classification of fungi isolated from stem tissue of cotton (*Gossypium hirsutum* L)
Unpublished

JOURNAL 3 (bases 1 to 506)
Becerra-Lopez Lavalley, L.A., Saleeba, J.A. and Lyon, B.R.
Direct Submission
Submitted (27-JUN-2002) School of Biological Sciences, The University of Sydney, Macleay Building A12, Science Road, Sydney, NSW 2006, Australia

FEATURES
source
1..506
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="49-2"
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/db_xref="taxon:5507"
/country="Australia"
<1..20
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21..158
/product="internal transcribed spacer 1"
159..316
/product="5.8S ribosomal RNA"
317..468
/product="internal transcribed spacer 2"
469..>506
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18
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350 CGTTAATTCGGCTTCCTC 367

DB

RESULT 56
AY555719 515 bp DNA linear PLN 20-MAR-2004

LOCUS Fusarium oxysporum strain f35 18S ribosomal RNA gene, partial
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.

ACCESSION AY555719

VERSION AY555719.1 GI:45445262

KEYWORDS Fusarium oxysporum

SOURCE Fusarium oxysporum

ORGANISM Fusarium oxysporum

REFERENCE 1 (bases 1 to 515)
Li, C.-T., Wang, Q.-J., Mo, E.-K., Xu, B.-J., Fang, Z.-M. and Sung, C.-K.
Taxol production by endophytes isolated from yew tree, *Taxus
cuspidata*
Unpublished

JOURNAL 2 (bases 1 to 515)
Li, C.-T.
Direct Submission
Submitted (24-FEB-2004) Antioxidants Research Lab, Korea Research
Institute of Bioscience and Biotechnology, Yuseong-gu, Daejeon,
Chungnam 305-333, South Korea
Location/Qualifiers

```


|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                |
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|                       | rRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                      | /strain="Pj5"<br>/specific_host="Taxus cuspidata"<br>/db_xref="taxon:5507"<br>/country="South Korea; Kang-Won" |
|                       | misc_RNA                                                                                                                                                                                                                                                                                                                                                                                                                                                  | <1..24<br>/product="18S ribosomal RNA"                                                                         |
|                       | rRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 25..174<br>/product="internal transcribed spacer 1"<br>175..332<br>/product="5.6S ribosomal RNA"               |
|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 333..482<br>/product="internal transcribed spacer 2"<br>483..>515<br>/product="28S ribosomal RNA"              |
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| Best Local Similarity | 100.0%; Pred. No. 27;                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                |
| Matches               | 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                |
| Oy                    | 1 CGTAATTCGCGTCCCTC 18<br>     <br>                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                |
| Dn                    | 365 CATTAAITTCGGTTCTC 382<br><br>                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                |
| RESULT 57             | FOUJ34566                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 520 bp DNA linear PLN 15-JUL-1998                                                                              |
| LOCUS                 | FUOJ34566                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Fusarium oxysporum NRRL 22902 internal transcribed spacer RNA.                                                 |
| DEFINITION            | U34566                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                |
| VERSION               | U34566.1 GI:1808932                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                |
| KEYWORDS              |                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                |
| SOURCE                |                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                |
| ORGANISM              | Fusarium oxysporum<br>Fusarium oxysporum<br>Eukaryota; Fungi; Ascomycetes; Pezizomycotina; Sordariomycetes;<br>Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;<br>Fusarium oxysporum complex.<br>1 (bases 1 to 520)<br>O'Donnell,K., Ciigelink,E. and Casper,H.H.<br>Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus Fusarium are nonorthologous<br>Mol. Phylogenet. Evol. 7 (1), 103-116 (1997) |                                                                                                                |
| REFERENCE             | PUBMED 9007025                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                |
| AUTHORS               | 2 (bases 1 to 520)<br>O'Donnell,K., Ciigelink,E. and Casper,H.H.<br>Molecular phylogenetic, morphological, and mycotoxin data support reidentification of the Quorn mycoprotein fungus as Fusarium venenatum<br>Fungal Genet. Biol. 23 (1), 57-67 (1998)                                                                                                                                                                                                  |                                                                                                                |
| TITLE                 | JOURNAL MEDLINE PUBMED 98162098                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                |
| MEDLINE               | 9501477                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                |
| REFERENCE             | 3 (bases 1 to 520)<br>O'Donnell,K., Ciigelink,E. and Nirenberg,H.I.<br>Molecular systematics and phyllogeography of the Gibberella fujikuroi species complex<br>Myologia 90 (3), 465-493 (1998)                                                                                                                                                                                                                                                           |                                                                                                                |
| AUTHORS               | 4 (bases 1 to 520)<br>O'Donnell,K. and Ciigelink,E.<br>Direct Submission<br>Submitted (21-AUG-1995) Kerry O'Donnell, NCAR, USDA, 1815 N. University St., Peoria, IL 61604, USA                                                                                                                                                                                                                                                                            |                                                                                                                |
| TITLE                 | JOURNAL JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                |
| FEATURES              | location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                |
| source                | 1..520<br>/organism="Fusarium oxysporum"<br>/mol_type="genomic DNA"<br>/strain="NRRL 22902"<br>/db_xref="taxon:5507"<br>1..520<br>/product="Internal transcribed spacer"                                                                                                                                                                                                                                                                                  |                                                                                                                |
|                       | misc_RNA                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                |


```

[illegible]

REFERENCE 2 (bases 1 to 523)
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
 FEATURES
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 1..523
 /organism="leaf litter ascomycete strain its330"
 /mol_type="genomic DNA"
 /strain="its330"
 /isolate="1000501231"
 /specific_host="Mammee americana"
 /db_xref="taxon:194113"
 /country="Puerto Rico"
 <1..163
 /product="internal transcribed spacer 1"
 164..318
 /product="5.8S ribosomal RNA"
 319..>523
 /product="internal transcribed spacer 2"
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CGTTAATTCGCGTTCCTC 18
 |||||
 354 CGTTAATTCGCGTTCCTC 371
 RESULT 60
 AF242876 531 bp DNA linear PLN 12-APR-2000
 LOCUS Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;
 DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 AF242876
 AF242876.1 GI:7542605
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1 (bases 1 to 531)
 Gomez-Ieyva,J.F., Ochoa-Sanchez,J.C., Loera-Quezada,M.,
 Leal-Klvezas,D.S., Abeyaratne,P., Nazari,R.N., Rodriguez-Garay,B.
 and Martinez-Soriano,J.P.
 Sensitive and specific PCR assay to detect the causal agent of the
 Agave tequilana root rot
 Unpublished
 2 (bases 1 to 531)
 Gomez-Ieyva,J.F., Ochoa-Sanchez,J.C., Leal-Klvezas,D.S. and
 Martinez-Soriano,J.P.
 Direct Submission
 Submitted (08-MAR-2000) Biotechnology y Bioluminica, Unidad de
 Biotecnologia e Ingenieria Genetica de Plantas, CINVESTAV-IPN, km
 9.6 Ibramlenito norte, carr. Irapuato-Leon, Irapuato, Gto 36500,
 Mexico
 FEATURES
 source
 1..531
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 /isolate="MMAVH13"
 /specific_host="Agave tequilana Weber var. Azul"
 /db_xref="taxon:5507"
 <1..26
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 27..174
 /product="internal transcribed spacer 1"

RNA 175..331
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 332..481
 /product="internal transcribed spacer 2"
 482..>531
 /product="28S ribosomal RNA"
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CGTTAATTCGCGTTCCTC 18
 |||||
 365 CGTTAATTCGCGTTCCTC 382
 Db

RESULT 61
 FOXYRNA 544 bp DNA linear PLN 14-JUN-2001
 LOCUS Fusarium oxysporum 18S rRNA gene (partial), 5.8S rRNA gene, 28S
 DEFINITION rRNA gene (partial), internal transcribed spacer 1 (ITS1) and
 internal transcribed spacer 2 (ITS2).
 X94173 X93902
 X94173.1 GI:1122871
 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
 internal transcribed spacer 2; ITS1; ITS2.
 SOURCE
 Fusarium oxysporum
 Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1
 Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W.
 Discordant groupings of Fusarium spp. from sections Riegans,
 Lissola and Diamina a based on ribosomal ITS1 and ITS2 sequences
 Mycologia 88, 361-368 (1996)
 2 (bases 1 to 544)
 Waalwijk,C.
 Direct Submission
 Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Plant
 Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS
 On Jun 15, 2001 this sequence version replaced gi:1103570.
 Overlaps with X78260.
 FEATURES
 source
 1..544
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 /specific_host="carnation"
 /db_xref="taxon:5507"
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 /gene="18S rRNA"
 <1..30
 /gene="16S rRNA"
 /product="18S ribosomal RNA"
 31..177
 /note="internal transcribed spacer 1, ITS1"
 178..335
 /gene="5.8 rRNA"
 178..335
 /gene="5.8 rRNA"
 /product="5.8 ribosomal RNA"
 336..486
 /note="internal transcribed spacer 2, ITS2"
 487..544
 /gene="28S rRNA"
 487..>544
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 /product="28S ribosomal RNA"
 ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 544;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 369 CGTTAATTCGCGTTCCTC 386

RESULT 62
 FOVCB58 545 bp DNA linear PLN 16-JAN-1996
 LOCUS F.oxysporum (f.sp.vasinflectum, BIE) 5.8S rRNA gene.
 DEFINITION X78260.1 GI:467737
 X78260 5.8S ribosomal RNA; 5.8S rRNA gene.
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.
 KEYWORDS Fusarium oxysporum
 SOURCE Fusarium oxysporum
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA
 JOURNAL Fungal Genet. Newsl. 42, 53-55 (1995)
 REFERENCE 2 (bases 1 to 545)
 AUTHORS Mitchelson,K.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK
 FEATURES
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 1. 545
 /organism="Fusarium oxysporum"
 /mol_type="genomic DNA"
 /strain="BIE"
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 /lab_host="Gossypium"
 /note="host from Bie, Angola"
 1. 545
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 /product="5.8S ribosomal RNA"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 370 CGTTAATTCGCGTTCCTC 387

RESULT 63
 FOVCB58 546 bp DNA linear PLN 16-JAN-1996
 LOCUS F.oxysporum (f.sp.vasinflectum, Cuanza Bul) 5.8S rRNA gene.
 DEFINITION X78259.1 GI:467738
 X78259 5.8S ribosomal RNA; 5.8S rRNA gene.
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.
 KEYWORDS Fusarium oxysporum
 SOURCE Fusarium oxysporum
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA

and adjacent ITS 1 and ITS 2 regions
 Fungal Genet. Newsl. 42, 53-55 (1995)
 REFERENCE 2 (bases 1 to 546)
 AUTHORS Mitchelson,K.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK
 FEATURES
 source
 1. 546
 /organism="Fusarium oxysporum"
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 /sub_species="f.sp.vasinflectum"
 /db_xref="taxon:5507"
 /tissue_type="Mycelium"
 /clone_lib="S.Moricca"
 /lab_host="Gossypium"
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 1. 546
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 1. 546
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 /product="5.8S ribosomal RNA"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGCGTTCCTC 18
 |||||
 Db 371 CGTTAATTCGCGTTCCTC 388

RESULT 64
 FOVCN58 546 bp DNA linear PLN 16-JAN-1996
 LOCUS F.oxysporum (f.sp.vasinflectum, Cuanza Norte) 5.8S rRNA gene.
 DEFINITION X78258.1 GI:467739
 X78258 5.8S ribosomal RNA; 5.8S rRNA gene.
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.
 KEYWORDS Fusarium oxysporum
 SOURCE Fusarium oxysporum
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA
 JOURNAL Fungal Genet. Newsl. 42, 53-55 (1995)
 REFERENCE 2 (bases 1 to 546)
 AUTHORS Mitchelson,K.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK
 FEATURES
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 1. 546
 /organism="Fusarium oxysporum"
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 /clone_lib="S.Moricca"
 /lab_host="Gossypium"
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 1. 546
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 /product="5.8S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 546;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 371 CGTTAATTCGGCTTCCTC 388

RESULT 65
 AY147369 552 bp DNA linear PLN 15-FEB-2003
 LOCUS Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;
 DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 ACCESSION AY147369 GI:28394595
 VERSION AY147369.1 GI:28394595
 KEYWORDS Fusarium oxysporum
 SOURCE Fusarium oxysporum
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Microsporici Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 552)
 Mishra, P.K.
 TITLE Genomics and Evolutionary Biology of Fusarium culmorum
 JOURNAL Thesis (2002) The University of Reading, Whiteknights, Reading,
 Berkshire, United Kingdom
 2 (bases 1 to 552)
 Mishra, P.K., Fox, R.T.V. and Culham, A.
 TITLE Development of a PCR-based assay for rapid and reliable
 identification of pathogenic Fusaria
 JOURNAL FEMS Microbiol. Lett. 218 (2), 329-332 (2003)
 22474178
 MEDLINE 12586412
 PUBMED 3 (bases 1 to 552)
 AUTHOR Mishra, P.K., Fox, R.T.V. and Culham, A.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-2002) School of Plant Sciences, The University of
 Reading, Whiteknights, Reading, Berkshire RG6 6AS, United Kingdom

FEATURES
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 1..552
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 /mol_type="genomic DNA"
 /db_xref="taxon:5507"
 <1..>552
 /note="contains 18S ribosomal RNA, internal transcribed
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
 2, and 28S ribosomal RNA"

misc_rna

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18
 |||||
 Db 386 CGTTAATTCGGCTTCCTC 403

RESULT 66
 AY462580 552 bp DNA linear PLN 06-DEC-2003
 LOCUS Fusarium oxysporum f. sp. vasinfectum isolate PA3 18S ribosomal RNA
 DEFINITION gene, partial sequence; internal transcribed spacer 1, 5.8S
 ribosomal RNA gene, and internal transcribed spacer 2, complete
 sequence; and 28S ribosomal RNA gene, partial sequence.
 ACCESSION AY462580 GI:38569372
 VERSION AY462580.1 GI:38569372
 KEYWORDS Fusarium oxysporum f. sp. vasinfectum
 SOURCE Fusarium oxysporum f. sp. vasinfectum

ORGANISM Fusarium oxysporum f. sp. vasinfectum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Microsporici Hypocreales; Fusarium;
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 552)
 AUTHOR Catal, M. and Schilder, A.M.C.
 TITLE A PCR-based method to distinguish Eutypa lata and Eutypella vitis
 from grapevine
 JOURNAL Unpublished
 2 (bases 1 to 552)
 AUTHOR Catal, M. and Schilder, A.M.C.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-2003) Plant Pathology, Michigan State University,
 Wilson Road, East Lansing, MI 48823, USA
 LOCATION/Qualifiers
 1..552
 /organism="Fusarium oxysporum f. sp. vasinfectum"
 /mol_type="genomic DNA"
 /isolate="PA3"
 /specific_host="Vitis vinifera"
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 /country="USA: PA"
 /note="forma specialis: vasinfectum"
 /product="18S ribosomal RNA"
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 204..361
 /product="5.8S ribosomal RNA"
 362..511
 /product="internal transcribed spacer 2"
 512..>552
 /product="28S ribosomal RNA"

misc_rna

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18
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 Db 394 CGTTAATTCGGCTTCCTC 411

RESULT 67
 AY462579 555 bp DNA linear PLN 06-DEC-2003
 LOCUS Fusarium oxysporum f. sp. vasinfectum isolate PA1 18S ribosomal RNA
 DEFINITION gene, partial sequence; internal transcribed spacer 1, 5.8S
 ribosomal RNA gene, and internal transcribed spacer 2, complete
 sequence; and 28S ribosomal RNA gene, partial sequence.
 ACCESSION AY462579 GI:38569371
 VERSION AY462579.1 GI:38569371
 KEYWORDS Fusarium oxysporum f. sp. vasinfectum
 SOURCE Fusarium oxysporum f. sp. vasinfectum
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Microsporici Hypocreales; Fusarium;
 Fusarium oxysporum complex.
 1 (bases 1 to 555)
 AUTHOR Catal, M. and Schilder, A.M.C.
 TITLE A PCR-based method to distinguish Eutypa lata and Eutypella vitis
 from grapevine
 JOURNAL Unpublished
 2 (bases 1 to 555)
 AUTHOR Catal, M. and Schilder, A.M.C.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-2003) Plant Pathology, Michigan State University,
 Wilson Road, East Lansing, MI 48823, USA
 LOCATION/Qualifiers
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 /organism="Fusarium oxysporum f. sp. vasinfectum"
 /mol_type="genomic DNA"

/isolate="PA1"
/specific_host="vitis vinifera"
/db_xref="taxon:61374"
/country="USA: PA"
/note="forma_specialis: vasinfectum"
<1..53
/product="18S ribosomal RNA"
54..202
/product="internal transcribed spacer 1"
203..360
/product="5.8S ribosomal RNA"
361..510
/product="internal transcribed spacer 2"
511..555
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 392 CGTTAATTCGCGTTCCTC 409

RESULT 68
AF322074 616 bp DNA linear PLN 13-DEC-2000
LOCUS
DEFINITION Fusarium oxysporum f. sp. vasinfectum strain Ag149-18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence.
AF322074
AF322074.1 GI:11692812

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 616)
Ying, L., Hong, Y. and Guohua, G.
Comparison of ribosomal RNA gene sequences between a heterokaryon
and two segregants of Fusarium oxysporum f. sp. vasinfectum
Unpublished
2 (bases 1 to 616)
Ying, L., Hong, Y. and Guohua, G.
Direct Submission
Submitted (20-NOV-2000) Department of Microbiology, College of
Biological Sciences, China Agricultural University, No. 2,
Yuanmingyuan West Road, Beijing 100094, P.R. China
Location/Qualifiers

FEATURES
source
1..616
/organism="Fusarium oxysporum f. sp. vasinfectum"
/mol_type="genomic DNA"
/strain="Ag149-1"
/db_xref="taxon:61374"
/country="China: Henan Province, isolated from a cotton
field"
/note="forma_specialis: vasinfectum"
<1..112
/product="18S ribosomal RNA"
113..250
/product="internal transcribed spacer 1"
251..408
/product="5.8S ribosomal RNA"
409..558
/product="internal transcribed spacer 2"
559..5616
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 441 CGTTAATTCGCGTTCCTC 458

RESULT 69
AF322075 616 bp DNA linear PLN 13-DEC-2000
LOCUS
DEFINITION Fusarium oxysporum f. sp. vasinfectum strain Ag149-18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence.
AF322075
AF322075.1 GI:11692813

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 616)
Ying, L., Hong, Y. and Guohua, G.
Comparison of ribosomal RNA gene sequences between a heterokaryon
and two segregants of Fusarium oxysporum f. sp. vasinfectum
Unpublished
2 (bases 1 to 616)
Ying, L., Hong, Y. and Guohua, G.
Direct Submission
Submitted (20-NOV-2000) Department of Microbiology, College of
Biological Sciences, China Agricultural University, No. 2,
Yuanmingyuan West Road, Beijing 100094, P.R. China
Location/Qualifiers

FEATURES
source
1..616
/organism="Fusarium oxysporum f. sp. vasinfectum"
/mol_type="genomic DNA"
/strain="Ag149-1"
/db_xref="taxon:61374"
/note="nuclear type segregant
forma_specialis: vasinfectum"
<1..112
/product="18S ribosomal RNA"
113..250
/product="internal transcribed spacer 1"
251..408
/product="5.8S ribosomal RNA"
409..558
/product="internal transcribed spacer 2"
559..5616
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 616;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18
|||||
Db 441 CGTTAATTCGCGTTCCTC 458

RESULT 70
AF322076 616 bp DNA linear PLN 13-DEC-2000
LOCUS
DEFINITION Fusarium oxysporum f. sp. vasinfectum strain Ag149-18S
ribosomal RNA gene, partial sequence; internal transcribed spacer
1, 5.8S ribosomal RNA gene and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence.
AF322076
AF322076.1 GI:11692814

ORIGIN

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Fusarium oxysporum f. sp. vasinfectum
Fusarium oxysporum f. sp. vasinfectum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 616)
Yang, L., Hong, Y., and Guohua, G.
Comparison of ribosomal RNA gene sequences between a heterokaryon
and two segregants of Fusarium oxysporum f. sp. vasinfectum
Unpublished
2 (bases 1 to 616)
Yang, L., Hong, Y., and Guohua, G.
Direct Submission
Submitted (20-NOV-2000) Department of Microbiology, College of
Biological Sciences, China Agricultural University, No. 2,
Yuanmingyuan West Road, Beijing 100094, P.R. China
Location/Qualifiers
1. 616
/organism="Fusarium oxysporum f. sp. vasinfectum"
/mol_type="genomic DNA"
/strain="Ag149-111"
/db_xref="taxon:61374"
/note="nuclear type segregant
forma specialis: vasinfectum"
1. 112
/product="18S ribosomal RNA"
113. 250
/product="internal transcribed spacer 1"
251. 408
/product="5.8S ribosomal RNA"
409. 558
/product="internal transcribed spacer 2"
559. 616
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 616;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||
Db 441 CGTTAATTCGGCTTCCTC 458

RESULT 71
AF443071/c
LOCUS
DEFINITION
Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.
AF443071
AF443071.1 GI:17227116

ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 636)
Quader, M. and Riley, I.T.
Direct Submission
Submitted (06-NOV-2001) Applied and Molecular Ecology, Adelaide
University, Waite Campus, Glen Osmond, Adelaide, SA 5064, Australia
Location/Qualifiers
1. 636
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/db_xref="taxon:5507"
/cissue_type="galled roots"
complement(<1..>636)

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 636;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||
Db 200 CGTTAATTCGGCTTCCTC 183

RESULT 72
AY669120
LOCUS
DEFINITION
Fusarium oxysporum strain F-T.1.7-030520 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
AY669120
AY669120.1 GI:50313229

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Fusarium oxysporum
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 655)
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
Comparison of ribosomal RNA gene sequences among the strains of
Fusarium oxysporum from different hosts
Unpublished
2 (bases 1 to 655)
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
Direct Submission
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agriculture Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China
Location/Qualifiers
1. 655
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="F-T.1.7-030520"
/specific host="Cucumis melo L."
/db_xref="taxon:5507"
/country="China: Fujian, Fuzhou, Yongtai"
1. 171
/product="18S ribosomal RNA"
172. 310
/product="internal transcribed spacer 1"
311. 468
/product="5.8S ribosomal RNA"
469. 618
/product="internal transcribed spacer 2"
619. 655
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 655;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18
|||||
Db 501 CGTTAATTCGGCTTCCTC 518

RESULT 73
AY667489
LOCUS
DEFINITION
Fusarium oxysporum isolate 12-152 internal transcribed spacer 1,
partial sequence; 5.8S ribosomal RNA gene, complete sequence; and

```
internal transcribed spacer 2, partial sequence.
ACCESSION AY667489 GI:50313404
VERSION AY667489.1
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 666)
AUTHORS Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,
P.R. China
FEATURES
source location/Qualifiers
1..666
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-152"
/species_host="cowpea plant"
/db_xref="taxon:5507"
<1..319
/product="internal transcribed spacer 1"
320..477
/product="5.8S ribosomal RNA"
478..566
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 666;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGGCTTCCTC 18
Db 511 CGTTAATTCGGCTTCCTC 528
RESULT 74 671 bp DNA linear PLN 20-JUL-2004
AY669122
LOCUS Fusarium oxysporum strain F-W.6.2-030304 18S ribosomal RNA gene,
DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.
ACCESSION AY669122 GI:50313231
VERSION AY669122.1
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 671)
AUTHORS Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
TITLE Comparison of ribosomal RNA gene sequences among the strains of
JOURNAL Fusarium oxysporum from different hosts
REFERENCE 2 (bases 1 to 671)
AUTHORS Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agriculture Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China
FEATURES
source location/Qualifiers
1..671
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="F-W.6.2-030304"
/species_host="Pisum sativum L."
/db_xref="taxon:5507"
/country="China: Fujian, Zhangzhou, Zhangpu"
<1..186
internal transcribed spacer 2, partial sequence.
ACCESSION AY667489 GI:50313404
VERSION AY667489.1
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 666)
AUTHORS Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,
P.R. China
FEATURES
source location/Qualifiers
1..666
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/isolate="12-152"
/species_host="cowpea plant"
/db_xref="taxon:5507"
<1..319
/product="internal transcribed spacer 1"
320..477
/product="5.8S ribosomal RNA"
478..566
/product="internal transcribed spacer 2"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 666;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGGCTTCCTC 18
Db 511 CGTTAATTCGGCTTCCTC 528
RESULT 75 678 bp DNA linear PLN 20-JUL-2004
AY669125
LOCUS Fusarium oxysporum strain F-X.1.7-030520-12 18S ribosomal RNA gene,
DEFINITION partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION AY669125 GI:50313234
VERSION AY669125.1
KEYWORDS
SOURCE Fusarium oxysporum
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 678)
AUTHORS Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
TITLE Comparison of ribosomal RNA gene sequences among the strains of
JOURNAL Fusarium oxysporum from different hosts
REFERENCE 2 (bases 1 to 678)
AUTHORS Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of
Agriculture Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China
FEATURES
source location/Qualifiers
1..678
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="F-X.1.7-030520-12"
/species_host="Citrus limonatus (Thunb) Mansfeld"
/db_xref="taxon:5507"
/country="China: Fujian, Fuzhou, Yongtai"
<1..187
/product="18S ribosomal RNA"
188..326
/product="internal transcribed spacer 1"
327..484
/product="5.8S ribosomal RNA"
485..634
/product="internal transcribed spacer 2"
635..678
/product="28S ribosomal RNA"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGGCTTCCTC 18
Db 517 CGTTAATTCGGCTTCCTC 534
```

RESULT 76
AY188919 1134 bp DNA linear PLN 30-NOV-2003
LOCUS Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial
DEFINITION sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION AY188919 GI:37778811
VERSION AY188919.1 GI:37778811
KEYWORDS
SOURCE Fusarium oxysporum f. sp. melonis
ORGANISM Fusarium oxysporum f. sp. melonis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
AUTHORS Hartsch, D., Phalip, V. and Jeltsch, J.M.
TITLE Study of the genes encoding cellobiohydrolase-C and topoisomerase
11 as target for phylogenetic analysis and identification of
Fusarium at a species level
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1134)
AUTHORS Hartsch, D., Phalip, V. and Jeltsch, J.M.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Laboratoire de Phytopathologie, UMR 7100 -
IFR 85 - ESBS - ULP, Boulevard Sebastien Brant,
Illkirch-Graffenstaden, Alsace 67400, France
location/Qualifiers
1. 1134
/organism="Fusarium oxysporum f. sp. melonis"
/mol_type="genomic DNA"
/db_xref="taxon:61369"
/note="forma_specialis: melonis"
<1. .29
/product="18S ribosomal RNA"
30. 169
/product="internal transcribed spacer 1"
170. 326
/product="5.8S ribosomal RNA"
327. .474
/product="internal transcribed spacer 2"
475. .>1134
/product="28S ribosomal RNA"
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 1134;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
|||
Db 369 CGTTAATTCGCGTTCCTC 386
|||||
RESULT 77
FOS88RNA 1471 bp DNA linear PLN 20-JAN-1997
LOCUS F. oxysporum 5.8S rRNA, ITS2, and 26S rRNA.
DEFINITION Y07991
ACCESSION Y07991.1 GI:1805769
VERSION Y07991.1 GI:1805769
KEYWORDS 26S ribosomal RNA; 5.8S ribosomal RNA; ITS2.
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
AUTHORS Iglesias, M. and Ballesta, J.P.G.
JOURNAL Unpublished
REFERENCE 2
AUTHORS Ballesta, J.P.G.
TITLE Direct Submission

JOURNAL Submitted (12-SEP-1996) J.P.G. Ballesta, Universidad Autonoma De
Madrid, Centro De Biologia Molecular, Canto Blanco,, Madrid, 28049,
SPAIN
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 1471)
AUTHORS Ballesta, J.P.G.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1997) J.P.G. Ballesta, Universidad Autonoma De
Madrid, Centro De Biologia Molecular, Canto Blanco,, Madrid, 28049,
SPAIN
COMMENT On Jan 29, 1997 this sequence version replaced gi:1550626.
FEATURES
source location/Qualifiers
1. 1471
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
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/clone_11b="CA3"
1. 144
/gene="5.8S rRNA"
/gene="5.8S rRNA"
1. 144
/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
145. .683
/note="intergenic region ITS2"
684. .1042
/gene="26S rRNA"
684. .1042
/gene="26S rRNA"
/product="26S rRNA"
/product="26S ribosomal RNA"
1043. .>1471
/codon_start=3
/product="hypothetical protein"
/protein_id="CAA69270.1"
/db_xref="GI:1805770"
/db_xref="EMBL:P78651"
/translation="HSHQRRGHLIEIVQPEKQYPRAGIQPRSRNRNSKSLPIYVD
ICIGQISKLVHLRTPTPEVXSQLSKTKPTVLEASQSEYLYRIRIRHQSSPE
SILGALKSIANKGTAKIMHENVYLRAELREVRANILSR"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 1471;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGCGTTCCTC 18
|||
Db 178 CGTTAATTCGCGTTCCTC 195
|||||
Search completed: December 7, 2004, 14:42:58
Job time : 1413 secs

XX Example 1; Page 22; 45bp; English.

PS Probes AAV83677-708 are derived from the internal transcribed spacer 2

CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes

CC are species-specific, and can be used for identifying a species selected

CC from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,

CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,

CC *M. indicus*, *M. circinalis*, *F. circinalis*, *Rhizopus oryzae*, *R.*

CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Ascidia*

CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph

CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*

CC *schenkii*. The probes can be used for differentiating filamentous fungal

CC species from each other and from other medically important fungi

XX Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTAAATTCGGCTTCCTC 18

DB 1 CGTAAATTCGGCTTCCTC 18

RESULT 2

AAA72783

ID AAA72783 standard; DNA; 382 BP.

AC AAA72783;

XX

DT 13-DEC-2000 (first entry)

XX

DE 5.8s rRNA gene sequence.

XX

XX Black spot disease; brown spot disease; fungi; fruit vegetable;

KW field crop; *Alternaria*; 5.8s rRNA; detection; ds.

XX

OS *Fusarium oxysporum*.

XX

PN WO20046397-A1.

XX

PD 10-AUG-2000.

XX

PF 24-JAN-2000; 2000WO-US001466.

XX

PR 02-FEB-1999; 99US-00241427.

XX

PA (TECR) TECHNIION RES & DEV FOUND LTD.

XX (KASHI) KASHI Y.

PI Kashi Y, Zur G, Sharf R, Hallerman E,

XX

DR WPI; 2000-499381/44.

XX

PT Nucleic acid based assay and kit for detection of *Alternaria*

PT contamination in food products involves analyzing the sample of food

PT product for nucleic acid sequences unique to *Alternaria*.

XX

PS Example; Fig 1; 47bp; English.

XX

CC The invention relates to a nucleic acid based method for the detection of

CC *Alternaria* contamination in a food product. The method involves obtaining

CC and analyzing a food product sample for a nucleic acid sequence unique to

CC *Alternaria*. Detectable levels of the nucleic acid sequence can be used as

CC an indication of *Alternaria* contamination. Fungi from the genus

CC *Alternaria* are ubiquitous saprophytes and are economically important

CC pathogens affecting a wide range of plants. *Alternaria* are the causative

CC agents of black or brown spot disease in many fruits, vegetables and

CC field crops. The method is used for the detection of *Alternaria*

CC contamination in food products. The present sequence represents the

CC *Fusarium oxysporum* 5.8s rRNA gene, used in examples illustrating the

CC invention

XX

SQ Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 U; 0 Other;

CC

Query Match 100.0%; Score 18; DB 3; Length 382;

Best Local Similarity 100.0%; Pred. No. 8.3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTAAATTCGGCTTCCTC 18

DB 287 CGTAAATTCGGCTTCCTC 304

RESULT 3

ABQ37055/C

ID ABQ37055 standard; DNA; 538 BP.

XX

AC ABQ37055;

XX

DT 12-JUL-2002 (first entry)

XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 23646.

XX

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

KW drug; side effect; cancer; central nervous system; cardiovascular;

KW gastrointestinal; respiratory system; single nucleotide polymorphism;

KW SNP; cell differentiation; ds.

XX

OS Homo sapiens.

XX

PN WO200218632-A2.

XX

PD 07-MAR-2002.

XX

PF 01-SEP-2001; 2001WO-EP010074.

XX

PR 01-SEP-2000; 2000DE-01043826.

XX

PR 05-SEP-2000; 2000DE-01044543.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K, Gueutig D,

XX

DR WPI; 2002-371829/40.

XX

PT Determining the degree of cytosine methylation in genomic DNA, useful for

PT diagnosis and prognosis, comprises selective hybridization of amplicons

PT from chemically treated DNA.

XX

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX

CC This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a

CC genomic sample of DNA. The sample is treated chemically to convert

CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one member,

CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

CC degree of hybridisation to both classes is determined from the label on

CC the amplicon. From the ratio of labels hybridised to the two classes of

CC oligomers, the degree of methylation is calculated. The method is used:

CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs

CC and of a wide range of diseases, e.g. cancer, disorders of the central

CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

CC particularly by detecting mutations or single nucleotide polymorphisms

CC (SNP's); and (ii) for differentiation of cell or tissue types and for

CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. ABQ3440-

CC ABQ54121 represent genomic DNA sequences used to illustrate the method

CC for determining the degree of cytosine methylation described in the

CC disclosure of the invention

XX

SQ Sequence 538 BP; 256 A; 160 C; 61 G; 61 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 538;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTATTGCGCTTCTC 18
DB 105 GTTAAATCGCGTTCCTC 89

RESULT 4

ABQ37054
ID ABQ37054 standard; DNA; 538 BP.

AC ABQ37054;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 23645.

KM Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

KM drug; side effect; cancer; central nervous system; cardiovascular;

KM gastrointestinal; respiratory system; single nucleotide polymorphism;

KM SNP; cell differentiation; ds.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP010074.

PR 01-SEP-2000; 2000DE-01043826.

PR 05-SEP-2000; 2000DE-01044543.

PA (EPG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Gietig D;

DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for

PT diagnosis and prognosis, comprises selective hybridization of amplicons

PT from chemically treated DNA.

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a

CC genomic sample of DNA. The sample is treated chemically to convert

CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one member,

CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

CC degree of hybridisation to both classes is determined from the label on

CC the amplicon. From the ratio of labels hybridised to the two classes of

CC oligomers, the degree of methylation is calculated. The method is used:

CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs

CC and of a wide range of diseases, e.g. cancer, disorders of the central

CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

CC particularly by detecting mutations or single nucleotide polymorphisms

CC (SNP's); and (11) for differentiation of cell or tissue types and for

CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. AB013410-

CC ABQ5121 represent genomic DNA sequences used to illustrate the method

CC for determining the degree of cytosine methylation described in the

CC disclosure of the invention

CC Sequence 538 BP; 61 A; 61 C; 160 G; 256 T; 0 U; 0 Other;

CC Query Match 85.6%; Score 15.4; DB 6; Length 538;

CC Best Local Similarity 94.1%; Pred. No. 2.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTATTGCGCTTCTC 18
DB 434 GTTAAATCGCGTTCCTC 450

RESULT 5

ACA13108/C
ID ACA13108 standard; DNA; 127 BP.

AC ACA13108;

DT 27-OCT-2003 (revised)

DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene antisense oligonucleotide #978.

KM Antisense; ss; prokaryotic essential gene; cell proliferation;

KM drug design.

OS Archaea.

PN WO200271183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-034923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

PS Claim 1; SEQ ID NO 978; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation; (7) identifying a gene in an operon required for

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or its gene product lies

CC pathway in which a proliferation-regulated gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213
CC antisense sequences of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to
CC standardise OS field)

XX
SQ Sequence 127 BP; 42 A; 31 C; 22 G; 32 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 8; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTCC 16
DB 117 GTTAATTCGGCTTCC 103

RESULT 6
AAS48419/C
ID AAS48419 standard; DNA, 128 BP.

XX AAS48419;
AC 13-FEB-2002 (first entry)
XX
XX Enterococcus faecalis cellular proliferation inhibitory sequence #989.
DE Enterococcus faecalis cellular proliferation inhibitory sequence #989.
XX
XX Antisense; ss; prokaryotic cellular proliferation; antibiotic;
KW antibacterial; drug design.
XX
XX Enterococcus faecalis.
OS
XX WO200170955-A2.
FN
XX
XX 27-SEP-2001.
PD
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0245278P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Claim 1; SEQ ID NO 996; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence is an antisense oligonucleotide of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTCC 16
DB 118 GTTAATTCGGCTTCC 104

RESULT 7
AAS47978/C
ID AAS47978 standard; DNA, 250 BP.

XX AAS47978;
AC 13-FEB-2002 (first entry)
XX
XX Enterococcus faecalis cellular proliferation inhibitory sequence #548.
DE Enterococcus faecalis cellular proliferation inhibitory sequence #548.
XX
XX Antisense; ss; prokaryotic cellular proliferation; antibiotic;
KW antibacterial; drug design.
XX
XX Enterococcus faecalis.
OS
XX WO200170955-A2.
FN
XX
XX 27-SEP-2001.
PD
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0245278P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Claim 1; SEQ ID NO 555; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence is an antisense oligonucleotide of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;
SQ
Query Match 83.3%; Score 15; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 GTTAATTCGCGTTCC 16
|||||
54 GTTAATTCGCGTTCC 40
Db
RESULT 8
ACAI2661/c
ID ACAI2661 standard; DNA; 250 BP.
XX
ACAI2661:
XX
27-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene antisense oligonucleotide #531.
XX
XX Antisense; ss; prokaryotic essential gene; cell proliferation;
XX drug design.
XX
XX Archaea.
XX
XX MO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002MO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen K, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 1; SEQ ID NO 531; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway;
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213
CC antisense sequences of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;
SQ
Query Match 83.3%; Score 15; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 GTTAATTCGCGTTCC 16
|||||
54 GTTAATTCGCGTTCC 40
Db
RESULT 9
ADH82429
ID ADH82429 standard; DNA; 615 BP.
XX
XX ADH82429;
XX
XX 22-APR-2004 (first entry)
XX
XX Enterococcus faecalis polynucleotide #314.
XX
XX Enterococcus faecalis infection; transcription regulatory element;
XX antibacterial; gene; ds.
XX
XX Enterococcus faecalis.
XX
XX US6617156-B1.
XX
XX 09-SEP-2003.
XX
XX 13-AUG-1998; 98US-00134000.
XX
XX 15-AUG-1997; 97US-0055778P.
XX
XX (DOUC/) DOUCETTE-STAMM L A.
XX (BUSH/) BUSH D.
XX
XX Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-895394/82.
XX
XX P-PsDB; ADH85834.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
XX polypeptide, useful for preparing a composition for diagnosing or
XX treating *E. faecalis* infection.
XX
XX Disclosure; SEQ ID NO 314; 193pp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
XX polypeptides. The invention also relates to a recombinant expression
XX vector comprising a polynucleotide operably linked to a transcription
XX regulatory element, a cell comprising a recombinant vector, a method for
XX producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising
XX a sequence not given in the specification, a recombinant vector
XX comprising the nucleic acid and a cell comprising the recombinant vector.
XX The polynucleotides can be used to detect the presence of *E. faecalis* in
XX a sample. The sequences are useful for preparing a composition for
XX diagnosing or treating Enterococcus faecalis infection. This sequence
XX represents an *E. faecalis* polynucleotide of the invention.

XX Sequence 615 BP; 187 A; 115 C; 123 G; 190 T; 0 U; 0 Other;
SQ Query Match 83.3%; Score 15; DB 10; Length 615;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GTTAATTCGCGTTCC 16
|||||
Db 172 GTTAATTCGCGTTCC 166
RESULT 10
ACAI8462
ID ACAI8462 standard; DNA; 1467 BP.
AC ACAI8462;
XX 19-JUN-2003 (first entry)
XX 19-JUN-2003 (first entry)
XX Prokaryotic essential gene #119.
XX DE Prokaryotic essential gene #119.
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX Enterococcus faecalis.
XX OS Enterococcus faecalis.
XX PN WO200271193-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX P-PSDB; ABU14592.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 14; SEQ ID NO 6332; 1766bp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1467 BP; 464 A; 268 C; 311 G; 424 T; 0 U; 0 Other;
SQ Query Match 83.3%; Score 15; DB 8; Length 1467;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GTTAATTCGCGTTCC 16
|||||
Db 1027 GTTAATTCGCGTTCC 1041
RESULT 11
AAI3271
ID AAI3271 standard; DNA; 9212 BP.
XX AAI3271;
XX 19-MAR-1999 (first entry)
XX Enterococcus faecalis genome contig SEQ ID NO:334.
XX DE Enterococcus faecalis; contig; detection; Enterococcal infection;
XX Enterococcus faecalis; contig; detection; Enterococcal infection;
XX vaccine; attenuation; computer readable medium; ds.
XX OS Enterococcus faecalis.
XX PN WO9805055-A2.
XX 12-NOV-1998.
XX 04-MAY-1998; 98WO-US008985.
XX 06-MAY-1997; 97US-0044031P.
XX 16-MAY-1997; 97US-0046555P.
XX 14-NOV-1997; 97US-0066009P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Kunsch CA, Dillon PJ, Barash SC;
PI WPI; 1999-045171/04.
XX New isolated Enterococcus faecalis polynucleotides and polypeptides -
PT used to develop products for the detection of Enterococcus and for use in
PT vaccines for prevention or attenuation of Enterococcus infection.
XX Claim 1; Page 1436-1441; 2084bp; English.
XX A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC AAI12938 to AAI13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence of
CC Enterococcus faecalis in samples. They can also be used for diagnosing
CC Enterococcal infection in an animal and monitoring progression of
CC disease, and for identifying agents which can be used to modulate the
CC growth or pathogenicity of Enterococcus faecalis, or another related
CC organism, in vivo or in vitro. In particular the polypeptides encoded by
CC the Enterococcus faecalis nucleotide sequences can be used in vaccines to
CC prevent or attenuate an Enterococcal infection

XX Sequence 9212 BP, 3045 A, 1564 C, 2061 G, 2529 T, 0 U, 13 Other;
SQ Query Match 83.3%; Score 15; DB 2; Length 9212;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16
DB 4989 GTTAATTCGCGTTCC 5003

RESULT 12
ABS99066 standard; DNA; 9212 BP.
XX ABS99066;
AC
XX 18-DEC-2002 (first entry)
DT
XX Enterococcus faecalis contig sequence #334.
DE
XX Computer readable medium; Enterococcus faecalis; microbe; growth;
KW pathogenicity; vaccine; resistance; Enterococcal infection; commercial;
KW therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;
KW biotech technology; antibacterial; modulator of nucleic acid expression;
KW contig; ds.
KM
XX Enterococcus faecalis.
OS
XX US2002120116-A1.
PN
XX 29-AUG-2002.
PD
XX 04-MAY-1998; 98US-00070927.
PF
XX 04-MAY-1998; 98US-00070927.
PR
XX (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
XX
XX Kunsch CA, Dillon PJ, Barash S;
PI WPI; 2002-750065/81.
XX
XX Computer readable medium having recorded on it a Enterococcus faecalis
PT nucleotide sequence useful for detecting diseases related to Enterococcus
XX infections in animals.
XX
XX Claim 1; Page; 119pp; English.
PS
XX The present invention relates to a new computer readable medium with an
CC Enterococcus faecalis nucleotide sequence. The invention is useful to
CC diagnose the presence of E. faecalis in a sample or determining the
CC presence of a specific microbe in a sample. The invention is also useful
CC for modulating the growth or pathogenicity of E. faecalis, in a vaccine to
CC confer resistance to Enterococcal infection, for commercial, therapeutic
CC and industrial purposes, and for fermenting a particular sugar source or
CC to produce a particular metabolite. The invention is useful for detecting
CC diseases related to Enterococcus infections in animals, and for detecting
CC E. faecalis using biotech technology. The present nucleic acid sequence
CC represents an Enterococcus faecalis contig DNA sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at http://seqdata.uspto.gov
XX
SQ Sequence 9212 BP, 3045 A, 1564 C, 2061 G, 2529 T, 0 U, 13 Other;
XX
XX Query Match 83.3%; Score 15; DB 6; Length 9212;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16
DB 4989 GTTAATTCGCGTTCC 5003

RESULT 13
ADC92275/C
ID ADC92275 standard; DNA; 207 BP.
XX ADC92275;
AC
XX 01-JAN-2004 (first entry)
DT
XX E. faecium DNA sequence SEQ ID 1902.
DE
XX ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
KW
XX Enterococcus faecium.
OS
XX US6583275-B1.
PN
XX 24-JUN-2003.
PD
XX 30-JUN-1998; 98US-00107532.
PF
XX 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Doucette-Stamm LA, Bush D;
PI WPI; 2003-799836/75.
XX
XX P-PSDB; ADC95929.
DR
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
XX Example 1; SEQ ID NO 1902; 243pp; English.
PS
XX The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection), and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antitense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium nucleic acids.
XX
SQ Sequence 207 BP, 68 A, 36 C, 47 G, 55 T, 0 U, 1 Other;
XX
XX Query Match 82.2%; Score 14.8; DB 10; Length 207;
XX Best Local Similarity 88.9%; Pred. No. 4.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18
DB 84 CGTTAATTCGCGTTCTC 67

RESULT 14
 ABQ14482
 ID ABQ14482 standard; DNA; 554 BP.
 AC
 XX
 AC ABQ14482;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1073.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 KM
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PR 05-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D,
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ14410-
 CC ABQ14412 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 CC
 SQ Sequence 554 BP; 76 A; 67 C; 169 G; 242 T; 0 U; 0 Other;
 XX
 XX
 Query Match 82.2%; Score 14.8; DB 6; Length 554;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CGTTAATTCGGCTTCCTC 18
 |||||
 DB 113 CGTTAATTCGGCTTCATC 130

RESULT 15
 ABQ14483/c
 ID ABQ14483 standard; DNA; 554 BP.

XX
 AC ABQ14483;
 XX
 AC
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1074.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 KM
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PR 05-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D,
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ14411 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 CC
 SQ Sequence 554 BP; 242 A; 169 C; 67 G; 76 T; 0 U; 0 Other;
 XX
 XX
 Query Match 82.2%; Score 14.8; DB 6; Length 554;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CGTTAATTCGGCTTCCTC 18
 |||||
 DB 442 CGTTAATTCGGCTTCATC 425

Search completed: December 8, 2004, 11:13:42
 Job time : 231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:28:40 ; Search time 60 Seconds
(without alignments)
213.237 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcttcctc 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCITUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	15	83.3	615	US-08-134-000C-314	Sequence 114, App
3	14.8	82.2	207	US-09-107-532A-1902	Sequence 1902, Ap
4	14.8	82.2	650	US-09-669-751-103	Sequence 103, App
5	14.8	82.2	2457	US-09-134-000C-2950	Sequence 2950, Ap
6	14.4	80.0	939	US-09-710-279-3059	Sequence 3059, Ap
7	14.4	80.0	963	US-09-134-001C-1367	Sequence 1367, Ap
8	14.4	80.0	2815	US-09-710-279-3819	Sequence 3819, Ap
9	14	77.8	3208	US-07-972-791-3	Sequence 3, Appl
10	14	77.8	3345	US-07-972-791-7	Sequence 7, Appl
11	14	77.8	3346	US-07-972-791-5	Sequence 5, Appl
12	14	77.8	3347	US-07-972-791-2	Sequence 2, Appl
13	14	77.8	3347	US-07-972-791-8	Sequence 8, Appl
14	14	77.8	3361	US-07-972-791-6	Sequence 6, Appl
15	14	77.8	3434	US-06-543-681A-4125	Sequence 4125, Ap
16	13.8	76.7	702	US-09-328-352-1886	Sequence 1886, Ap
17	13.8	76.7	1386	US-09-134-001C-984	Sequence 984, App
18	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
19	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
20	13.8	76.7	6642	US-09-809-665A-80	Sequence 80, Appl
21	13.8	76.7	6642	US-08-844-274-13	Sequence 13, Appl
22	13.8	76.7	6723	US-08-844-274-13	Sequence 14, Appl
23	13.8	76.7	6723	US-09-598-421-13	Sequence 13, Appl
24	13.8	76.7	6723	US-09-598-421-14	Sequence 14, Appl
25	13.8	76.7	7560	US-08-844-274-20	Sequence 20, Appl
26	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl
27	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl

28	13.8	76.7	9423	US-09-377-066-6	Sequence 6, Appl
29	13.8	76.7	9704	US-09-814-951A-3	Sequence 3, Appl
30	13.8	9717	3	US-09-251-645-1	Sequence 1, Appl
31	13.8	76.7	12666	US-08-961-527-137	Sequence 137, App
32	13.8	76.7	49795	US-08-453-702B-60	Sequence 60, Appl
33	13.6	75.6	3378	US-07-972-791-1	Sequence 1, Appl
34	13.4	74.4	341	US-09-270-767-8188	Sequence 8188, Ap
35	13.4	74.4	341	US-09-270-767-23470	Sequence 23470, A
36	13.4	74.4	350	US-09-270-767-1708	Sequence 1708, Ap
37	13.4	74.4	350	US-09-270-767-16990	Sequence 16990, A
38	13.4	74.4	492	US-09-248-796A-4921	Sequence 4921, Ap
39	13.4	74.4	549	US-09-328-352-3243	Sequence 3243, Ap
40	13.4	74.4	720	US-09-134-000C-1003	Sequence 1003, Ap
41	13.4	1293	4	US-09-489-039A-409	Sequence 409, App
42	13.4	74.4	1411	US-09-270-767-11617	Sequence 11617, A
43	13.4	74.4	2430	US-09-620-312D-176	Sequence 176, App
44	13.4	74.4	2967	US-09-185-501B-12	Sequence 12, Appl
45	13.4	74.4	10144	US-10-204-708-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-09-423-233-50
Sequence 50, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium oxysporum
US-09-423-233-50

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATCGCGTTCTC 18
Db 1 CGTTAATCGCGTTCTC 18

RESULT 2
US-09-134-000C-314
Sequence 314, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 314
LENGTH: 615
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-314

Query Match 83.3%; Score 15; DB 4; Length 615;

Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 16
Db 172 GTTAATTCGGCTTC 186

RESULT 3

US-09-107-532A-1902/c

; Sequence 1902, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Arinlele, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 1902:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...207

; SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

US-09-107-532A-1902

Query Match 82.2%; Score 14.8; DB 4; Length 207;

Best Local Similarity 88.9%; Pred. No. 56;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTC 18

Db 84 CGTTAATTCGGCTTC 67

RESULT 4

US-09-669-751-103

; Sequence 103, Application US/09669751

; Patent No. 6551575

; GENERAL INFORMATION:

; APPLICANT: Greenspan, Ralph J.

; TITLE OF INVENTION: Methods for Identifying Compounds for Motion Sickness, Vertigo and Other Disorders Related to Balance and the Perception of Gravity

; FILE REFERENCE: P-NI 3864

; CURRENT APPLICATION NUMBER: US/09/669,751

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 60/168,579

; PRIOR FILING DATE: 1999-12-02

; NUMBER OF SEQ ID NOS: 261

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 103

; LENGTH: 650

; TYPE: DNA

; ORGANISM: Drosophila

US-09-669-751-103

Query Match 82.2%; Score 14.8; DB 4; Length 650;

Best Local Similarity 88.9%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTC 18

Db 69 CGTTAATTCGGCTTC 86

RESULT 5

US-09-134-000C-2950/c

; Sequence 2950, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2950

; LENGTH: 2457

; TYPE: DNA

; ORGANISM: Enterococcus faecalis

US-09-134-000C-2950

Query Match 82.2%; Score 14.8; DB 4; Length 2457;

Best Local Similarity 88.9%; Pred. No. 71;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTC 18

Db 963 CGTTAATTCGGCTTC 946

RESULT 6

US-09-710-279-3059/c

; Sequence 3059, Application US/09710279

; Patent No. 6703492

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PUS480US

; CURRENT APPLICATION NUMBER: US/09/710,279

; CURRENT FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3059

LENGTH: 939
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3059

Query Match 80.0%; Score 14.4; DB 4; Length 939;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18
|||||
DB 616 TTAATTCGCGTTCCTC 601

RESULT 7
US-09-134-001C-1367/c
Sequence 1367, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1367
LENGTH: 963
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1367

Query Match 80.0%; Score 14.4; DB 3; Length 963;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18
|||||
DB 640 TTAATTCGCGTTCCTC 625

RESULT 8
US-09-710-279-3819
Sequence 3819, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 3819
LENGTH: 2815
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3819

Query Match 80.0%; Score 14.4; DB 4; Length 2815;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18
|||||
DB 792 TTAATTCGCGTTCCTC 807

RESULT 9
US-07-972-791-3/c
Sequence 3, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAYEL, GAMBRELL, HEMITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3208 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 1 (S2308)
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15
|||||
DB 1488 GTTAATTCGCGTTC 1475

RESULT 10
US-07-972-791-7/c
Sequence 7, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3345 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella melitensis
STRAIN: biovar 1
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATCGCGTTC 15
|||||
DB 1487 GTTAATCGCGTTC 1474

RESULT 11
US-07-972-791-5/c
Sequence 5, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3346 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella neotomae
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATCGCGTTC 15
|||||
DB 1488 GTTAATCGCGTTC 1475

RESULT 12
US-07-972-791-2/c
Sequence 2, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 5
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATCGCGTTC 15
|||||

Db 1488 GTTAATTCGCGTTC 1475

RESULT 13

US-07-972-791-8/c

Sequence 8, Application US/07972791

Patent No. 5348857

GENERAL INFORMATION:

APPLICANT: Ficht, Thomas A.

APPLICANT: Sowa, Blair A.

APPLICANT: Adams, L. Gary

TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING SPECIES AND BIOVARS OF BRUCELLA

TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER

STREET: 1177 West Loop South, 10th Floor

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77027

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/972,791

FILING DATE: 19921106

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Denise M.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165

TELEX: 792026

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3347 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Brucella suis

STRAIN: biovar 1

US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15

Db 1488 GTTAATTCGCGTTC 1475

RESULT 14

US-07-972-791-6/c

Sequence 6, Application US/07972791

Patent No. 5348857

GENERAL INFORMATION:

APPLICANT: Ficht, Thomas A.

APPLICANT: Sowa, Blair A.

APPLICANT: Adams, L. Gary

TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING SPECIES AND BIOVARS OF BRUCELLA

TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER

STREET: 1177 West Loop South, 10th Floor

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77027

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/972,791

FILING DATE: 19921106

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Denise M.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165

TELEX: 792026

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 3361 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Brucella ovis

US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15

Db 1503 GTTAATTCGCGTTC 1490

RESULT 15

5310649-1/c

Patent No. 5310649

APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, Garry L.

TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS OF BRUCELLA

NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/527,017

FILING DATE: 22-MAY-1990

SEQ ID NO: 1;

LENGTH: 3434

5310649-1

Query Match 77.8%; Score 14; DB 6; Length 3434;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15

Db 1692 GTTAATTCGCGTTC 1679

Search completed: December 8, 2004, 11:09:45
Job time: 61 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:31:11 ; Search time 257 Seconds
(without alignments)
386.161 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18
Sequence: 1 cgtcaattccgcgtccctc 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4085731 seqs, 2756760397 residues

Total number of hits satisfying chosen parameters: 8171462

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-046-955-50	Sequence 50, Appl
2	15.4	85.6	538	US-10-363-345A-23645	Sequence 23645, A
3	15.4	85.6	538	US-10-363-345A-23646	Sequence 23646, A
4	15.4	85.6	4461	US-10-437-963-93618	Sequence 93618, A
5	15	83.3	127	US-10-282-122A-978	Sequence 978, App
6	15	83.3	128	US-09-815-242-996	Sequence 996, App
7	15	83.3	250	US-09-815-242-555	Sequence 555, App
8	15	83.3	250	US-10-282-122A-531	Sequence 531, App
9	15	83.3	1467	US-10-282-122A-6332	Sequence 6332, Ap
10	15	83.3	9212	US-09-070-927A-334	Sequence 334, App
11	14.8	82.2	262	US-09-535-459-1371	Sequence 1371, Ap
12	14.8	82.2	438	US-10-424-599-43896	Sequence 43896, A

13	14.8	82.2	554	US-10-363-345A-1073	Sequence 1073, Ap
14	14.8	82.2	554	US-10-363-345A-1074	Sequence 1074, Ap
15	14.8	82.2	585	US-10-437-963-81762	Sequence 81762, A
16	14.8	82.2	650	US-10-255-536-103	Sequence 103, App
17	14.8	82.2	816	US-10-425-115-60210	Sequence 60210, A
18	14.8	82.2	1231	US-10-363-345A-14681	Sequence 14681, A
19	14.8	82.2	1231	US-10-363-345A-14682	Sequence 14682, A
20	14.8	82.2	1445	US-10-425-115-145901	Sequence 145901, A
21	14.8	82.2	3135	US-10-282-122A-20853	Sequence 20853, A
22	14.8	82.2	3138	US-09-815-242-6520	Sequence 6520, Ap
23	14.8	82.2	2731748	US-10-287-465A-1	Sequence 1, Appli
24	14.4	80.0	65	US-10-032-585-259	Sequence 259, App
25	14.4	80.0	230	US-10-242-535A-247	Sequence 247, App
26	14.4	80.0	230	US-10-085-783A-247	Sequence 247, App
27	14.4	80.0	306	US-09-974-300-6603	Sequence 6603, Ap
28	14.4	80.0	540	US-10-363-345A-4913	Sequence 4913, Ap
29	14.4	80.0	540	US-10-363-345A-4914	Sequence 4914, Ap
30	14.4	80.0	559	US-10-029-386-7594	Sequence 7594, Ap
31	14.4	80.0	601	US-10-363-345A-20645	Sequence 20645, A
32	14.4	80.0	601	US-10-363-345A-20646	Sequence 20646, A
33	14.4	80.0	651	US-10-027-632-266929	Sequence 266929, A
34	14.4	80.0	651	US-10-027-632-266929	Sequence 266929, A
35	14.4	80.0	914	US-10-369-493-35000	Sequence 35000, A
36	14.4	80.0	948	US-10-424-599-78398	Sequence 78398, A
37	14.4	80.0	1520	US-10-424-599-116221	Sequence 116221, A
38	14.4	80.0	6711	US-10-341-200-42	Sequence 42, Appl
39	14.4	80.0	8440	US-10-341-200-19	Sequence 19, Appl
40	14.4	80.0	1163020	US-10-398-221-10	Sequence 10, Appl
41	14.4	80.0	3011208	US-10-398-221-2058	Sequence 2058, Ap
42	14	77.8	549	US-10-363-345A-15973	Sequence 15973, A
43	14	77.8	704	US-10-363-345A-15974	Sequence 15974, A
44	14	77.8	704	US-10-363-345A-23187	Sequence 23187, A
45	14	77.8	704	US-10-363-345A-23188	Sequence 23188, A

ALIGNMENTS

RESULT 1
US-10-046-955-50
Sequence 50, Application US/10046955
Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di.
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Etrol
APPLICANT: Aldorevich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium oxysporum
US-10-046-955-50
Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTAATTCGCGTTCCTC 18
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Db 1 CCTAATTCGCGTTCCTC 18

RESULT 2

US-10-363-345A-23645
; Sequence 23645, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23645
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23645
US-10-363-345A-23645

Query Match 85.6%; Score 15.4; DB 18; Length 538;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GTTAATTCGCGTTCCTC 18
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Db 434 GTTAATTCGCGTTCCTC 450

RESULT 3

US-10-363-345A-23646/c
; Sequence 23646, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23646
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23646
US-10-363-345A-23646

Query Match 85.6%; Score 15.4; DB 18; Length 538;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GTTAATTCGCGTTCCTC 18
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Db 105 GTTAATTCGCGTTCCTC 89

RESULT 4

US-10-437-963-93618/c
; Sequence 93618, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 93618
; LENGTH: 4461
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91986C.1
US-10-437-963-93618

Query Match 85.6%; Score 15.4; DB 17; Length 4461;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5

US-10-282-122A-978/c
; Sequence 978, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

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Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 978
; LENGTH: 127
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-978
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Query Match      83.3%; Score 15; DB 16; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      117 GTTAATCGCGTTCC 103
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RESULT 6
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; Patent No. US20020061569A1
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GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 14110
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996
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Query Match      83.3%; Score 15; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 555, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
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; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-555
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Query Match      83.3%; Score 15; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 GTTAATCGCGTTCC 16
      |||||
Db      54 GTTAATCGCGTTCC 40
```

```
RESULT 8
US-10-282-122A-531/c
; Sequence 531, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
```

```

; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 531
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-531

Query Match
Best Local Similarity 83.3%; Score 15; DB 16; Length 250;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCC 16
Db 54 GTTAATTCGCGTTCC 40

RESULT 9
US-10-282-122A-6332
; Sequence 6332, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO: 6332
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-6332

Query Match
Best Local Similarity 83.3%; Score 15; DB 16; Length 1467;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCC 16
Db 1027 GTTAATTCGCGTTCC 1041

RESULT 10
US-09-070-927A-334
; Sequence 334, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 334:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 334:
US-09-070-927A-334

Query Match
Best Local Similarity 83.3%; Score 15; DB 9; Length 9212;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCC 16
Db 4989 GTTAATTCGCGTTCC 5003
```

```
RESULT 11
US-09-535-459-1371/c
; Sequence 1371, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleagane, Angelo M.
; APPLICANT: Stueart, Susan G.
; APPLICANT: Stueart, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1371
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m13c_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371

Query Match      82.2%; Score 14.8; DB 10; Length 262;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
Db      102 CCTTAATTCGCGTTCTC 85

RESULT 12
US-10-424-599-43896
; Sequence 43896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovallig, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43896
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139637C.1
US-10-424-599-43896

Query Match      82.2%; Score 14.8; DB 16; Length 438;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
Db      297 CGTTAATTCGCGTTCTC 314

RESULT 13
US-10-363-345A-1073
; Sequence 1073, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1073
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1073
US-10-363-345A-1073

Query Match      82.2%; Score 14.8; DB 18; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
Db      113 CGTTAATTCGCGTTATC 130

RESULT 14
US-10-363-345A-1074/c
; Sequence 1074, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1074
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1074
US-10-363-345A-1074

Query Match      82.2%; Score 14.8; DB 18; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
Db      442 CGTTAATTCGCGTTATC 425

RESULT 15
US-10-437-963-81762
; Sequence 81762, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovallig, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
```

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81762
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81256C.1
US-10-437-963-81762

Query Match      82.2%; Score 14.8; DB 17; Length 585;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATCGCGCTCTC 18
        |||||
Db      230 CGTTCATTGCGCTCCAC 247

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Search completed: December 8, 2004, 11:18:07
 Job time : 261 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:26:55 ; Search time 1781 Seconds
(without alignments)
368.285 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgtccctc 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	667	5	BQ483402 WHE3508_B
2	16.4	91.1	949	9	CL460875 SAT1.11
3	16.4	88.9	685	9	CL707833 OR_BBA002
4	16.4	88.9	701	9	CL708823 OR_BBA003
5	16.4	88.9	740	9	CL714278 OR_BBA003
6	16.4	88.9	750	9	CL788163 OR_BBA010
7	15.4	85.6	262	8	AZ359925 IM0103B02
8	15.4	85.6	277	8	BH452985 BOHGA60TF
9	15.4	85.6	367	7	CN746869 SAL_US027
10	15.4	85.6	402	9	CG858920 ZMMBC026
11	15.4	85.6	493	8	CG858920 ZMMBC026
12	15.4	85.6	499	8	AZ498171 IM0335P13
13	15.4	85.6	547	7	BH144783 TDGEO91TH
14	15.4	85.6	547	7	CK701447 USDA-PP_4
15	15.4	85.6	588	8	BZ508556 BONS38TF
16	15.4	85.6	669	3	AY440797 Armigeres
17	15.4	85.6	740	9	AG042918 Pan_trog1
18	15.4	85.6	753	3	AY440799 Armigeres
19	15.4	85.6	819	3	CG810640 FSA082TF
20	15.4	85.6	902	6	CA278228 SCBPSD03
21	15.4	85.6	921	7	CK288913 EST751635
22	15.4	85.6	968	7	CK286745 EST749467
23	15.4	85.6	1000	5	BP512280 BP512280
24	15.4	85.6	1278	2	BM543811 AGERCORT
			311	2	AW833312 RC2-TT000

25	15	83.3	543	4	BI881942	BI881942 fm89g12.x
26	15	83.3	547	6	CB406133	CB406133 OSTR064C7
27	15	83.3	563	6	CB406152	CB406152 OSTR064C7
28	15	83.3	611	9	CR257810	CR257810 Forward s
29	15	83.3	636	2	BE557132	BE557132 Fk94g09.y
30	15	83.3	728	4	BG723264	BG723264 602650884
31	15	83.3	870	7	CK200815	CK200815 FGAS00933
32	15	83.3	928	9	CL729708	CL729708 OR_BBA006
33	15	83.3	1057	9	AG081712	AG081712 Pan_trog1
34	14.8	82.2	140	6	CB066245	CB066245 PVBE11E11
35	14.8	82.2	187	4	BM616169	BM616169 170006871
36	14.8	82.2	206	8	AZ991070	AZ991070 2M0275N03
37	14.8	82.2	206	8	AZ991080	AZ991080 2M0275P03
38	14.8	82.2	239	9	CR203507	CR203507 Forward s
39	14.8	82.2	282	6	CB066239	CB066239 PVBE11E04
40	14.8	82.2	296	9	CR045592	CR045592 Forward s
41	14.8	82.2	298	9	CR180215	CR180215 Forward s
42	14.8	82.2	303	1	AA785231	AA785231 95h08a1.f
43	14.8	82.2	322	9	BX965280	BX965280 Forward s
44	14.8	82.2	338	1	AJ502973	AJ502973
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ALIGNMENTS

RESULT 1
BQ483402/c 667 bp mRNA linear EST 03-JUN-2002
LOCUS WHE3508 B09 D18ZS Wheat untranscribed root cDNA library Triticum
DEFINITION aetivum cDNA clone WHE3508_B09_D18, mRNA sequence.

ACCESSION BQ483402 GI:21119338
VERSION BQ483402.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Anderson, O.D., Chao, S., Close, T.J., Crossman, C., Fenton, R.D., Lazo, G.R., Nguyen, H.T., Rauech, C.J., Wilson, C., Woo, J. and Zhang, D. The structure and function of the expressed portion of the wheat genomes - Untranscribed root cDNA library

JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

FEATURES
source Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1. 667
/organism="Triticum aestivum"
/mol_type="mRNA"
/cuiovar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE3508_B09_D18"
/tissue_type="Roots"
/dev_stage="Full tillering"
/lab_host="E. coli SOLR"
/clone_lib="Wheat untranscribed root cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK(-), Site 1: EcoRI, Site 2: XhoI. Plants were grown until full tillering stage and root tissue was collected at Texas Tech University (Zhang, H.T. Nguyen Lab). Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemide in the T7

Close lab (Close, Fenton) at the University of California, Riverside. Colony plating, plasmid preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 91.1%; Score 16.4; DB 5; Length 667;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
|||||
Db 243 CGTTAATTCGGCTTCCTC 226

RESULT 2
LOCUS CL460875 949 bp DNA linear GSS 31-MAR-2004
DEFINITION SAIL_111.C06.v1 SAIL Collection Arabidopsis thaliana genomic clone
CL460875
VERSION CL460875.1 GI:45863780
ACCESSION
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsis;
1 (bases 1 to 949)

REFERENCE
AUTHORS Sessions, A., Burke, E., Presting, G., Aux, G., McEliver, J., Patton, D., Dietrich, B., Ho, P., Bacwarden, J., Ko, C., Clarke, J. D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutcheson, D., Kimmery, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
12356987
JOURNAL MEDLINE
PUBMED 12468722

COMMENT

Applied Trait Genetics
Contact: Sessions A
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS805419; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

1..949
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_111.C06.v1"
/clone_1ib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 949;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18
|||||
Db 578 CGTTAATTCGGCTTCCTC 595

RESULT 3
LOCUS CL707833/c 685 bp DNA linear GSS 26-JUL-2004
DEFINITION OR_BB40027F10.r OR_BB4 Oryza rufipogon genomic clone OR_BB40027F10

3', genomic survey sequence.
ACCESSION CL707833
VERSION CL707833.1 GI:50594871
KEYWORDS GSS.

SOURCE

Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 685)

REFERENCE

AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.

TITLE

OMAP Project
Unpublished (2004)

JOURNAL

Contact: Rod A. Wing
Arizona Genomics Institute

University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0027 row: F column: 10
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES

Location/Qualifiers
1..685
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BB40027F10"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_1ib="OR_BB4"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGGCTTCCT 17
|||||
Db 32 GTTAATTCGGCTTCCT 17

RESULT 4
LOCUS CL708823/c 701 bp DNA linear GSS 26-JUL-2004
DEFINITION OR_BB40030B15.r OR_BB4 Oryza rufipogon genomic clone OR_BB40030B15
3', genomic survey sequence.
ACCESSION CL708823
VERSION CL708823.1 GI:50595861
KEYWORDS GSS.

SOURCE

Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.

TITLE

OMAP Project
Unpublished (2004)

JOURNAL

Contact: Rod A. Wing
Arizona Genomics Institute

COMMENT

University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259

Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 161 Std Error: 0.00
Plate: 0030 row: B column: 15
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1..701
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa0030B15"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 701;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCCT 17
|||||
32 GTTAATTCGCGTTCCT 17

Db

RESULT 5
CL714278 740 bp DNA linear GSS 26-JUL-2004
LOCUS OR_BBa0038P08.r OR_BBa Oryza rufipogon genomic clone OR_BBa0038P08
DEFINITION 3' genomic survey sequence.
CL714278
CL714278.1 GI:50601316

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 740)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 161 Std Error: 0.00
Plate: 0030 row: P column: 08
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1..740
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa0038P08"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 740;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCCT 17
|||||
32 GTTAATTCGCGTTCCT 17

Db

RESULT 6
CL788163 750 bp DNA linear GSS 30-JUL-2004
LOCUS OR_BBa106I12.r OR_BBa Oryza rufipogon genomic clone OR_BBa106I12
DEFINITION 3' genomic survey sequence.
CL788163
CL788163.1 GI:50867814

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 750)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 161 Std Error: 0.00
Plate: 0106 row: I column: 12
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1..750
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa106I12"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 750;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCCT 17
|||||
34 GTTAATTCGCGTTCCT 19

Db

RESULT 7
AZ359925 262 bp DNA linear GSS 02-OCT-2000
LOCUS IM0103B02F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM10103B02 F, genomic survey sequence.
AZ359925
AZ359925.1 GI:10473625

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: B column: 02
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 262.
Location/Qualifiers

FEATURES

source

1. 262
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0103B02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCM1 library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 262;
Best Local Similarity 94.1%; Pred. No. 6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTCCTC 18
|||||
Db 214 GTTAATTCGGCTTCCTC 198

RESULT 8
BH452985/c
LOCUS BH452985 277 bp DNA linear GSS 12-DEC-2001
DEFINITION BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, genomic
survey sequence.
ACCESSION BH452985
VERSION BH452985.1 GI:17638696
KEYWORDS GSS
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 277)
Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHGA60TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers

FEATURES

source

1. 277
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHGA60"
/clone_1ib="BOHG"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 277;
Best Local Similarity 94.1%; Pred. No. 6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCT 17
|||||
Db 94 CGTTAATTCGGCTTCCT 78

RESULT 9
CN746869
LOCUS CN746869 367 bp mRNA linear EST 19-MAY-2004
DEFINITION SAL_US027xg21fl.ab1 SAL_US N. Benthamia Nicotiana benthamiana cDNA
5', mRNA sequence.
ACCESSION CN746869
VERSION CN746869.1 GI:47511866
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 367)
Opperman,C.H., Lommel,S.A., Burke,M., Feulner,G., Carlson,J.,
George,C., Gove,S., Houfek,T.D., Jefferys,S.R., Kalat,S., King,R.,
Levin,J., Little,P.C., Lumpkin,A., Ross,T., Salestad,A.,
Scholl,E.H., Sosinski,B.R., Stephens,P.J. and Zekans,S.H.
Tobacco Genome Initiative (TGI) Nicotiana benthamiana ESTs
Unpublished (2004)
Contact: Dr. Steven A. Lommel
Tobacco Genome Initiative
North Carolina State University
Box 7253, NCSU, Raleigh, NC 27606, USA
Tel: 9195130006
Fax: 9195159500
Email: Steve_Lommel@ncsu.edu
Homology: e-val = 7.0e-022. Description = asparaginyl-tRNA
synthetase, cytoplasmic (asparagine-tRNA ligase), putative
[Arabidopsis thaliana] gi|20140327|sp|Q9SSK1|SYN1_ARATH
Asparaginyl-tRNA synthetase, cytoplasmic 3 (Asparagine--tRNA ligase
3) [AenRS 3] gi|25406088|pir|B96734 hypothetical prote Homology:
e-val = 2.4e-022. Description = putative asparaginyl-tRNA
synthetase [Oryza sativa (japonica cultivar-group)]
gi|14587206|dbj|BAB61140.1| putative asparaginyl-tRNA synthetase
[Oryza sativa (japonica cultivar-group)]

g[15408636|dbj|BAB64053.1| putative asparaginyl-tRNA synthetase
[Oryza row: 9 column: 21
High quality sequence stop: 367.
Location/Qualifiers
1..367
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/cultivar="berkeley"
/db_xref="taxon:4100"
/cissue_type="expanding leaf tissue"
/clone_lib="SAL US N.Bentheme"
/note="Vector: pBluescript S/K +; Site_1: EcoRI; Site_2:
XhoI; Total RNA isolated from tissue, poly A fraction
isolated on oligo-dT column. mRNA reverse transcribed and
double stranded. Poly A dsRNA ranging in size from
400-4000 bp directionally cloned into EcoRI and XhoI
restricted into pBluescript. EcoRI site at the 5' end of
the cDNA and XhoI on the 3' side."

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 367;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATCGCGTCTCTC 18
|||||
DB 207 GTTCATTCGCGTCTCTC 223

RESULT 10 402 bp DNA linear GSS 19-NOV-2003
CG858920 ZMMBC0267L01f ZMMBC (EcoRI) Zea mays genomic clone ZMMBC0267L01
LOCUS ZMMBC0267L01f ZMMBC (EcoRI) Zea mays genomic clone ZMMBC0267L01
DEFINITION 5', genomic survey sequence.
ACCESSION CG858920
VERSION CG858920.1 GI:38431633
KEYWORDS GSS.

SOURCE

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 402)
Bharti,A.K., Young,S., Kavchok,S., Keiser,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PCR (2003c)
Unpublished (2003)

JOURNAL

Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu

Seg primer: T7
Class: BAC ends
High quality sequence start: 110.

FEATURES

Location/Qualifiers
1..402
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBC0267L01"
/lab_host="E.coli DH10B"
/clone_id="ZMMBC (EcoRI)"
/note="Vector: pYRABAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 402;
Best Local Similarity 94.1%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTAATTCGCGTCTCT 17
|||||
DB 69 CGTAATTCGCGTCTCT 85

RESULT 11 493 bp DNA linear GSS 05-OCT-2000
AZ498171c 1M0335P13f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION 1M0335P13f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0335P13 F, genomic survey sequence.
AZ498171.1 GI:10675786
GSS.

ACCESSION AZ498171
VERSION AZ498171.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 493)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0335 row: P column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 493.

JOURNAL

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0335 row: P column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 493.

FEATURES

Location/Qualifiers
1..493
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0335P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid library"
/note="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g[14732114|db|AF120072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 493;
Best Local Similarity 94.1%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18
 |||||
 Db 383 GTTAATTCGCGTTCCTC 367

RESULT 12
 BH144783 499 bp DNA linear GSS 16-AUG-2001
 LOCUS TDBEO91TH CTOG Lycopersicon esculentum genomic clone CTOG30P13,
 DEFINITION genomic survey sequence.
 ACCESSION BH144783
 VERSION BH144783.1 GI:15200046
 KEYWORDS GSS.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 499)
 van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Romning,C. and
 Tanksley,S.
 Tomato demethylated genomic DNA sequences
 Unpublished (2001)
 CONTACT: CUGI
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 tomato demethylated genomic DNA
 Insert length: 1270 Std Error: 0.00
 Seq primer: M13-F-R
 Class: shotgun.

FEATURES
 source
 1..499
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /cultiivar="R6203"
 /db_xref="taxon:4081"
 /clone="CTOG30P13"
 /tissue_type="young leaves"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="E.coli JM109"
 /clone_id="CTOG"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; This library was made from short EcoRI digested
 fragments of the genome of Lycopersicon esculentum ligated
 into pBS (SK-). The fragments were cloned into the
 methylation restrictive E.coli strain JM109 with the
 purpose of enriching the library for non-methylated DNA
 fragments. This procedure may enrich the pool of cloned
 fragments in JM109 cells for sequences representing
 expressed genes. Average insert size 1.27 kb."

ORIGIN
 Query Match 85.6%; Score 15.4; DB 8; Length 499;
 Best Local Similarity 94.1%; Pred. No. 6.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18
 |||||
 Db 116 GTTAATTCGCGTTCCTC 132

RESULT 13
 CK701447 547 bp mRNA linear EST 09-FEB-2004
 LOCUS CK701447/c
 DEFINITION USDA-FP 4707 Ridge pineapple sweet orange entire seedling Citrus
 sinensis cDNA clone RSE3JA08 5', mRNA sequence.
 ACCESSION CK701447
 VERSION CK701447.1 GI:42477392
 KEYWORDS EST.
 SOURCE Citrus sinensis

ORGANISM
 Citrus sinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Sapindales; Rutaceae; Citrus.
 1 (bases 1 to 547)
 Bausher,M., Shalters,R., Chaparro,J., Dang,P., Hunter,W. and
 Medz,R.
 An expressed sequence tag (EST) set from Citrus sinensis L. Osbeck
 whole seedlings and the implications of further perennal source
 investigations
 Plant Sci. 165, 415-422 (2003)
 CONTACT: Michael Bausher
 US Horticultural Research
 USDA - ARS
 2001 South Rock Rd., Fort Pierce, FL 34945, USA
 Tel: (772) 462-5918
 Fax: (772) 462-5961
 Email: mbausher@usnr1.ars.usda.gov
 Seq primer: T3 Universal.

FEATURES
 source
 1..547
 /organism="Citrus sinensis"
 /mol_type="mRNA"
 /cultiivar="Ridge pineapple"
 /db_xref="taxon:2711"
 /clone="RSE3JA08"
 /tissue_type="entire seedling"
 /dev_stage="50 days after germination"
 /lab_host="X11-Blue"
 /clone_id="Ridge pineapple sweet orange entire seedling"
 /note="Vector: pBluescript IT SK+; Site 1: EcoRI; Site 2:
 XhoI; A high quality EST with at least 200 contiguous
 bases at Trace Tuner score of 20 or better"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 7; Length 547;
 Best Local Similarity 94.1%; Pred. No. 6.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18
 |||||
 Db 491 GTTAATTCGCGTTCCTC 475

RESULT 14
 BZ508556/c 588 bp DNA linear GSS 16-DEC-2002
 LOCUS BZ508556
 DEFINITION BZ508556 BO_1.6_2_KB_for Brassica oleracea genomic clone BZ508556,
 genomic survey sequence.
 ACCESSION BZ508556
 VERSION BZ508556.1 GI:27031477
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 588)
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Frazer,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other GSSs: BZ508556R
 CONTACT: Chris Town.
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: shared ends.

FEATURES
 source
 1..588
 Location/Qualifiers

ORIGIN

```

/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T0100DH3"
/db_xref="taxon:3712"
/clone="BONSH38"
/clone_lib="BO_1.6-2_KB_tot"
/notes="Vector: PHOS1, Site 1: BatXI, 1.6-2 kb sheared
total DNA inserted into PHOS1 using BatXI linkers"

```

Query Match 85.6%; Score 15.4; DB 8; Length 588;
 Best Local Similarity 94.1%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17
 |||||
 Db 445 CGTTAATTCGCGTTCT 429

RESULT 15
 AY440797 669 bp mRNA linear HTC 24-JUN-2004
 LOCUS Armigeres subalbatus ASAP ID: 40469 putative: alanine
 DEFINITION aminotransferase mRNA sequence.
 ACCESSION AY440797 GI:42765826
 VERSION AY440797.1 GI:42765826
 KEYWORDS HTC.
 SOURCE Armigeres subalbatus
 ORGANISM Armigeres subalbatus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Armigeres.
 1 (bases 1 to 669)
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
 Fuchs,J.F., Liss,P., Ruech,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
 Christensen,B.M.
 Description of the Transcriptomes of Immune Response-Activated
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
 subalbatus
 JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)
 PUBMED 15213157
 2 (bases 1 to 669)
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
 Liss,P., Ruech,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
 Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
 Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
 Direct Submission
 Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
 53706, USA
 COMMENT More information about this sequence is available in ASAP (A
 Systematic Annotation Package for community analysis of genomes)
 from the University of Wisconsin-Madison at
<https://asap.ahabs.wisc.edu/annotation/pnp/logon.php>.
 location/Qualifiers

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ORIGIN

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Db 32 CGTTAATTCGCGTTCT 48

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 171.043 Seconds

(without alignments)
5321.503 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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2	21	100.0	21	6 BD083636	BD083636 Nucleic a
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5	21	100.0	319	6 BD083591	BD083591 Nucleic a
6	21	100.0	319	6 AF117921	AF117921 Nectria h
7	21	100.0	468	8 AY426972	AY426972 Fusarium
8	21	100.0	471	8 AF161222	AF161222 Nectria h
9	21	100.0	471	8 AY043472	AY043472 Nectria h
10	21	100.0	471	8 AY043473	AY043473 Nectria h
11	21	100.0	471	8 AY043478	AY043478 Nectria h
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32	21	100.0	481	8 AY210327	AY210327 Nectria s
33	21	100.0	483	8 AY043477	AY043477 Nectria h
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ACCESSION AR206445
VERSION AR206445.1 GI:21505049
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ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Morrison,C.J., Reies,E., Aldorevich,L. and Choi,J.Soo.
JOURNAL Nucleic acids for detecting Aspergillus species and other
Patent: US 6372430-A 51 16-APR-2002;
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DEFINITION	BD083636 21 bp DNA linear PAT 27-AUG-2002	
ACCESSION	BD083636	
VERSION	BD083636.1 GI:22629246	
KEYWORDS	JP 2001525665-A/51.	
SOURCE	Fusarium solani	
ORGANISM	Fusarium solani	
REFERENCE	Eunaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
AUTHORS	1 (bases 1 to 21)	
TITLE	Morrison C.J., Reiss E., Aldorevich L. and Choi J.S.	
JOURNAL	Nucleic acids for detecting Aspergillus species and other filamentous fungi.	
COMMENT	Patent: JP 2001525665-A 51 11-DEC-2001; THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE	
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PN	JP 2001525665-A/51	
PD	11-DEC-2001	
PF	01-MAY-1998 JP 1998548275	
PR	02-MAY-1997 US 60/045400	
PI	CHRISTINE J MORRISON,ERROL REISS,LILIANA ALDOREVICH,JONG SOO	
PI	CHOI	
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ACCESSION	AY226096	
VERSION	AY226096.1 GI:29293692	
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KEYWORDS	LOCUS	REFERENCE	FEATURES	ORIGIN	LOCUS	REFERENCE	FEATURES	ORIGIN
<p>NECTRIA haematococca</p> <p>Nectria haematococca</p> <p>Euxaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.</p> <p>1 (bases 1 to 298)</p> <p>Millar,B.C., Xu,J. and Moore,J.E.</p> <p>Direct Submission</p> <p>Submitted (28-JUN-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK</p> <p>Location/Qualifiers</p> <p>1..298</p> <p>/organism="Nectria haematococca"</p> <p>/mol_type="genomic DNA"</p> <p>/strain="260499/24"</p> <p>/db_xref="taxon:140110"</p> <p><1..132</p> <p>/product="5.8S ribosomal RNA"</p> <p>133..245</p> <p>/product="internal transcribed spacer 2"</p> <p>246..>298</p> <p>/product="28S ribosomal RNA"</p>	<p>Query Match</p> <p>Best Local Similarity 100.0%; Score 21; DB 8; Length 298;</p> <p>Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>1 CTACACCTCGCAACTGAGA 21</p> <p> </p> <p>195 CTACACCTCGCAACTGAGA 215</p>	<p>Query Match</p> <p>Best Local Similarity 100.0%; Score 21; DB 6; Length 319;</p> <p>Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>1 CTACACCTCGCAACTGAGA 21</p> <p> </p> <p>222 CTACACCTCGCAACTGAGA 242</p>				

ORGANISM Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 319)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other
filamentous fungi
Patent: JP 2001525665-A 6 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O
CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND
PREVENTION TECHNOLOGY TRANSFER OFFICE
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PD 11-DEC-2001
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PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
PI CHOI
PC C12Q1/68
CC Strandedness: Single;
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Db 222 CTAACACCTCGCAACTGGAGA 242
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DEFINITION internal transcribed spacer 2, complete sequence; and 28S ribosomal
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ACCESSION AF117921
VERSION AF117921.1 GI:8570107
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SOURCE Fusarium solani
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 319)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
Rapid differentiation of filamentous fungi using species-specific
DNA probes
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE 2 (bases 1 to 319)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
TITLE Direct Submission
AUTHORS Choi,J.S., Westerman,J.M. and Morrison,C.J.
JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA
JOURNAL
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ACCESSION AY426972.1 GI:38018121
VERSION AY426972.1
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 468)
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.
and Zhang,Z.Q.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium sp. from
vanilla plantation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 468)
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.
and Zhang,Z.Q.
TITLE Direct Submission
AUTHORS Submitted (02-OCT-2003) Department of Plant Pathology, Yunnan
Agricultural University, Longtuo Street, Kunming, Yunnan 650201, P.
R. China
JOURNAL
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DEFINITION 5.8S ribosomal RNA gene, complete sequence; internal transcribed
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ACCESSION AF161222
VERSION AF161222.1 GI:6941832
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ORGANISM Fusarium solani
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
AUTHORS 1 (bases 1 to 471)
TITLE Grunden, E., Chen, W., and Crane, J. L.
JOURNAL Fungi Colonizing Microclerotia of Verticillium dahliae
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 471)
TITLE Grunden, E., Chen, W., and Crane, J. L.
JOURNAL Direct Submission
TITLE Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural
History Survey, IL Dept. Natural Resources, 607 E. Peabody Dr.,
Champaign, IL 61820, USA
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VERSION AY043472.1 GI:15450333
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE rDNA sequence variability in Fusarium solani populations associated
with eumattii wilt and dry rot of potato in Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Submitted (03-JUN-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil
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VERSION AY043473.1 GI:15450334
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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REFERENCE 1 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE rDNA sequence variability in Fusarium solani populations associated
with eumattii wilt and dry rot of potato in Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Submitted (03-JUN-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil
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Db 60 CTACACCTCGCACTGGAGA 40
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ACCESSION AY043478
VERSION AY043478.1 GI:15450339
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ORGANISM Fusarium solani (anamorph: Fusarium solanii)
Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE rDNA sequence variability in Fusarium solani populations associated

with eumartii wilt and dry rot of potato in Brazil

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
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Brazil

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Db 59 CTAACACCTCGCACTGGAGA 39

RESULT 12
FSU38558 477 bp DNA linear **PLN 08-NOV-1995**
LOCUS Fusarium solani 5.8S ribosomal RNA gene, complete sequence and
DEFINITION Internal transcribed spacers 1 and 2.
ACCESSION U38558
VERSION U38558.1 GI:1054930
KEYWORDS

SOURCE

ORGANISM

Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 477)
AUTHORS Duggal, A.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1995) Arti Duggal, Forestry, Univ. of Toronto, 33
Willcocks St., Toronto, Ont. M5S 3B3, Canada

FEATURES
source
Location/Qualifiers
1..477
/organism="Fusarium solani"
/mol_type="genomic DNA"
/db_xref="taxon:169388"
1..150
/note="internal transcribed spacer 1; ITS1"
151..306
/product="5.8S ribosomal RNA"
307..477
/note="internal transcribed spacer 2; ITS2"

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 477;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGGAGA 21
|||||
Db 418 CTAACACCTCGCACTGGAGA 438

RESULT 13
AF132801 478 bp DNA linear PLN 20-JAN-2000
LOCUS Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal
DEFINITION RNA, and internal transcribed spacer 2, complete sequence.

ACCESSION AF132801
VERSION AF132801.1 GI:4809015
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 478)
AUTHORS Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
TITLE Molecular Identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
JOURNAL Plant Dis. 84 (1), 83-89 (2000)
2 (bases 1 to 478)
Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.
Direct Submission
Submitted (03-MAR-1999) Plant Pathology, Iowa State University,
Room 351 Bessey Hall, Ames, IA 50011, USA

FEATURES
source
Location/Qualifiers
1..478
/organism="Fusarium solani"
/mol_type="genomic DNA"
/isolate="P185"
/specific_host="Glycine max"
/db_xref="taxon:169388"
/tissue_type="mycelium"
/country="USA: Iowa, Lee County"
1..149
/product="internal transcribed spacer 1"
/note="ITS1"
150..306
/product="5.8S ribosomal RNA"
307..478
/product="internal transcribed spacer 2"
/note="ITS2"

misc_RNA

RNA

misc_RNA

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGGAGA 21
|||||
Db 419 CTAACACCTCGCACTGGAGA 439

RESULT 14
AF150459 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150459
VERSION AF150459.1 GI:7650157
KEYWORDS

SOURCE

ORGANISM

Nectria haematococca
Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Hyakumachi, M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
2 (bases 1 to 478)
Suga, H., Hyakumachi, M. and Kageyama, K.
Direct Submission
Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan

FEATURES
source
Location/Qualifiers
1..478
/organism="Nectria haematococca"
/mol_type="genomic DNA"
/strain="K-1"

/db xref="taxon:140110"
 /note="anamorph: Fusarium solani"
 1. .149
 /product="internal transcribed spacer 1"
 150. .307
 /product="5.8S ribosomal RNA"
 308. .478
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21
 |||||
 Db 419 CTACACCTCGCACTGGAGA 439

RESULT 15

AF150460 478 bp DNA linear PLN 05-JAN-2001
 LOCUS Nectria haematococca strain FI internal transcribed spacer 1, 5.8S
 DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
 sequence.

ACCESSION AF150460
 VERSION AF150460
 KEYWORDS AF150460.1 GI:7650158

SOURCE

Nectria haematococca
 Nectria haematococca
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE

1 (bases 1 to 478)
 Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
 Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
 based on the rDNA-ITS region
 Mycol. Res. 104 (10), 1175-1183 (2000)

JOURNAL

2 (bases 1 to 478)
 Suga,H., Hyakumachi,M. and Kageyama,K.
 Direct Submission
 Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
 University, Gifu 501-1112, Japan
 Location/Qualifiers

FEATURES

source
 1. .478
 /organism="Nectria haematococca"
 /mol_type="genomic DNA"
 /strain="FI"
 /db_xref="taxon:140110"
 /note="anamorph: Fusarium solani"
 1. .149
 /product="internal transcribed spacer 1"
 150. .307
 /product="5.8S ribosomal RNA"
 308. .478
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21
 |||||
 Db 419 CTACACCTCGCACTGGAGA 439

Search completed: October 1, 2004, 05:17:03
 Job time : 172.543 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 37.2571 Seconds
(without alignments)
2394.501 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21
Sequence: 1 ctaacactcgcactgagaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002s:*
7: geneeqn2003as:*
8: geneeqn2003bs:*
9: geneeqn2003cs:*
10: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	2	AAV83698 Species-s
2	21	100.0	319	2	AAV70850 Internal
3	19	90.5	502	3	AA61893 Fusarium
4	19	90.5	561	2	AAV59009 F. avenac
5	19	90.5	659	6	ABV78724 C. sinens
6	17	81.0	510	3	AA637182 Arabidops
7	17	81.0	2706	3	AA645891 Arabidops
8	16.2	77.1	1144	5	ADD44826 Rat gene
9	16.2	77.1	33769	5	ABA82622 Human HBM
10	16.2	77.1	33769	7	ABK22781 Human hlg
11	16.2	77.1	33769	7	ACC45363 Human HBM
12	16.2	77.1	33769	9	ADB82432 HBM-relat
13	16.2	77.1	33769	9	ADB82432 Human DNA
14	16	76.2	1118	6	ABQ45159 Oligonuc
15	16	76.2	1118	6	ABQ45158 Oligonuc
16	15.8	75.2	879	7	ACA45356 Prokaryot
17	15.8	75.2	1399	4	ABL09973 Drosophi
18	15.8	75.2	1815	4	ABL02877 Drosophi
19	15.8	75.2	3399	4	ABL09972 Drosophi
20	15.8	75.2	3405	6	AA595263 long term
21	15.8	75.2	3947	4	ABL02976 Drosophi
22	15.8	75.2	4394	4	ABL08778 Drosophi
23	15.8	75.2	4494	7	ADA70422 Rice gene

24	15.8	75.2	4763	4	ABL08780 Drosophi
25	15.4	73.3	989	4	ABL18503 Prokaryot
26	15.4	73.3	1110	7	ACA37427 Prokaryot
27	15.4	73.3	1260	4	ABL11645 Drosophi
28	15.4	73.3	1388	9	AD658528 Human gen
29	15.4	73.3	1388	9	ADD47423 Human gen
30	15.4	73.3	1884	4	AA553358 Staphyloc
31	15.4	73.3	2034	7	ABV73338 M. sexta
32	15.4	73.3	2310	4	AA552105 Staphyloc
33	15.4	73.3	2787	7	ACT73619 Staphyloc
34	15.4	73.3	2790	4	AA554538 Staphyloc
35	15.4	73.3	2790	4	AA555168 Staphyloc
36	15.4	73.3	2790	7	ACA19827 Prokaryot
37	15.4	73.3	2853	4	ABL15238 Drosophi
38	15.4	73.3	3061	4	ABL18502 Drosophi
39	15.4	73.3	3433	4	ABL11644 Drosophi
40	15.4	73.3	3713	4	ABL15001 Drosophi
41	15.4	73.3	4676	4	ABL08318 Drosophi
42	15.4	73.3	6325	4	ABL06620 Drosophi
43	15.4	73.3	2955	2	AAV74517 Staphyloc
44	15.4	73.3	36181	9	ADB74371 Mycobacte
45	15.4	73.3	38494	9	ADB74275 Mycobacte

ALIGNMENTS

RESULT 1	AAV83698	standard; DNA; 21 BP.
ID	AAV83698	
XX	AAV83698;	
XX	26-FEB-1999	(first entry)
DT	Species-specific probe targeted to the internal transcribed spacer 2.	
DE	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;	
XX	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;	
XX	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;	
XX	M. circinellioideus F. circinellioideus; Rhizopus oryzae; R. microsporus;	
XX	R. circinans; R. stolonifer; Rhizomucor pusillus; Abidia corymbifera;	
XX	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;	
XX	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.	
XX	Synthetic.	
OS	Fusarium solani.	
XX	Key	Location/Qualifiers
FT	modified_base	1 /tag= a
FT		/note= "labelled with digoxigenin"
XX	W09850584-A2.	
XX	12-NOV-1998.	
XX	01-MAY-1998;	98WO-US008926.
XX	02-MAY-1997;	97US-0045400P.
XX	(USSH)	US DEPT HEALTH & HUMAN SERVICES.
XX	Morrison CJ, Reiss E, Aldorevich L, Choi JS;	
XX	WPI, 1999-034737/03.	
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.	
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,	
XX	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix	
XX	species.	
PS	Example 1; Page 22; 45pp; English.	

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
 CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
 CC are species-specific, and can be used for identifying a species selected
 CC from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,
 CC *M. indicus*, *M. circinellioidei*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abisidia*
 CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*
 CC *schenkii*. The probes can be used for differentiating filamentous fungal
 CC species from each other and from other medically important fungi
 XX

Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGAGAGA 21
 Db 1 CTAACACCTCGCAACTGAGAGA 21

RESULT 2
 ID AAV70850 standard; DNA; 319 BP.
 XX AAV70850;
 AC 26-FEB-1999 (first entry)
 XX

Internal transcribed spacer 2 (ITS2) and adjacent regions.

XX Internal transcribed spacer 2; ITS2; probe: *Aspergillus flavus*; *A. niger*;
 KM *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*;
 KM *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;
 KM *M. circinellioidei*; *Rhizopus oryzae*; *R. microsporus*;
 KM *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abisidia corymbifera*;
 KM *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;
 KM *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.
 XX

Fusarium solani.
 OS
 XX
 PN MO9850584-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 01-MAY-1998; 98WO-US008926.
 XX
 PR 02-MAY-1997; 97US-0045400P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Morrison CJ, Reiss E, Aidorevich L, Choi JS;
 PT WPI; 1999-034737/03.
 DR
 XX
 PT New nucleic acid probes for filamentous fungi - for detecting e.g.
 PT *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abisidia*,
 PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*
 PT species.
 XX
 PS
 XX Claim 1; Page 12; 45pp; English.

The present sequence represents an internal transcribed spacer 2 (ITS2)
 CC and adjacent regions. Probes can be derived from the present sequence
 CC which are species-specific. The specification also describes ITS2
 CC sequence-derived probes for identifying a species selected from
 CC *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,
 CC *M. indicus*, *M. circinellioidei*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abisidia*
 CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*
 CC *schenckii*. The probes can be used for differentiating filamentous fungal
 CC species from each other and from other medically important fungi
 XX

CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*
 CC *schenckii*. The probes can be used for differentiating filamentous fungal
 CC species from each other and from other medically important fungi
 XX

Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 0.77; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCAACTGAGAGA 21
 Db 222 CTAACACCTCGCAACTGAGAGA 242

RESULT 3
 ID AAA61893 standard; DNA; 502 BP.
 XX AAA61893;
 AC 15-SEP-2003 (revised)
 DT 14-NOV-2000 (first entry)
 XX

Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
 DE
 XX
 XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
 KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
 KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
 KM symptomatic infection; asymptomatic infection; potential HIV exposure;
 KM combination therapy; ds.
 XX

Fusarium sp. MF6381.
 OS
 XX
 PN WO200036132-A1.
 XX
 PD 22-JUN-2000.
 XX
 PF 09-DEC-1999; 99WO-US029356.
 XX
 PR 14-DEC-1998; 98US-0112168P.
 XX
 PA (MERCK) MERCK & CO INC.
 XX
 PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
 PT Dombrowski AW;
 PT WPI; 2000-431606/37.
 DR
 XX
 PT New steroid compounds are HIV integrase inhibitors used for treating HIV
 PT infection and AIDS.
 XX
 PS Disclosure; Page 14; 113pp; English.

The invention relates to novel steroid compounds derived from the African
 CC soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of
 CC HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381.
 CC The invention also relates to a composition comprising a compound of the
 CC invention in combination with an AIDS antiviral agent, an immunomodulator
 CC and an anti-infective agent. The compounds of the invention may be used in
 CC the inhibition of HIV integrase and in the prevention and treatment of
 CC HIV infection. A wide range of state of HIV infection may be treated:
 CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
 CC both symptomatic and asymptomatic HIV infection; and actual or potential
 CC exposure to HIV. The compounds may be used to isolate HIV integrase
 CC mutants which are potentially useful as screening tools for antiviral
 CC compounds. The compounds may also be used to establish or determine the
 CC site at which other antivirals bind to HIV integrase (e.g., by
 CC competitive inhibition). The present sequence represents the ribosomal
 CC DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp.
 CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
 CC to standardise OS field)


```

XX SQ Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match 90.5%; Score 19; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAACCTCGCAACTGGA 19
Db 410 CTAAACCTCGCAACTGGA 428

RESULT 4
AAVS9009 ID AAVS9009 standard; DNA; 561 BP.
XX AC AAVS9009;
XX DT 17-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 06-JAN-1999 (first entry)
XX DE F. avenaceum internal transcribed spacer.
XX KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX KW fungal pathogen identification; infection identification; ss.
XX OS Gibberella avenacea.
XX FH Key Location/Qualifiers
XX FT misc_feature 31..181
XX FT /*tag= a
XX FT /note= "ITS1"
XX FT misc_feature 339..504
XX FT /*tag= b
XX FT /note= "ITS2"
XX PN US5827695-A.
XX PD 27-OCT-1998.
XX PF 04-AUG-1997; 97US-00905314.
XX PR 04-AUG-1997; 97US-00905314.
XX PA (NOVS ) NOVARTIS FINANCE CORP.
XX PI Beck JI;
XX DR WPI; 1998-593995/50.
XX PT Wheat pathogen internal transcribed spacer sequences - used as a basis
XX PT of primers for the species-specific polymerase chain reaction detection
XX PS Claim 1; Col 29-30; 20pp; English.
XX CC This sequence represents an internal transcribed spacer (ITS) sequence of
XX CC the invention. The primer pairs, based on the ITS sequences, are used for
XX CC the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX CC pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX CC avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX CC strains of fungi show different symptoms during infection, which may or
XX CC may not be due to infection. Early identification of the strain causing
XX CC the infection allows early, and more specific fungicidal treatment.
XX CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;
Query Match 90.5%; Score 19; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 CTAAACCTCGCAACTGGA 19
Db 445 CTAAACCTCGCAACTGGA 463

RESULT 5
ABV78724 ID ABV78724 standard; rRNA; 659 BP.
XX AC ABV78724;
XX DT 14-JAN-2003 (first entry)
XX DE C. sinensis rRNA sequence #23.
XX KW Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;
XX KW Cordyceps sinensis; ss.
XX OS Cordyceps sinensis.
XX PN JP2002204696-A.
XX PD 23-JUL-2002.
XX PF 12-JAN-2001; 2001JP-00004805.
XX PR 12-JAN-2001; 2001JP-00004805.
XX PA (HEAL-) HEALTRWAY KK.
XX PA (KANE/) KANESHIRO N.
XX DR WPI; 2002-639075/69.
XX PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
XX PT of seeds of Cordyceps sinensis.
XX PS 26; Page 25; 33pp; Japanese.
XX CC The invention relates to a novel base sequence which is part of a fully
XX CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.
XX CC The base sequences can be used for the classification of Cordyceps
XX CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
XX CC invention
XX SQ Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;
Query Match 90.5%; Score 19; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAACCTCGCAACTGGA 19
Db 473 CTAAACCTCGCAACTGGA 491

RESULT 6
AAC37182 ID AAC37182 standard; DNA; 510 BP.
XX AC AAC37182;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16470.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.

```

XX 06-SEP-2000.
PD
XX
PR 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125768P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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PR 18-JUN-1999; 99US-0139750P.
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PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
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PR 09-AUG-1999; 99US-0147493P.
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PR 10-AUG-1999; 99US-0148171P.
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Best Local Similarity	100.0%	Pred. No. 89		
Matches 17	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	37	CACCTCGCACTGGAGA	53	
RESULT 7				
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ID	AAC45891	standard; DNA; 2706 BP.		
XX				
AC	AAC45891;			
XX				
DT	18-OCT-2000	(first entry)		
DE	Arabidopsis thaliana DNA Fragment SEQ ID NO: 48143.			
XX				
KM	Hybridisation assay; genetic mapping; gene expression control;			
XX	protein identification; signal transduction pathway; metabolic pathway;			
KM	promoter; termination sequence; ss.			
XX				
OS	Arabidopsis thaliana.			
XX				
PN	EP1033405-A2.			
XX				
PD	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-00301439.			
XX				
FR	25-FEB-1999; 99US-0121825P.			
XX				
FR	05-MAR-1999; 99US-0123180P.			
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Query Match 81.0%; Score 17; DB 3; Length 2706;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CACCTGCACTGGAGA 21
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Db 20 CACCTGCACTGGAGA 36

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RESULT 8
ADD44826
ID ADD44826 standard; DNA; 1144 Bp.
XX AC ADD44826;
XX DT 29-JAN-2004 (first entry)
XX DE Rat gene Y00311, SEQ ID NO 10257.
XX KW Rat; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX

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DR	WPI; 2003-268312/26.
XX	GENDANK; Y00311.
FT	New composition comprising two or more isolated polypeptides, useful for
PT	preparing a medicament for treating pain in an animal.
PS	
XX	Claim 1; Page: 1017pp; English.
XX	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC	injury (CCI) and spared nerve injury (SN)) in an animal (e.g. gene
CC	therapy). The sequence presented is a rat DNA (shown in Table 2 of the
CC	specification) which encodes one of the polypeptides of the invention
CC	which is differentially expressed during pain. Note: The sequence data
CC	for this patent did not form part of the printed specification, but was
CC	obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
SO	
XX	Sequence 1144 BP; 310 A; 256 C; 291 G; 287 T; 0 U; 0 Other;
QY	
Db	
1	CTAACACCTCGCACTGAGAGA 21
33	CTTAACAACCTCACAAATGGAGA 53
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ID	ABA82622
AB	ABA82622 standard; DNA; 33769 BP.
AC	
XX	ABA82622;
DT	
XX	25-JAN-2002 (first entry)
DE	
XX	Human HBM gene region b527d12-h_contig308G.
KM	
KV	Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW	sequence tagged site; SIS; osteoporosis; osteopathic; gene therapy;
XX	antibense therapy; vaccine; bone disorder; Paget's disease; sclerostosis;
XX	osteomalacia; fibrous dysplasia; ds.
OS	
XX	Homo sapiens.
PN	
XX	WO200177327-A1.
PD	
XX	18-OCT-2001.
PF	
XX	21-JUN-2000; 2000WO-US016951.
PR	
XX	05-APR-2000; 2000US-00543771.
RR	
XX	05-APR-2000; 2000US-00544398.

(GENO-) GENOME THERAPEUTICS CORP.
Càtullì JP, Little RD, Recker RR, Johnson MT,
WPI, 2001-657171/75.

New high bone mass (HBM) and Zmax1 genes and proteins useful for modulating bone mass for the treatment of e.g. osteoporosis.

Claim 51; Page 237-257; 443pp; English.

The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13. The Zmax1 and HBM genes have osteoprotective activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.

AB82028 to AB89700 and AAG68168 to AAG68193 represent sequences used in the exemplification of the present invention

Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 5; Length 33769;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0

1 CTAAACACTCGCACTGGAGA 21
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25831 CTAGCACCTCTCACTGACGA 25851

RESULT 10
ABK22781
ID ABK22781 standard; cDNA; 33769 BP.
AC
XX ABK22781;
DT
XX 09-APR-2002 (first entry)
DE Human high bone mass (HBM) polynucleotide clone #4.
KW Human; mouse; Zmax1, HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
OS Homo sapiens.
XX
XX WO200192891-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016946.
PF
XX 26-MAY-2000; 2000US-00578900.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
PI Carulli JP, Little RD, Recker RR, Johnson MT,
PI WPI, 2002-097784/13.
DR
XX Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX Example 2; Page 259-283; 409pp; English.
XX

CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX

SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 6; Length 33769;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTACACCTCGCACTGAGA 21
DB 25831 CTAGCACCCTCTCACTGAC 25851

RESULT 11
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ID ACCA5363 standard; DNA; 33769 BP.

AC 45363;

DT 02-JUN-2003 (first entry)

DE Human HBM gene fragment #4.

KM Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KM bone size; bone tissue connectivity; bone disease; osteoporosis;
KM osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.

OS Homo sapiens.

PN WO200292764-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014876.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

PI Babilj P, Bex FJ, Yaworsky PJ, Bodine PV;

DR WPI; 2003-129276/12.

XX New transgenic animals (e.g. mice), useful as models for studying bone

XX density modulation, developing drugs for treating or preventing bone

XX diseases (e.g. osteoporosis), or diagnosing diseases characterized by

XX reduced bone density.

XX Example 2; Page 323-334; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high

CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,

CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterized by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX

SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 7; Length 33769;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTACACCTCGCACTGAGA 21
DB 25831 CTAGCACCCTCTCACTGAC 25851

RESULT 12
ADB98063
ID ADB98063 standard; DNA; 33769 BP.

AC 98063;

DT 04-DEC-2003 (first entry)

DE HBM-related clone contig b527d12-h contig308G.

KM Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;

KW bone mass modulation; osteoporosis; human; ds.

OS Homo sapiens.

PN WO200292000-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014877.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;

DR WPI; 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for

XX diagnosing a HBM-like phenotype in a subject and for preparing a

XX composition for modulating bone mass and/or lipid levels in a subject

XX suffering from e.g. osteoporosis.

XX Example 3; SEQ ID NO 8; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and

CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a

CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid

CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence was used to illustrate the invention.

XX Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 9; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGAGAGA 21

DB 25831 CTAGCACCCTCACTGAGACA 25851

RESULT 13
ADE82432 ADE82432 standard; DNA; 33769 BP.

XX ADE82432;

XX 29-JAN-2004 (first entry)

XX Human DNA sequence related to the invention #4.

XX LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory;
XX Antiarthritic; Bone mass disorders; Osteoporosis; hypercalcaemia;
XX hyperostosis; osteogenesis; Wnt signaling; ds.

XX Homo sapiens.

XX WO200292015-A2.

XX 21-NOV-2002.

XX 17-MAY-2002; 2002WO-US015982.

XX 17-MAY-2001; 2001US-0291311P.

XX 01-FEB-2002; 2002US-0353058P.

XX 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX (AMHP) WYETH.

XX Allen K, Anisowicz A, Bhat BM, Damagnez V, Robinson JA,
XX Yaworsky PJ;
XX WPI; 2003-129219/12.

XX Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating
XX lipid levels and/or bone mass, and for in treating bone mass disorders,
XX e.g. osteoporosis, comprises administering a composition which modulates
XX a Dkk activity.

XX Disclosure; SEQ ID NO 8; 173pp; English.

XX The present invention relates to regulating LRP5, LRP6 or HBM activity in
XX a subject comprising administering a composition which modulates a Dkk
XX activity. The method is useful for modulating lipid levels and/or bone
XX mass, and is useful in treating or diagnosing abnormal lipid levels and
XX bone mass disorders, such as osteoporosis, bone fracture, age-related
XX loss of bone, a chondrodysplasia, drug-induced bone disorder, high bone
XX turnover, hypercalcaemia, hyperostosis, osteogenesis, imperforata,
XX osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and
XX rickets. Modulators of Dkk activity are useful for as reagents in
XX studying bone mass and lipid level modulation, in modulating Wnt
XX signaling, or treating Dkk-mediated disorders. The present sequence
XX represents a human DNA sequence related to the invention.

XX Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 9; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGAGAGA 21

DB 25831 CTAGCACCCTCACTGAGACA 25851

RESULT 14

ABQ45159 ABQ45159 standard; DNA; 1118 BP.

XX ABQ45159;

XX 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 31750.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPIDEMIOLOGICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's), and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention

XX Sequence 1118 BP; 389 A; 464 C; 144 G; 121 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 6; Length 1118;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTACACCTCGCAACT 16
 |||||
 DB 396 CTACACCTCGCAACT 411

Search completed: October 1, 2004, 03:41:21
 Job time : 42.2571 secs

RESULT 15
 ABQ45158/c
 ID ABQ45158 standard; DNA; 1118 BP.

XX ABQ45158;

XX 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31749.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

PR 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPICENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

XX Sequence 1118 BP; 121 A; 144 C; 464 G; 389 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 6; Length 1118;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

OY 1 CTACACCTCGCAACT 16
 |||||
 DB 723 CTACACCTCGCAACT 708

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 / Search time 6.92045 Seconds
(without alignments)
1683.989 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaccacctgcacactgagaga 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-09-423-233-51	Sequence 51, Appl
2	21	100.0	319	US-09-423-233-6	Sequence 6, Appl
3	19	90.5	561	US-08-905-314A-24	Sequence 24, Appl
4	15.4	73.3	29555	US-08-956-171E-206	Sequence 206, App
5	15.4	73.3	36181	US-08-311-731A-120	Sequence 120, App
6	15.4	73.3	38494	US-08-311-731A-24	Sequence 134, Appl
7	15.4	73.3	38675	US-08-311-731A-135	Sequence 135, Appl
8	15.2	72.4	1173	US-09-398-858-13	Sequence 13, Appl
9	14.8	70.5	927	US-09-252-991A-6522	Sequence 6522, Ap
10	14.8	70.5	41171	US-08-311-731A-122	Sequence 122, App
11	14.8	70.5	1230025	US-09-198-452A-1	Sequence 1, Appl
12	14.8	70.5	4403765	US-09-103-840A-2	Sequence 2, Appl
13	14.8	70.5	4411529	US-09-103-840A-1	Sequence 1, Appl
14	14.6	69.5	357	US-09-489-039A-5642	Sequence 5642, Ap
15	14.6	69.5	517	US-09-276-531-122	Sequence 123, App
16	14.6	69.5	525	US-09-621-976-2520	Sequence 2520, App
17	14.6	69.5	535	US-09-833-381-881	Sequence 881, App
18	14.6	69.5	804	US-09-833-381-1461	Sequence 1461, App
19	14.6	69.5	1661	US-09-149-476-246	Sequence 246, App
20	14.6	69.5	1766	PCT-US93-00601-1	Sequence 1, Appl
21	14.6	69.5	1765	PCT-US94-07107A-1	Sequence 1, Appl
22	14.6	69.5	1767	US-08-083-945C-1	Sequence 1, Appl
23	14.6	69.5	1784	US-08-554-612C-13	Sequence 13, Appl
24	14.6	69.5	2201	US-09-149-476-245	Sequence 245, App
25	14.6	69.5	2264	US-09-833-381-883	Sequence 883, App
26	14.6	69.5	2337	US-09-489-039A-1284	Sequence 1284, App
27	14.6	69.5	2636	US-08-554-612C-12	Sequence 12, Appl

C 28	14.6	69.5	2898	1	US-08-554-612C-51	Sequence 51, Appl
C 29	14.6	69.5	2909	1	US-08-554-612C-10	Sequence 10, Appl
C 30	14.6	69.5	2909	1	US-08-554-612C-11	Sequence 11, Appl
C 31	14.6	69.5	5613	4	US-09-562-702A-13	Sequence 13, Appl
C 32	14.6	69.5	5613	4	US-09-561-818A-13	Sequence 13, Appl
C 33	14.6	69.5	5613	4	US-09-561-709B-10	Sequence 10, Appl
C 34	14.6	69.5	5843	4	US-08-554-612C-2	Sequence 2, Appl
C 35	14.4	68.6	7796	4	US-09-521-511C-12	Sequence 12, Appl
C 36	14.2	67.6	20	4	US-09-198-452A-4305	Sequence 4305, Ap
C 37	14.2	67.6	402	4	US-09-252-991A-6809	Sequence 6809, Ap
C 38	14.2	67.6	519	4	US-09-252-991A-8273	Sequence 8273, Ap
C 39	14.2	67.6	644	3	US-09-386-493-9	Sequence 9, Appl
C 40	14.2	67.6	654	4	US-09-543-681A-2368	Sequence 2368, Ap
C 41	14.2	67.6	738	4	US-09-252-991A-13238	Sequence 13238, A
C 42	14.2	67.6	837	4	US-09-252-991A-5983	Sequence 5983, Ap
C 43	14.2	67.6	1001	4	US-09-671-317-284	Sequence 284, App
C 44	14.2	67.6	1095	3	US-08-928-383B-3	Sequence 3, Appl
C 45	14.2	67.6	1104	4	US-09-252-991A-6759	Sequence 6759, Ap

ALIGNMENTS

RESULT 1
US-09-423-233-51
Sequence 51, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 21
TYPE: DNA
ORGANISM: Fusarium solani
US-09-423-233-51

Query Match 100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCTCGCACTGAGA 21
Db 1 CTAACCTCGCACTGAGA 21

RESULT 2
US-09-423-233-6
Sequence 6, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-09-423-233-6

Query Match 100.0%; Score 21; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGA 21
Db 222 CTACACCTCGCACTGAGA 242

RESULT 3

US-08-905-314A-24
; Sequence 24, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: DNA (genomic)
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..181
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182..338
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 339..504
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 505..561
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 90.5%; Score 19; DB 1; Length 561;

Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGA 19
Db 445 CTACACCTCGCACTGGA 463

RESULT 4

US-08-956-171E-206/c
; Sequence 206, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-956-171E-206

Query Match 73.3%; Score 15.4; DB 4; Length 29555;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAACACCTCGCACTGG 18
Db 1809 TAACACCTCGCACTGG 1793

RESULT 5

US-08-311-731A-120/c
; Sequence 120, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 36181 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-120

Query Match 73.3%; Score 15.4; DB 4; Length 36181;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AACACCTCGCACTGGA 19
Db 28405 AACACCGCGCAACTGGA 28389

RESULT 6
US-08-311-731A-24/c
Sequence 24, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 38494 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-24

Query Match 73.3%; Score 15.4; DB 4; Length 38494;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CACCTCGCACTGGAGA 21
Db 23279 CACCTCGCACTGGCGA 23263

RESULT 7
US-08-311-731A-135/c
Sequence 135, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 38675 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-135

Query Match 73.3%; Score 15.4; DB 4; Length 38675;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CACCTCGCACTGGAGA 21
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Db 3801 CACCTCGCACTGGAGA 3785

RESULT 8
US-09-398-858-13
; Sequence 13, Application US/09398858
; Patent No. 6518487
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McEliver, John A.
; APPLICANT: Hoelter, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926
; CURRENT APPLICATION NUMBER: US/09/398,858
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
; US-09-398-858-13

Query Match 72.4%; Score 15.2; DB 4; Length 1173;
Best Local Similarity 85.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACTCGCACTGGAG 20
|||||
Db 550 CTAACACTCGCACTGGAG 569

RESULT 9
US-09-252-991A-6522
; Sequence 6522, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 31142
; SEQ ID NO 6522
; LENGTH: 927
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6522

Query Match 70.5%; Score 14.8; DB 4; Length 927;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AACACTCGCACTGGAGA 21
|||||
Db 875 AACACTCGCACTGGAGA 892

RESULT 10
US-08-311-731A-122
; Sequence 122, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
; US-08-311-731A-122

Query Match 70.5%; Score 14.8; DB 4; Length 41171;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACACTCGCACTGGAG 20
|||||
Db 30961 AACACTCGCACTGGAG 30978

RESULT 11
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:

APPLICANT: Grifais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) .. (15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001) .. (30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001) .. (45000)
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature
LOCATION: (300001) .. (315000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (315001) .. (330000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (615001) .. (630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (630001) .. (645000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (645001) .. (660000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

US-09-489-039A-5642

Query Match 69.5%; Score 14.6; DB 4; Length 357;
Best Local Similarity 81.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGA 21
|||
Db 212 CTGACACCCCGCAACCGGAAA 232

RESULT 15

US-09-276-531-122
Sequence 122, Application us/09276531
Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Guejler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276, 531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079, 677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE/DOCKET NUMBER: PA-0008 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 122:

SEQUENCE CHARACTERISTICS:

LENGTH: 517 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGPUT08

CLONE: 2642108

US-09-276-531-122

Search completed: October 1, 2004, 08:06:04
Job time : 26.9205 secs

Query Match 69.5%; Score 14.6; DB 3; Length 517;
Best Local Similarity 81.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGA 21
|||
Db 442 CTAAACTTGTACTGAGA 462

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 85.5213 Seconds
(Without alignments)
1244.847 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaccactcgcaactggaga 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-10-046-955-51	Sequence 51, Appl
2	21	100.0	319	US-10-046-955-6	Sequence 123319,
3	16.2	77.1	403	US-10-424-599-123319	Sequence 123319,
4	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
5	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
6	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
7	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
8	16.2	77.1	894	US-10-437-963-41403	Sequence 41403, A
9	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
10	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
11	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,
12	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
13	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
14	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,

15	16.2	77.1	2985	17	US-10-437-963-99074	Sequence 99074, A
16	16.2	77.1	33769	13 <td>US-10-182-936A-8</td> <td>Sequence 8, Appl1</td>	US-10-182-936A-8	Sequence 8, Appl1
17	16.2	77.1	33769	17 <td>US-10-374-979-8</td> <td>Sequence 8, Appl1</td>	US-10-374-979-8	Sequence 8, Appl1
18	16.2	77.1	33769	17 <td>US-10-731-739-8</td> <td>Sequence 8, Appl1</td>	US-10-731-739-8	Sequence 8, Appl1
19	16.2	77.1	152759	17 <td>US-10-322-281-10</td> <td>Sequence 10, Appl</td>	US-10-322-281-10	Sequence 10, Appl
20	16.2	77.1	156843	13 <td>US-10-087-192-1408</td> <td>Sequence 1408, Ap</td>	US-10-087-192-1408	Sequence 1408, Ap
21	15.8	75.2	341	16 <td>US-10-369-493-23617</td> <td>Sequence 23617, A</td>	US-10-369-493-23617	Sequence 23617, A
22	15.8	75.2	879	13 <td>US-10-282-122A-33226</td> <td>Sequence 33226, A</td>	US-10-282-122A-33226	Sequence 33226, A
23	15.8	75.2	1858	13 <td>US-10-087-192-656</td> <td>Sequence 656, App</td>	US-10-087-192-656	Sequence 656, App
24	15.8	75.2	2571	13 <td>US-10-424-599-95510</td> <td>Sequence 95510, A</td>	US-10-424-599-95510	Sequence 95510, A
25	15.8	75.2	2811	15 <td>US-10-156-761-6673</td> <td>Sequence 6673, Ap</td>	US-10-156-761-6673	Sequence 6673, Ap
26	15.8	75.2	5802	17 <td>US-10-437-963-3724</td> <td>Sequence 3724, Ap</td>	US-10-437-963-3724	Sequence 3724, Ap
27	15.8	75.2	5822	17 <td>US-10-437-963-3724</td> <td>Sequence 3724, Ap</td>	US-10-437-963-3724	Sequence 3724, Ap
28	15.8	75.2	71678	13 <td>US-10-087-192-655</td> <td>Sequence 655, App</td>	US-10-087-192-655	Sequence 655, App
29	15.8	75.2	9025608	15 <td>US-10-156-761-1</td> <td>Sequence 1, Appl1</td>	US-10-156-761-1	Sequence 1, Appl1
30	15.4	73.3	1110	13 <td>US-10-282-122A-25297</td> <td>Sequence 25297, A</td>	US-10-282-122A-25297	Sequence 25297, A
31	15.4	73.3	1884	9 <td>US-09-815-242-8995</td> <td>Sequence 8995, Ap</td>	US-09-815-242-8995	Sequence 8995, Ap
32	15.4	73.3	2034	9 <td>US-09-815-242-8995</td> <td>Sequence 8995, Ap</td>	US-09-815-242-8995	Sequence 8995, Ap
33	15.4	73.3	2310	9 <td>US-09-815-242-8995</td> <td>Sequence 4687, Ap</td>	US-09-815-242-8995	Sequence 4687, Ap
34	15.4	73.3	2790	9 <td>US-09-815-242-8175</td> <td>Sequence 8175, Ap</td>	US-09-815-242-8175	Sequence 8175, Ap
35	15.4	73.3	2790	9 <td>US-09-815-242-8175</td> <td>Sequence 8175, Ap</td>	US-09-815-242-8175	Sequence 8175, Ap
36	15.4	73.3	2790	13 <td>US-10-282-122A-7697</td> <td>Sequence 7697, Ap</td>	US-10-282-122A-7697	Sequence 7697, Ap
37	15.4	73.3	2941	17 <td>US-10-437-963-16977</td> <td>Sequence 16977, A</td>	US-10-437-963-16977	Sequence 16977, A
38	15.4	73.3	29555	8 <td>US-08-781-986A-206</td> <td>Sequence 206, App</td>	US-08-781-986A-206	Sequence 206, App
39	15.4	73.3	29555	13 <td>US-10-329-624-206</td> <td>Sequence 206, App</td>	US-10-329-624-206	Sequence 206, App
40	15.2	72.4	39	13 <td>US-10-252-155-724</td> <td>Sequence 724, App</td>	US-10-252-155-724	Sequence 724, App
41	15.2	72.4	39	13 <td>US-10-252-155-725</td> <td>Sequence 725, App</td>	US-10-252-155-725	Sequence 725, App
42	15.2	72.4	598	16 <td>US-10-027-632-224405</td> <td>Sequence 224405,</td>	US-10-027-632-224405	Sequence 224405,
43	15.2	72.4	630	15 <td>US-10-027-632-224405</td> <td>Sequence 224405,</td>	US-10-027-632-224405	Sequence 224405,
44	15.2	72.4	630	15 <td>US-10-061-043A-32</td> <td>Sequence 32, Appl</td>	US-10-061-043A-32	Sequence 32, Appl
45	15.2	72.4	630	16 <td>US-10-060-634C-32</td> <td>Sequence 32, Appl</td>	US-10-060-634C-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-10-046-955-51

Sequence 51, Application US/10046955

Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the

APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease

APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.

APPLICANT: Reiss, Errol

APPLICANT: Aidorevich, Liliانا

TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

TITLE OF INVENTION: Other Filamentous Fungi

FILE REFERENCE: 6395-62064

CURRENT APPLICATION NUMBER: US/10/046,955

CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US 09/423,233

PRIOR FILING DATE: 2000-06-27

PRIOR APPLICATION NUMBER: PCT/US98/08926

PRIOR FILING DATE: 1998-05-01

PRIOR APPLICATION NUMBER: US 60/045,400

PRIOR FILING DATE: 1997-05-02

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 51

LENGTH: 21

TYPE: DNA

ORGANISM: Fusarium solani

US-10-046-955-51

Query Match 100.0%; Score 21; DB 15; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTACACCTCGCACTGGAGA 21

Db 1 CTAACCTCGCACTGGAGA 21

```
RESULT 2
US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Liliانا
; APPLICANT: Choi, Jong Seo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6
```

```
Query Match 100.0%; Score 21; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CTAACCTCGCACTGGAGA 21
DB 222 CTAACCTCGCACTGGAGA 242

```
RESULT 3
US-10-424-599-123319
; Sequence 123319, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 123319
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82365C.1
US-10-424-599-123319
```

```
Query Match 77.1%; Score 16.2; DB 13; Length 403;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 CTAACCTCGCACTGGAGA 21
DB 107 CTAACGACACCACTGGAGA 127

```
RESULT 4
US-10-027-632-136133
; Sequence 136133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136133
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136133
```

```
Query Match 77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 CTAACCTCGCACTGGAGA 21
DB 55 CTAACCTCGCCCACTGGAGA 75

```
RESULT 5
US-10-027-632-136134
; Sequence 136134, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136134
; LENGTH: 499
```

TYPE: DNA
ORGANISM: Human
US-10-027-632-136134

Query Match 77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGAGA 21
DB 55 CTAACTCCTCCCACTGAGAGA 75

RESULT 6

US-10-027-632-136133
Sequence 136133, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 136133
LENGTH: 499
TYPE: DNA
ORGANISM: Human
US-10-027-632-136133

Query Match 77.1%; Score 16.2; DB 16; Length 499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGAGA 21
DB 55 CTAACTCCTCCCACTGAGAGA 75

RESULT 7

US-10-027-632-136134
Sequence 136134, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 136134
LENGTH: 499
TYPE: DNA
ORGANISM: Human
US-10-027-632-136134

RESULT 8

US-10-437-963-41403/C
Sequence 41403, Application US/10437963
Publication No. US2004012345A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 41403
LENGTH: 894
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_44751C.1
US-10-437-963-41403

Query Match 77.1%; Score 16.2; DB 16; Length 499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGAGA 21
DB 55 CTAACTCCTCCCACTGAGAGA 75

RESULT 9

US-10-027-632-259445
Sequence 259445, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12

```
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 259445
;; LENGTH: 1037
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-259445
```

```
Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CTAACACCTGCACTGGAGA 21
Db 496 CTTACCCCTTGCACTGGAGA 516
```

```
RESULT 10
US-10-027-632-259446
;; Sequence 259446, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 259446
;; LENGTH: 1037
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-259446
```

```
Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CTAACACCTGCACTGGAGA 21
Db 496 CTTACCCCTTGCACTGGAGA 516
```

```
RESULT 11
US-10-027-632-259447
```

```
;; Sequence 259447, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 259447
;; LENGTH: 1037
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-259447
```

```
Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CTAACACCTGCACTGGAGA 21
Db 496 CTTACCCCTTGCACTGGAGA 516
```

```
RESULT 12
US-10-027-632-259445
;; Sequence 259445, Application US/10027632
;; Publication No. US20030204075A9
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 259445
;; LENGTH: 1037
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-259445
```

Query Match 77.1%; Score 16.2; DB 16; Length 1037;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21
|||
Db 496 CTTACCCCTTGCACTGGAGA 516

RESULT 13

US-10-027-632-259446
; Sequence 259446, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259446
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259446

Query Match 77.1%; Score 16.2; DB 16; Length 1037;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21
|||
Db 496 CTTACCCCTTGCACTGGAGA 516

RESULT 14

US-10-027-632-259447
; Sequence 259447, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259447
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259447

Query Match 77.1%; Score 16.2; DB 16; Length 1037;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21
|||
Db 496 CTTACCCCTTGCACTGGAGA 516

RESULT 15

US-10-437-963-99074
; Sequence 99074, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 99074
; LENGTH: 2985
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96920C.1
US-10-437-963-99074

Query Match 77.1%; Score 16.2; DB 17; Length 2985;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21
|||
Db 1071 CTTACTCCTCGCACTGGAGA 1091

Search completed: October 1, 2004, 08:54:03
Job time : 93.5213 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 : Search time 294 Seconds

(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctcaacctcgcaactgagga 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hcc:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_hcc:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_esthum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	84.8	762	29	CE746752 tigr-gss
2	17.4	82.9	540	28	B2896386 NARP9_013
3	17	81.0	606	14	CB256360 81-E01166
4	16.8	80.0	313	29	AG225492 Locust cor

Result No.	Score	Query Match	Length	DB ID	Description
5	16.8	80.0	362	10	BE070797 RC3-BT050
6	16.8	80.0	458	28	AO681735 HS_2142_A
7	16.8	80.0	552	28	AZ191211 SP_1019_A
8	16.8	80.0	586	9	AL955976
9	16.8	80.0	610	12	BM440563
10	16.8	80.0	639	29	CG294089
11	16.8	80.0	646	13	BU47567
12	16.8	80.0	668	13	BU235239
13	16.8	80.0	679	13	BU482142
14	16.8	80.0	784	13	BU311672
15	16.8	80.0	811	13	BU030991
16	16.8	80.0	829	29	CG14705
17	16.8	80.0	883	13	BU142471
18	16.8	80.0	907	28	BZ659389
19	16.8	80.0	951	29	CG14704
20	16.8	80.0	972	29	CNS0777Y
21	16.8	80.0	973	28	CC396411
22	16.8	80.0	1321	12	B1490849
23	16.4	78.1	174	9	AT001540
24	16.4	78.1	300	9	AV179460
25	16.4	78.1	376	9	AV191390
26	16.4	78.1	380	12	BU154339
27	16.4	78.1	394	12	BU125969
28	16.4	78.1	469	10	AW582687
29	16.4	78.1	586	9	AU218666
30	16.4	78.1	587	10	BF619904
31	16.4	78.1	713	28	BH064238
32	16.4	78.1	771	29	CC546447
33	16.4	78.1	787	28	BH061459
34	16.4	78.1	819	28	BH061403
35	16.2	77.1	252	28	AZ468148
36	16.2	77.1	266	9	AV043034
37	16.2	77.1	293	10	BB089128
38	16.2	77.1	323	10	BB572305
39	16.2	77.1	326	28	AQ260963
40	16.2	77.1	349	28	AQ013861
41	16.2	77.1	384	29	CC930150
42	16.2	77.1	430	28	AQ836420
43	16.2	77.1	437	9	AA840330
44	16.2	77.1	439	9	AW081834
45	16.2	77.1	452	10	BF320988

ALIGNMENTS

RESULT 1
LOCUS CE746752 762 bp DNA linear GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000369563878 Dog library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE746752
VERSION CE746752.1 GI:37087099
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org

```

FEATURES
  source
    Class: shotgun.
    Location/Qualifiers
      1..762
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from
        peripheral blood"

ORIGIN
  Query Match
    84.8%; Score 17.8; DB 29; Length 762;
  Best Local Similarity 90.5%; Pred. No. 7.1e+02;
  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
  1 CTACACCTCGCACTGGAGA 21
  ||||| ||||| ||||| |||||
  ||||| ||||| ||||| |||||
  Db
  88 CTACACCTCGCACTGGAGA 108

RESULT 2
BZ896386 540 bp DNA linear GSS 30-JUL-2003
LOCUS
DEFINITION
  NARP9_0137 Na pUC18 Library Natrialba asiatica genomic 5', genomic
  survey sequence.
ACCESSION
  BZ896386
VERSION
  BZ896386.1 GI:33346862
KEYWORDS
  GSS.
SOURCE
  Natrialba asiatica
  Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Natrialba.
  1 (bases 1 to 540)
REFERENCE
  Goer, Y., Roach, J., Glusman, G., Baliga, N.S., Deutsch, K., Pan, M.,
  DasSarma, S., Ng, W.V. and Hood, L.
  Low-pass Sequencing for Microbial Comparative Genomics
  Unpublished (2003)
  Contact: Goer Y
  Institute for Systems Biology
  1441 North 34th Street, Seattle, WA 98103, USA
  Tel: 206 732 1412
  Fax: 206 732 1299
  Email: ygoer@systemsbiology.org
  Seq primer: M13 Forward
  Class: Shotgun.
FEATURES
  source
    Location/Qualifiers
      1..540
        /organism="Natrialba asiatica"
        /mol_type="genomic DNA"
        /strain="ATCC 700177"
        /db_xref="taxon:64602"
        /clone_lib="Na pUC18 Library"
        /note="Vector: pUC18; Site_1: SmaI; A shotgun library was
        constructed from Natrialba asiatica genomic DNA using
        pUC18/SmaI/BAP plasmid"

ORIGIN
  Query Match
    82.9%; Score 17.4; DB 28; Length 540;
  Best Local Similarity 94.7%; Pred. No. 9.9e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  3 AACACCTCGCACTGGAGA 21
  ||||| ||||| ||||| |||||
  ||||| ||||| ||||| |||||
  Db
  323 AACACCTCGCACTGGAGA 341

RESULT 3
CB256360 606 bp mRNA linear EST 06-NOV-2003
LOCUS
DEFINITION
  81-E011664-027-006-A22-T7R MP1Z-ADIS-027 Arabidopsis thaliana cDNA
  clone MP1Zp772A226Q 5-PRIME, mRNA sequence.
ACCESSION
  CB256360

```

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VERSION
  CB256360.1 GI:32881133
KEYWORDS
  Arabidopsis thaliana (thale cress)
SOURCE
  Arabidopsis thaliana
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 606)
REFERENCE
  Schmidt, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
  Mitchell-Olds, T. and Weisshaar, B.
  Large-scale identification and analysis of genome-wide
  single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL
  MEDLINE
PUBMED
  12799357
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 606 Std Error: 0.00
  Plate: 6 Row: A Column: 22
  Seq primer: T7R; CTACACCTCGCACTGGAGA.
  Location/Qualifiers
    1..606
      /organism="Arabidopsis thaliana"
      /mol_type="mRNA"
      /cultivar="Eifel-2 (B1-2)"
      /db_xref="GABI:593758"
      /db_xref="taxon:3702"
      /clone="MP1Zp772A226Q"
      /cissue_type="whole plant"
      /dev_stage="adult plant, mixed stresses"
      /lab_host="E. coli TOP10"
      /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI, cDNA
      library from Arabidopsis thaliana, accession Eifel-2; ten
      week old total plants grown under long-day conditions in
      soil, whole adult plants were treated for 24 hours with
      different stresses: (1) at 4M-0 C in the dark, (2), at 37
      Grad C in the dark, (3) lying in the lab after removing
      from soil, (4) in the greenhouse after wounding leaves
      with a forceps, (5) in the lab watering with a 150 mM
      NaCl solution, (6) at 26 M-0C in the light/UV, equal
      quantities of stressed plant material were pooled; library
      was made at the Max-Planck-Institute for Plant Breeding
      Research, Cologne, Germany; cloning sites SalI-NotI,
      primer sites and orientation:
      T7-Sali-CCACGCGCCG-Sp1me-cDNA-polyA-CC-NotI-Sp6; Note:
      Sequencing granted in the context of the GABI Arabidopsis
      Verbund I: Genetic Diversity. 'Establishment of
      high-efficiency SNP-based mapping tools and development of
      methods for genome-wide mutation detection'. PI: Bernd
      Weisshaar Sequence submission managed by RZPD/GABI-Primary
      database: http://gabi.rzpd.de. This clone is available
      from RZPD; contact RZPD (clone@rzpd.de) for further
      information."

ORIGIN
  Query Match
    81.0%; Score 17; DB 14; Length 606;
  Best Local Similarity 100.0%; Pred. No. 1.6e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  5 CACCTCGCACTGGAGA 21
  ||||| ||||| ||||| |||||
  ||||| ||||| ||||| |||||
  Db
  115 CACCTCGCACTGGAGA 131

RESULT 4
AG225492 313 bp DNA linear GSS 19-JUL-2003
LOCUS
DEFINITION
  Lotus corniculatus var. japonicus DNA, clone: LjB12n04_E, genomic

```


survey sequence.

AG225492
 AG225492.1 GI:26536116
 GSS.

Lotus corniculatus var. japonicus (Lotus japonicus)
 Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
 Lotus.

REFERENCE
 1
 Sato, S., Nakamura, Y. and Tabata, S.
 Lotus japonicus BAC End sequences
 Published Only in Database (2002)
 2 (bases 1 to 313)
 Sato, S.
 Direct Submission
 Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
 The First Laboratory for Plant Gene Research; 2-6-7
 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
 (E-mail: sato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
 Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)
 Location/Qualifiers
 1..313
 /organism="Lotus corniculatus var. japonicus"
 /mol_type="genomic DNA"
 /strain="Miyakojima NC-20"
 /variety="japonicus"
 /db_xref="taxon:34305"
 /clone="LjB12H04.F"
 /clone_lib="genomic BAC library"
 /note="VECTOR: pBelobAC11-synonym: Lotus japonicus"

ORIGIN

Query Match 80.0%; Score 16.8; DB 29; Length 313;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAG 20
 |||||
 Db 234 CTACACCTCGCACTGGAG 215

RESULT 5
 BE070797 362 bp mRNA linear EST 09-JUN-2000
 LOCUS RC3-BT0502-251199-011-b12 BT0502 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE070797
 VERSION BE070797.1 GI:8415443
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 362)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britona, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=ec2=RC3-BT0502-251
 199-011-b12&c3=1999-11-25&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 28
 High quality sequence stop: 362.
 Location/Qualifiers
 1..362
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BT0502"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 80.0%; Score 16.8; DB 10; Length 362;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAG 20
 |||||
 Db 39 CTACCTTCGCACTGGAG 58

RESULT 6
 AO681735 458 bp DNA linear GSS 28-JUN-1999
 LOCUS HS_2142_A2 E04 MR CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=2142 Col=8 Row=I, genomic survey
 sequence.
 ACCESSION AO681735
 VERSION AO681735.1 GI:5257718
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 458)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end web server: http://www.husc.washington.edu
 Plate: 2142 row: I column: 8
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 458.
 Location/Qualifiers
 1..458
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

FEATURES
 source

```

/clone="Plate=2142 Col=8 Row=1"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
E-Coli DH10B"
ORIGIN
Query Match      80.0%; Score 16.8; DB 28; Length 458;
Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTAACACCTCGCACTGGAG 20
    |||||
    439 CTAACACCTCGCACTGGAG 458
RESULT 7
A2191211      552 bp  DNA  linear  GSS 30-AUG-2000
LOCUS
DEFINITION
SP 1019_A1 A04 SP6E Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=1019 Col=7 Row=A, genomic survey sequence.
ACCESSION
A2191211
VERSION
A2191211.1 GI:8374390
KEYWORDS
GSS.
SOURCE
Strongylocentrotus purpuratus
ORGANISM
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 552)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Pouska,A.J., Livingston,B.T.,
Wray,G.A., Ertensohn,C.A., Lehrach,H., Bittlen,R.J., Davidson,E.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
10920195
COMMENT
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1019 Row: A Column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 552.
Location/Qualifiers
1..552
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
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/clone="Plate=1019 Col=7 Row=A"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/notes="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
DH10B"
ORIGIN
Query Match      80.0%; Score 16.8; DB 28; Length 552;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTAACACCTCGCACTGGAG 21
    |||||
    407 CTAACACCTCGCACTGGAG 427
RESULT 8

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AL955976
LOCUS
DEFINITION
AL955976 XGC-gastrula Silurana tropicalis cDNA clone Tga6124m04 5',
mRNA sequence.
ACCESSION
AL955976
VERSION
AL955976.1 GI:25779571
KEYWORDS
EST.
SOURCE
Silurana tropicalis (western clawed frog)
ORGANISM
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 586)
Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
COMMENT
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tga6124m04.plcSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1..586
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="Tga6124m04"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
ORIGIN
Query Match      80.0%; Score 16.8; DB 9; Length 586;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTAACACCTCGCACTGGAG 20
    |||||
    551 CTAACACCTCGCACTGGAG 570
RESULT 9
LOCUS
DEFINITION
BM440563      610 bp  mRNA  linear  EST 01-FEB-2002
pgryn.pK003.h4 Normalized Chicken Reproductive Tract cDNA Library
(pgryn) Gallus gallus cDNA clone pgryn.pK003.h4 5' similar to no
significant hits (plog(p) 4), mRNA sequence.
ACCESSION
BM440563
VERSION
BM440563.1 GI:18471338
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 610)
Cogburn,L.A. and Nys,Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
COMMENT
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335

```

Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers

FEATURES

source

1. 610
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler and layer"
/db_xref="taxon:9031"
/clone="pgrin.pk003.h4"
/sex="Male and Female"
/tissue_type="testis, ovary and oviduct"
/dev_stage="Various stages; embryonic, post-hatch, immature and sexually-mature"
/lab_host="E. coli EMDH10B"
/clone_lib="Normalized Chicken Reproductive Tract cDNA library (pgrin)"
/note="Vector: PCMVSPORT6; library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and oviduct 50% of final RNA pool); single pass sequencing from 5'-end"

ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 610;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TAACACCTCGCACTGAGA 21
|||||
550 TAACACCTCGCAATGAGA 569

RESULT 10

LOCUS CG394089 639 bp DNA linear GSS 25-AUG-2003
DEFINITION CG1B182TV ZM 0.7.1.5 KB Zea mays genomic clone ZMMBM0723N19,
genomic survey sequence.

ACCESSION CG294089
VERSION CG294089.1 GI:34208303

KEYWORDS GSS.
SOURCE

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 639)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utepack, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, V.A., Rohlfing, T.,
Cleck, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSes: OG1B182TV
Contact: Cathy Whitelaw

JOURNAL

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@igr.org
Seq primer: TR
Class: sheared ends.

FEATURES

source

1. 639
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBM0723N19"
/clone_lib="ZM_0.7.1.5_KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 80.0%; Score 16.8; DB 29; Length 639;
Best Local Similarity 90.0%; Pred. No. 2e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TAACACCTCGCACTGAGA 21
|||||
435 TAACACCGAGCACTGAGA 454

RESULT 11

LOCUS BU407567 646 bp mRNA linear EST 27-NOV-2002
DEFINITION 60414084B1 CSEQCHN59 Gallus gallus cDNA clone CHEST973012 5', mRNA
sequence.

ACCESSION BU407567

VERSION BU407567.1 GI:25776623

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE

22335534

PUBMED

12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 10D, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1. 646
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adaptors, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., EMAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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Query Match 80.0%; Score 16.8; DB 13; Length 646;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TAACACCTCGCACTGAGA 21
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286 TAACACCTCGCAATGAGA 305

Db

RESULT 12
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LOCUS BU235239

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DEFINITION 603793039F1 CSEQCHN24 Gallus gallus cDNA clone CHEST759n10 5', mRNA
SEQUENCE
BU235239
BU235239.1 GI:25480437
EST
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 668)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
CURR. BIOL. 12 (22), 1965-1969 (2002)
JOURNAL MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@mist.ac.uk.
location/Qualifiers
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methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and EORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
ORIGIN
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Best Local Similarity 90.0%; Pred. No. 2.1e+03;
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| | | | | | | | | | | | | | | | | | | |
Db 633 TAAGACCTCGCAATGAGAGA 652
RESULT 13 679 bp mRNA linear EST 30-NOV-2002
BU482142 LOCUS
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SEQUENCE
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Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

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REFERENCE 1 (bases 1 to 679)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL CURR. BIOL. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@mist.ac.uk.
location/Qualifiers
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/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST823d10"
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/lab_host="DH10B"
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1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was bluntend, ligated to
NotI adapters, digested with EORI, size-selected, and
cloned into the NotI and EORI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."
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RESULT 14 784 bp mRNA linear EST 28-NOV-2002
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SEQUENCE
BU111672
BU111672.1 GI:25819673
EST
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 784)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL CURR. BIOL. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392

```

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

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synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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ORIGIN

Query Match 80.0%; Score 16.8; DB 13; Length 784;
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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db 717 TAAGACCTCGCAATGGAGA 736

RESULT 15

BU330991

LOCUS

DEFINITION 603870435F1 CSEQCHN65 Gallus gallus cDNA clone CHEST896e9 5', mRNA

ACCESSION

BU330991

KEYWORDS

SOURCE

ORGANISM

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

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Gallus gallus

Gallus gallus

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synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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ORIGIN

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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db 55 TAAGACCTCGCAATGGAGA 74

Search completed: October 1, 2004, 08:01:59
Job time : 302.333 secs

FEATURES

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 146.608 Seconds
(without alignments)
5321.503 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctatgacgcttcgcct 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBank: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vt: *
30: em_hcg_hum: *
31: em_hcg_inv: *
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40: em_hcgo_mus: *
41: em_hcgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	AR206443	AR206443 Sequence
2	18	100.0	18	BD083634	BD083634 Nucleic a
3	16.4	91.1	310	AR206401	AR206401 Sequence
4	16.4	91.1	310	BD083592	BD083592 Nucleic a
5	16.4	91.1	310	AF117922	AF117922 Gibberella
6	16.4	91.1	351	AF162903	AF162903
7	16.4	91.1	392	AF502843	AF502843 Leaf 11tc
8	16.4	91.1	393	AF502789	AF502789 Leaf 11tc
9	16.4	91.1	402	AF502677	AF502677 Leaf 11tc
10	16.4	91.1	418	AF502716	AF502716 Leaf 11tc
11	16.4	91.1	419	AF111060	AF111060 Fusarium
12	16.4	91.1	421	AF430128	AF430128 Fusarium
13	16.4	91.1	421	AF430129	AF430129 Fusarium
14	16.4	91.1	427	AF502877	AF502877 Leaf 11tc
15	16.4	91.1	434	AF243055	AF243055 Ascomycet
16	16.4	91.1	451	AF502788	AF502788 Leaf 11tc
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19	16.4	91.1	457	AF502641	AF502641 Leaf 11tc
20	16.4	91.1	458	AF008562	AF008562 Fusarium
21	16.4	91.1	458	AF502805	AF502805 Leaf 11tc
22	16.4	91.1	462	AF502875	AF502875 Leaf 11tc
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24	16.4	91.1	463	AF493964	AF493964 Calonectr
25	16.4	91.1	463	AF493965	AF493965 Cyindroc
26	16.4	91.1	464	AF261740	AF261740 Calonectr
27	16.4	91.1	466	NGA228662	NGA228662 Nectria g
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32	16.4	91.1	466	NGA228667	NGA228667 Nectria g
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35	16.4	91.1	466	NGA228670	NGA228670 Nectria g
36	16.4	91.1	466	NGA228671	NGA228671 Nectria g
37	16.4	91.1	466	NGA228672	NGA228672 Nectria g
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ALIGNMENTS

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LOCUS AR206443 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6372430.
ACCESSION AR206443
VERSION AR206443.1 GI:21505046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
Morrison,C.O., Reiss,E., Alderevich,L. and Choi,J.Soo.
TITLE Nucleic acids for detecting Aspergillus species and other
filamentous fungi
JOURNAL Patent: US 6372430-A 49 16-APR-2002;

FEATURES
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1 TCTAGTGACGGCTCTCGCT 18

Db
1 TCTAGTGACGGCTCTCGCT 18

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LOCUS
DEFINITION
Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION
BD083634.1 GI:22629244
VERSION
UP 2001525665-A/49.
KEYWORDS
Gibberella fujikuroi
SOURCE
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
1 (bases 1 to 18)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other filamentous fungi
Patent: JP 2001525665-A 49 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
OS Fusarium moniliforme
PN JP 2001525665-A/49
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
PC CHOI
PC C1201/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key

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Location/Qualifiers
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Db
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LOCUS
DEFINITION
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ACCESSION
AR206401
VERSION
AR206401.1 GI:21504992
KEYWORDS
SOURCE
Unknown.

ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 310)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.
Nucleic acids for detecting Aspergillus species and other filamentous fungi
Patent: US 6372430-A 7 16-APR-2002;
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Db
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RESULT 4
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LOCUS
DEFINITION
Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION
BD083592.1 GI:22629202
VERSION
JP 2001525665-A/7.
KEYWORDS
Gibberella fujikuroi
SOURCE
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
1 (bases 1 to 310)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other filamentous fungi
Patent: JP 2001525665-A 7 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
OS Fusarium moniliforme
PN JP 2001525665-A/7
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
PC CHOI
PC C1201/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key

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Db
174 TCTAGTGACGGCTCTCGCT 191

RESULT 5

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 ACCESSION AF117922
 VERSION AF117922.1 GI:8570108
 KEYWORDS
 SOURCE
 ORGANISM *Gibberella fujikuroi*
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; *Gibberella*; *Gibberella fujikuroi* complex.
 1 (bases 1 to 310)
 Choi, J.S., Westerman, J.M. and Morrison, C.J.
 Rapid differentiation of filamentous fungi using species-specific DNA probes
 Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
 2 (bases 1 to 310)
 Choi, J.S., Westerman, J.M. and Morrison, C.J.
 Direct Submission
 Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA
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 Query Match 91.1%; Score 16.4; DB 8; Length 310;
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 TCTACTGACGGTCTCGCT 18
 |||||
 174 TCTAGTGGCGTCTCGCT 191

RESULT 6
 LOCUS AF162903 351 bp DNA linear PLN 04-AUG-1999
 DEFINITION *Fusarium proliferatum* 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
 ACCESSION AF162903
 VERSION AF162903.1 GI:5690392
 KEYWORDS
 SOURCE
 ORGANISM *Fusarium proliferatum*
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; *Gibberella*; *Gibberella fujikuroi* complex.
 1 (bases 1 to 351)
 Min, B.R.
 Direct Submission
 Submitted (28-JUN-1999) BIOLOGY, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
 Location/Qualifiers
 1..351
 /organism="Fusarium proliferatum"
 /mol_type="genomic DNA"
 /strain="6787"
 /db_xref="taxon:42674"

rRNA
 misc_RNA
 rRNA
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 8; Length 351;
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 TCTAGTACCGTCTCGCT 18
 |||||
 195 TCTAGTGGCGTCTCGCT 212

RESULT 7
 AF502843/c 392 bp DNA linear PLN 13-MAY-2002
 LOCUS AF502843/c
 DEFINITION *leaf litter ascomycete strain its332* isolate 1000096451 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AF502843
 VERSION AF502843.1 GI:20531650
 KEYWORDS
 SOURCE
 ORGANISM *leaf litter ascomycete strain its332*
 leaf litter ascomycete strain its332
 Eukaryota; Fungi; Ascomycota.
 1 (bases 1 to 392)
 Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and Dreyfuss, M.M.
 Biogeography of leaf litter fungi
 Unpublished
 2 (bases 1 to 392)
 Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and Dreyfuss, M.M.
 Direct Submission
 Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
 Location/Qualifiers
 1..392
 /organism="leaf litter ascomycete strain its332"
 /mol_type="genomic DNA"
 /strain="its332"
 /isolate="1000096451"
 /specific_host="Prestoea montana"
 /db_xref="taxon:194115"
 /country="Puerto Rico"
 <1..3592
 /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA and internal transcribed spacer 2"

misc_RNA
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 8; Length 392;
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 TCTAGTACCGTCTCGCT 18
 |||||
 51 TCTAGTGGCGTCTCGCT 34

RESULT 8
 AF502789 393 bp DNA linear PLN 13-MAY-2002
 LOCUS AF502789
 DEFINITION *leaf litter ascomycete strain its265* isolate 1000143643 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
 ACCESSION AF502789
 VERSION AF502789.1 GI:20531596

SOURCE	leaf litter ascomycete strain its6265
ORGANISM	leaf litter ascomycete strain its6265
REFERENCE	Eukaryota; Fungi; Ascomycota.
AUTHORS	1 (bases 1 to 393)
TITLE	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
JOURNAL	Biogeography of leaf litter fungi
REFERENCE	2 (bases 1 to 393)
AUTHORS	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
TITLE	Direct Submission
JOURNAL	Submitted (12-Apr-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
FEATURES	Location/Qualifiers
SOURCE	1..393
	/organism="leaf litter ascomycete strain its6265"
	/mol_type="genomic DNA"
	/strain="its6265"
	/isolate="1000143643"
	/specific_host="Prestoea montana"
	/db_xref="taxon:194061"
	/country="Puerto Rico"
	<1..149
	/product="internal transcribed spacer 1"
rRNA	150..304
	/product="5.8S ribosomal RNA"
misc_RNA	305..>393
	/product="internal transcribed spacer 2"
ORIGIN	
Query Match	91.1%; Score 15.4; DB 8; Length 393;
Best Local Similarity	94.4%; Pred. No. 3.3e+02;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 TCTAGTGACGGCTCGCT 18
Dd	1 TTTATGTCGGGTCTGCT 383
RESULT 9	
AF502667	
LOCUS	AF502667 402 bp DNA linear PLN 13-MAY-2002
DEFINITION	Leaf litter ascomycete strain its608 isolate 1000589588 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION	AF502667
VERSION	AF502667.1 GI:20531474
KEYWORDS	'
ORGANISM	leaf litter ascomycete strain its608
SOURCE	leaf litter ascomycete strain its608
REFERENCE	Eukaryota; Fungi; Ascomycota.
AUTHORS	1 (bases 1 to 402)
TITLE	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
JOURNAL	Biogeography of leaf litter fungi
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 402)
TITLE	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.
JOURNAL	Direct Submission
REFERENCE	Submitted (12-Apr-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
FEATURES	Location/Qualifiers
SOURCE	1..402
	/organism="leaf litter ascomycete strain its608"
	/mol_type="genomic DNA"
	/strain="its608"
	/isolate="1000589588"
	/specific_host="Prestiumm alicastrum"
	/db_xref="taxon:193939"

	misc_RNA	<1..120 /product="internal transcribed spacer 1" 121..275 /product="5.8S ribosomal RNA" 276..>402 /product="internal transcribed spacer 2"
ORIGIN		
Query Match	91.1%; Score 16.4; DB 8; Length 402;	
Best Local Similarity	94.4%; Pred. No. 3.3e+02;	
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
CY	1 TCTAGTACGCGTCGCCT 18 	
Db	342 TCTAGTGCGGTCTCCT 359	
RESULT 10		
AF502716	AF502716 418 bp DNA linear PLN 13-MAY-2002	
LOCUS DEFINITION	Leaf litter ascomycete strain its182 isolate 1000011379 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.	
ACCSSION VERSION	AF502716 GI:20531523	
SOURCE KEYWORDS	'leaf litter ascomycete strain its182 leaf litter ascomycete strain its182 Eukaryota; Fungi; Ascomycota.'	
ORGANISM	1 (bases 1 to 418)	
REFERENCE	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreiyfuss,M.M.	
AUTHORS	Bioecography of leaf litter fungi Unpublished	
TITLE JOURNAL	2 (bases 1 to 418)	
REFERENCE	Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreiyfuss,M.M.	
AUTHORS	Direct Submission Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA	
JOURNAL TITLE	Location/Qualifiers	
FEATURES SOURCE	1..418 /organism="leaf litter ascomycete strain its182" /mol_type="genomic DNA" /strain="its182" /isolate="1000011379" /specific_host="Conusarpa panamensis" /db_xref="Taxon:193988" /country="Panama" <1..137 /product="internal transcribed spacer 1" 138..292 /product="5.8S ribosomal RNA" 293..>418 /product="internal transcribed spacer 2"	
ORIGIN		
Query Match	91.1%; Score 16.4; DB 8; Length 418;	
Best Local Similarity	94.4%; Pred. No. 3.3e+02;	
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
CY	1 TCTAGTACGCGTCGCCT 18 	
Db	353 TCTAGTGCGGTCTCCT 370	
RESULT 11		
AF111060	AF111060 419 bp DNA linear PLN 20-JAN-1999	
LOCUS DEFINITION	Fusarium subglutatum var. subglutatum strain BBA62431 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,	

complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF11060
VERSION AF11060.1 GI:4160484
KEYWORDS
SOURCE Fusarium subglutinatum var. subglutinatum
ORGANISM Fusarium subglutinatum var. subglutinatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE
AUTHORS Bulat,S.A., Yli-Mattila,T. and Alekhina,I.A.
TITLE Molecular taxonomy of Fusarium strains by means of ribotyping, rDNA sequencing and UP-PCR analysis. A case study of *Sporotrichiella* section
Unpublished
2 (bases 1 to 419)
Bulat,S.A. and Alekhina,I.A.
Direct Submission
Submitted (03-DEC-1998) Department of Molecular and Radiation Biophysics, Petersburg Nuclear Physics Institute RAS, Gatchina, Leningrad Region 188350, Russia
Location/Qualifiers
1..419
/organism="Fusarium subglutinatum var. subglutinatum"
/mol_type="genomic DNA"
/strain="BBA62431"
/variety="subglutinatum"
/db_xref="taxon:86548"
<1..136
/product="internal transcribed spacer 1"
/note="ITS1"
137..294
/product="5.8S ribosomal RNA"
295..>419
/product="internal transcribed spacer 2"
/note="ITS2"

ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 419;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 TCTAGTGACGCTCGCT 18
|||||
365 TCTAGTGACGCTCGCT 382

RESULT 12
AF430128
LOCUS AF430128 421 bp DNA linear PLN 06-NOV-2002
DEFINITION Fusarium mangiferae strain MRC3477 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AF430128
VERSION AF430128.1 GI:24637153
KEYWORDS
SOURCE Fusarium mangiferae
ORGANISM Fusarium mangiferae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
TITLE Vegetative compatibility and distribution of two *Fusarium* species associated with mango malformation in South Africa
Unpublished
2 (bases 1 to 421)
Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
Direct Submission
Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria,

Gauteng 0002, South Africa
Location/Qualifiers
1..421
/organism="Fusarium mangiferae"
/mol_type="genomic DNA"
/strain="MRC3477"
/db_xref="taxon:192010"
/note="section 1iseola"
<1..24
/product="18S ribosomal RNA"
25..161
/product="internal transcribed spacer 1"
162..320
/product="5.8S ribosomal RNA"
321..>421
/product="internal transcribed spacer 2"

ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 421;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 TCTAGTGACGCTCGCT 18
|||||
387 TCTAGTGACGCTCGCT 404

RESULT 13
AF430129
LOCUS AF430129 421 bp DNA linear PLN 06-NOV-2002
DEFINITION Fusarium mangiferae strain MRC7035 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION AF430129
VERSION AF430129.1 GI:24637154
KEYWORDS
SOURCE Fusarium mangiferae
ORGANISM Fusarium mangiferae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
TITLE Vegetative compatibility and distribution of two *Fusarium* species associated with mango malformation in South Africa
Unpublished
2 (bases 1 to 421)
Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.
Direct Submission
Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria,

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 387 TCTAGTACGCGTCTCGCT 404

RESULT 14
AF502877
LOCUS
DEFINITION
AF502877 427 bp DNA linear PLN 13-MAY-2002
Leaf litter ascomycete strain its389 isolate 1000096987 internal
transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,
complete sequence; and internal transcribed spacer 2, partial
sequence.
AF502877.1 GI:20531684

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
leaf litter ascomycete strain its389
leaf litter ascomycete strain its389
Eukaryota; Fungi; Ascomycota.
1 (bases 1 to 427)
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and
Dreyfus,M.M.
Biogeography of leaf litter fungi
Unpublished
2 (bases 1 to 427)
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and
Dreyfus,M.M.
Direct Submission
Submitted (12-APR-2002) Environmental Studies, University of
California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA
Location/Qualifiers
1..427
/organism="leaf litter ascomycete strain its389"
/mol_type="genomic DNA"
/strain="its389"
/isolate="1000096987"
/specific_host="Prestoea montana"
/db_xref="taxon:194149"
/country="Puerto Rico"
<1..164
/product="internal transcribed spacer 1"
165..319
/product="5.8S ribosomal RNA"
320..>427
/product="internal transcribed spacer 2"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 427;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 380 TCTAGTACGCGTCTCGCT 397

RESULT 15
AY243055
LOCUS
DEFINITION
AY243055 434 bp DNA linear PLN 14-APR-2003
Ascomycete sp. A77 internal transcribed spacer 1, partial sequence;
5.8S ribosomal RNA gene, complete sequence; and internal
transcribed spacer 2, partial sequence.
AY243055
AY243055.1 GI:29826150

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

1
ascomycete sp. A77
ascomycete sp. A77
Eukaryota; Fungi; Ascomycota.
1 (bases 1 to 434)
Beckstead,J. and Parker,I.M.
Invasiveness of *Ammophila arenaria*: Release from soil-borne
pathogens?

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 434)
AUTHORS Gambleta,G., Gilbert,G.S. and Parker,I.M.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2003) Ecology and Evolutionary Biology,
University of California, Santa Cruz, 1156 High St., Santa
Cruz, CA 95064, USA

FEATURES
source
1..434
Location/Qualifiers
1..434
/organism="ascomycete sp. A77"
/mol_type="genomic DNA"
/strain="A77"
/isolation_source="plants grown in greenhouse in
unsterilized soil collected from Sunset State Beach,
California"
/specific_host="Ammophila arenaria"
/db_xref="taxon:227269"
<1..98
/product="internal transcribed spacer 1"
99..247
/product="5.8S ribosomal RNA"
248..>434
/product="internal transcribed spacer 2"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 434;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCGTCTCGCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 323 TCTAGTACGCGTCTCGCT 340

Search completed: October 1, 2004, 05:17:01
Job time : 149.108 secs

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallesheria boydii* (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.

SQ Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTAGTACGCTCGCT 18
1 TCTAGTACGCTCGCT 18

RESULT 2

AAV70851
ID AAV70851 standard; DNA; 310 BP.

AC AAV70851;

DT 17-OCT-2003 (revised)

DT 26-FEB-1999 (first entry)

XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

XX Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *A. fumigatus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallesheria boydii*, *Scedosporium apiospermum*, *Penicillium notatum*, *Sporothrix schenckii*; filamentous fungus; ss.

OS *Gibberella fujikuroi*.

PN W09850584-A2.

XX 12-NOV-1998.

XX 01-MAY-1998; 98WO-US008926.

XX 02-MAY-1997; 97US-0045400P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Morrison CJ, Reiss E, Aldorevich L, Choi JS;

XX WPI, 1999-034737/03.

XX New nucleic acid probes for filamentous fungi - for detecting e.g.

XX *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*,

XX *Cunninghamella*, *Pseudallesheria boydii*, *Penicillium* and *Sporothrix*

XX species.

XX Claim 1; Page 12; 45pp; English.

XX The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*

CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallesheria boydii* (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.
(Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 2; Length 310;
Best Local Similarity 94.4%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTACGCTCGCT 18
174 TCTAGTACGCTCGCT 191

RESULT 3

AAA61893
ID AAA61893 standard; DNA; 502 BP.

AC AAA61893;

DT 15-SEP-2003 (revised)

DT 14-NOV-2000 (first entry)

XX *Fusarium* sp. MF6381 rDNA internal transcribed spacer (ITS) region.

XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469; HIV integrase inhibitor; steroid compound; human immunodeficiency virus; acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex; symptomatic infection; asymptomatic infection; potential HIV exposure; combination therapy; ds.

XX *Fusarium* sp; MF6381.

XX W0200036132-A1.

XX 22-JUN-2000.

XX 09-DEC-1999; 99WO-US029356.

XX 14-DEC-1998; 98US-011268P.

XX (MERI) MERCK & CO INC.

XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;

XX Dombrowski AW;

XX WPI, 2000-431606/37.

XX New steroid compounds are HIV integrase inhibitors used for treating HIV infection and AIDS.

XX Disclosure; Page 14; 113pp; English.

XX The invention relates to novel steroid compounds derived from the African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381. The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator and an anti-infective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic and asymptomatic HIV infection; and actual or potential exposure to HIV. The compounds may be used to isolate HIV integrase mutants which are potentially useful as screening tools for antiviral compounds. The compounds may also be used to establish or determine the site at which other antivirals bind to HIV integrase (e.g., by competitive inhibition). The present sequence represents the ribosomal DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp.

```
CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
CC to standardise OS field)
SQ Sequence 502 BP, 127 A, 144 C, 118 G, 113 T, 0 U; 0 Other;
Query Match          91.1%; Score 16.4; DB 3; Length 502;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18
    |||||
Db 371 TCTAGTACGGCTCTCGCT 388

RESULT 4
ACC50001
ID ACC50001 standard; DNA; 534 BP.
XX
XX ACC50001;
AC
XX
XX 14-JUL-2003 (first entry)
DT
XX Internal transcribed spacer RNA encoding sequence #3.
DE
XX Mitochondria; fungal pathogen; ds.
XX
XX Pasaarium proliferatum.
OS
XX WO2003027635-A2.
XX
XX 03-APR-2003.
PD
XX 19-SEP-2002; 2002MO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX Beck JÜ, Barnett CJ;
PI
XX WPI; 2003-363229/34.
DR
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
XX Claim 5; Page 38-39; 44pp; English.
PS
XX
XX This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX Sequence 534 BP, 135 A, 149 C, 130 G, 120 T, 0 U; 0 Other;
SQ
Query Match          91.1%; Score 16.4; DB 7; Length 534;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18
    |||||
Db 402 TCTAGTACGGCTCTCGCT 419

RESULT 5
ABV78700
ID ABV78700 standard; rRNA; 647 BP.
XX
XX ABV78700;
AC
XX
XX 14-JAN-2003 (first entry)
DT
```

```
XX
XX C. crassispota rRNA sequence #2.
DE
XX Ribosome ribonucleic acid; rRNA; Cordyceps crassispota; classification;
XX Cordyceps sinensis; ss.
XX
XX Cordyceps crassispota.
OS
XX JP2002204696-A.
XX
XX 23-JUL-2002.
PD
XX
XX 12-JAN-2001; 2001JP-00004805.
XX
XX 12-JAN-2001; 2001JP-00004805.
XX
XX (HEAL-) HEALTHWAY KK.
PA
XX (KANE/) KANESHIRO N.
XX
XX WPI; 2002-639075/69.
DR
XX
XX Ribosome RNA gene base sequence of Cordyceps sinensis for classification
XX of seeds of Cordyceps sinensis.
PT
XX 2; Page 12; 33pp; Japanese.
PS
XX
XX The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispota.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. crassispota rRNA sequence of the
CC invention
XX
XX Sequence 647 BP, 166 A, 178 C, 160 G, 143 T, 0 U; 0 Other;
SQ
Query Match          91.1%; Score 16.4; DB 6; Length 647;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18
    |||||
Db 418 TCTAGTACGGCTCTCGCT 435

RESULT 6
AAS16211
ID AAS16211 standard; DNA; 2293 BP.
XX
XX AAS16211;
AC
XX
XX 29-JAN-2002 (first entry)
DT
XX
XX Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
DE
XX Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1; ITS2;
XX 5.8S rRNA; LTB-1027; species differentiation; GA_4; GA_3; GA_7;
XX flowering; fruit cell elongation; apple; pear; grape; fruit;
XX russet control; fungus; ds.
XX
XX Gibberella fujiikuroi.
XX
XX Key Location/Qualifiers
XX
XX misc_feature 1..1774
XX /*tag= a
XX /note= "18S rRNA gene"
XX 1775..1921
XX /*tag= b
XX /note= "ITS1 region"
XX 1922..2078
XX /*tag= c
XX /note= "5.8S rRNA gene"
XX 2079..2243
XX /*tag= d
XX /note= "ITS2 region"
XX
```

```
FT misc_feature 2244. .2293
FT /*tag= e
FT /note= "28S rRNA gene"
XX
XX US6287800-B1.
XX
XX 11-SEP-2001.
XX
XX 23-AUG-2000; 2000US-00645073.
XX
XX 31-AUG-1999; 99US-0151770P.
XX
XX (GALL/) GALLIAZZO J L.
XX (LEEM/) LEE M D.
XX
XX Galliazzo JL, Lee MD;
XX WPI; 2001-662197/76.
XX
XX A new method for producing a mixture of gibberellins from Gibberella
PT fujiikuroi results in high titers of GA4 and GA7 useful to promote
PT flowering and fruit growth in the fruit growing industry.
XX
XX Example 4; Col 9-12; 7yp; English.
XX
XX This sequence represents a genomic DNA sequence containing the 18S rRNA
CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC rRNA sequences from a mutant strain of Gibberella fujiikuroi (LTB-1027) of
CC the invention. This region of DNA is highly variable and can be used for
CC species and strain differentiation. The LTB-1027 mutant produces a
CC mixture of gibberellins which is at least 70 % GA 4 and GA 7.
CC Gibberellins GA 4 and GA 7 promote flowering and fruit cell elongation,
CC and are used by growers of apples, pears and grapes to produce larger
CC fruits and earlier harvests. The mixture of GA_3, GA 4 and GA 7 achieved
CC using the method of this invention should be particularly useful in the
CC apple industry where GA_4 has been found more effective in russet control
CC and in promoting fruit set. This method produces GA_4 and GA_7 in much
CC higher titers than prior art methods
XX
XX Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;
SO
Query Match 91.1%; Score 16.4; DB 4; Length 2293;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTAGTACGGTCTCGCT 18
Db 2145 TCTAGTGGCGGTCTCGCT 2162
RESULT 7
AAC42796
ID AAC42796 standard; DNA; 744 BP.
XX
XX AAC42796;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 36883.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
XX
XX 25-FEB-1999; 99US-0121825P.
PR
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PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
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PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
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PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140623P.
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PR 29-JUN-1999; 99US-0140991P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 14-JUL-1999; 99US-0143624P.
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 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
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 PR 21-JUL-1999; 99US-0145086P.
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 PR 02-AUG-1999; 99US-0146388P.
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 PR 31-AUG-1999; 99US-0151438P.
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 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
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 PR 16-SEP-1999; 99US-0154039P.
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 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
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 PR 04-OCT-1999; 99US-0157117P.

PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
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 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
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 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161982P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162124P.

Query Match 85.6%; Score 15.4; DB 3; Length 744;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CTAGTGACGCTTCGCT 18
 Db 218 CTAGTCCGCTTCGCT 234

RESULT 8
 ACH46296/c
 ID ACH46296 standard; cDNA; 386 BP.
 AC ACH46296;
 AC ACH46296;
 DT 13-OCT-2003 (first entry)
 XX
 XX Human infant brain cDNA #359.
 DE
 XX Human; seq; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS
 XX
 PN US2003073623-A1.
 XX
 PD 17-Apr-2003.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 PR 30-JUL-2001; 2001US-00918995.
 XX
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Dmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX DR WPI; 2003-615964/58.
 XX PT New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX PS Claim 1; SEQ ID NO 33508; 44bp; English.
 XX CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12769-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 CC XX
 SQ Sequence 386 BP; 101 A; 105 C; 116 G; 64 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 8; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 AGTGACGGCTCGCT 18
 |||||
 Db 208 AGTGACGGCTCGCT 194
 RESULT 9
 AD30089/c
 ID AD30089 standard; cDNA; 432 BP.
 XX
 AC AD30089;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human novel cDNA sequence, SEQ ID NO:171.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; antihaememic; anticoagulant; thrombolytic; vulnery;
 KM antifiber; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KM gene therapy; chromosome 6p21.3; gene; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO2003029271-A2.
 PN
 XX 10-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-US030474.
 PF
 XX 24-SEP-2001; 2001US-0324631P.
 PR
 XX (HSE-) HSEB INC.
 PA
 XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QH, Wang J, Wehman T,
 XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Halley-Vicente D, Drmanac RT;

XX DR WPI; 2003-371981/35.
 XX DR P-PSDB; AD301060.
 XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX PS Claim 1; SEQ ID NO 171; 1185bp; English.
 XX CC The invention relates to 971 novel human cDNA sequences (AD329919-
 CC AD30089) and the polypeptides they encode (AD30890-AD301860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention, the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the
 CC invention; methods for the identification of compounds that modulate the
 CC expression or activity of the polynucleotide and/or polypeptide; and 767
 CC config sequences corresponding to the cDNA sequences of the invention
 CC (AD31861-AD32627) and the polypeptides encoded by the configs (AD32628
 CC -AD33394). The nucleic acids and polypeptides of the invention are
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the
 CC identification of mutations responsible for genetic disorders or other
 CC traits, for assessing biodiversity, and in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They are
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's
 CC disease and other neurodegenerative diseases, anaemia, platelet
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 CC cancer. The nucleic acids may also be used as hybridisation probes or
 CC primers, and in the recombinant production of a protein. The polypeptides
 CC are also useful in generating antibodies, as molecular weight markers,
 CC and as food supplements. The present sequence represents a specifically
 CC claimed human cDNA sequence of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC XX
 SQ Sequence 432 BP; 118 A; 113 C; 123 G; 78 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 9; Length 432;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 AGTGACGGCTCGCT 18
 |||||
 Db 123 AGTGACGGCTCGCT 109
 RESULT 10
 ACH4705/c
 ID ACH4705 standard; cDNA; 449 BP.
 XX
 AC ACH4705;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human infant brain cDNA #1138.
 XX
 KM Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KM genome mapping; biodiversity; genetic disorder.
 KM
 XX Homo sapiens.
 OS
 XX US2003073623-A1.
 PN
 XX 17-APR-2003.
 PD

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XX 30-JUL-2001; 2001US-00918995.
PF
XX
XX 30-JUL-2001; 2001US-00918995.
PR
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 34287; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX Sequence 449 BP; 118 A; 124 C; 127 G; 77 T; 0 U; 3 Other;
SQ
XX
XX Query Match 83.3%; Score 15; DB 8; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGTGACGCTCGCT 18
Db 253 AGTGACGCTCGCT 239
XX
XX RESULT 11
ACH13812/c
XX ID ACH13812 standard; cDNA; 473 BP.
XX
XX ACH13812;
AC
XX 13-OCT-2003 (first entry)
DT
XX Human adult brain cDNA #1024.
DE
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS
XX US2003073623-A1.
XX
XX 17-APR-2003.
PD
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX
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```
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 1024; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX Sequence 473 BP; 126 A; 121 C; 145 G; 80 T; 0 U; 1 Other;
SQ
XX
XX Query Match 83.3%; Score 15; DB 8; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGTGACGCTCGCT 18
Db 230 AGTGACGCTCGCT 216
XX
XX RESULT 12
AAT99142/c
XX ID AAT99142 standard; cDNA to mRNA; 1182 BP.
XX
XX AAT99142;
AC
XX 26-MAR-1998 (first entry)
DT
XX S-adenosylmethionine synthase 2 gene.
DE
XX S-adenosylmethionine synthase 2 gene.
KW sam2; ss.
XX
XX Hordeum vulgare.
OS
XX JP09313186-A.
XX
XX 09-DEC-1997.
PD
XX 28-MAY-1996; 96JP-00133406.
XX
XX 28-MAY-1996; 96JP-00133406.
XX
XX (NIOC ) NIPPON OIL CO LTD.
PA
XX WPI; 1998-080077/08.
XX
```

DR P-PSDB; AAW34541.
 XX
 PT S-adenosyl-methionine synthase gene - useful in producing plants
 PT resistant to alkaline soil.
 XX
 PS Claim 5; Page 9-10; 13pp; Japanese.
 CC This sequence represents the S-adenosylmethionine synthase 2 (sam2) gene.
 CC This DNA sequence may be used in a vector to produce plants which are
 CC resistant to alkaline soil
 XX
 SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 2; Length 1182;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TAGTGACGGTCTCGC 17
 |||||
 Db 145 TAGTGACGGTCTCGC 131
 |||||
 RESULT 13
 AAS88320
 ID AAS88320 standard; cDNA; 1596 BP.
 XX
 AC AAS88320;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #24124.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG24133.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 24124; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1596 BP; 405 A; 350 C; 462 G; 379 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 5; Length 1596;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AGTGACGGTCTCGCT 18
 |||||
 Db 1378 AGTGACGGTCTCGCT 1392
 |||||
 RESULT 14
 ADC32008
 ID ADC32008 standard; cDNA; 2139 BP.
 XX
 AC ADC32008;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human novel cDNA contig sequence, SEQ ID NO:2090.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; antianemic; anticoagulant; thrombolytic; valnerary;
 KM antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KM gene therapy; chromosome 6p21.3; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029271-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-US030474.
 XX
 PR 24-SEP-2001; 2001US-0324631P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicente D, Drmanac RT;
 XX
 DR WPI; 2003-371981/35.
 DR P-PSDB; ADC32775.
 XX
 PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX
 PS Example 2; SEQ ID NO 2090; 1185pp; English.
 XX
 CC The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds
(without alignments)
1683.989 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcacgcttcgct 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	4	US-09-423-233-49
2	16.4	91.1	310	4	US-09-423-233-7
3	16.4	91.1	583	1	US-08-652-127C-8
4	16.4	91.1	594	1	US-08-652-127C-5
5	16.4	91.1	2293	3	US-09-645-073-1
6	14.8	82.2	531	1	US-08-652-127C-7
7	14.8	82.2	581	1	US-08-652-127C-6
8	14.4	80.0	1629	4	US-09-252-991A-2042
9	14.4	80.0	1908	4	US-09-252-991A-1914
10	14.4	80.0	4689	1	US-08-471-119A-1
11	14	77.8	636	2	US-08-737-129A-1
12	14	77.8	639	4	US-09-170-769A-1
13	14	77.8	645	4	US-09-170-769A-5
14	14	77.8	666	2	US-08-737-129A-5
15	14	77.8	717	5	PCT-US94-14106-58
16	14	77.8	735	5	PCT-US94-14106-50
17	14	77.8	735	5	PCT-US94-14106-54
18	14	77.8	777	2	US-08-860-882A-25
19	14	77.8	777	4	US-09-011-769A-20
20	14	77.8	798	1	US-08-133-011-99
21	14	77.8	798	1	US-08-322-730A-99
22	14	77.8	798	1	US-08-387-874-71
23	14	77.8	798	1	US-08-383-614-99
24	14	77.8	798	3	US-08-907-739-99
25	14	77.8	798	4	US-09-729-597-99
26	14	77.8	798	5	PCT-US93-08364-71
27	14	77.8	830	1	US-08-133-011-115

c 28	14	77.8	830	1	US-08-322-730A-115	Sequence 115, App
c 29	14	77.8	830	1	US-08-387-874-88	Sequence 88, Appl
c 30	14	77.8	830	3	US-08-383-619-115	Sequence 115, App
c 31	14	77.8	830	3	US-08-907-739-115	Sequence 115, App
c 32	14	77.8	830	4	US-09-729-597-115	Sequence 115, App
c 33	14	77.8	830	5	PCT-US93-08364-88	Sequence 88, Appl
c 34	14	77.8	923	5	PCT-US94-07659-1	Sequence 1, Appl
c 35	14	77.8	1077	4	US-09-489-039A-1514	Sequence 1514, Ap
c 36	14	77.8	1347	6	5455030-2	Patent No. 5455030
c 37	14	77.8	1443	2	US-08-403-853-19	Sequence 19, Appl
c 38	14	77.8	1446	3	US-09-171-945-130	Sequence 130, App
c 39	14	77.8	1572	1	US-08-353-400-23	Sequence 23, Appl
c 40	14	77.8	1632	2	US-08-792-824-8	Sequence 8, Appl
c 41	14	77.8	1641	2	US-08-792-824-5	Sequence 5, Appl
c 42	14	77.8	1672	2	US-08-792-824-2	Sequence 2, Appl
c 43	14	77.8	1797	1	US-08-442-542-17	Sequence 17, Appl
c 44	14	77.8	1797	3	US-08-765-469-17	Sequence 17, Appl
c 45	14	77.8	1800	2	US-08-579-940-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-423-233-49
Sequence 49, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
ORGANISM: Fusarium moniliforme
US-09-423-233-49

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCTAGTACGCTTCGCT 18
Db 1 TCTAGTACGCTTCGCT 18

RESULT 2
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
ORGANISM: Fusarium moniliforme
US-09-423-233-7
Query Match 91.1%; Score 16.4; DB 4; Length 310;
Best Local Similarity 94.4%; Pred. No. 6.3;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18
|||||
Db 174 TCTAGTACGGTCTCGCT 191

RESULT 3

US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match

Best Local Similarity 91.1%; Score 16.4; DB 1; Length 583;
Best Local Similarity 94.4%; Pred. No. 6.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18
|||||
Db 429 TCTAGTACGGTCTCGCT 446

RESULT 4

US-08-652-127C-5
; Sequence 5, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-5

Query Match

Best Local Similarity 91.1%; Score 16.4; DB 1; Length 594;
Best Local Similarity 94.4%; Pred. No. 6.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18
|||||
Db 439 TCTAGTACGGTCTCGCT 456

RESULT 5

US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
; US-09-645-073-1

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 3; Length 2293;
Best Local Similarity 94.4%; Pred. No. 7.5;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18
|||||
Db 2145 TCTAGTACGGTCTCGCT 2162

RESULT 6

US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean

STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-7

Query Match 82.2%; Score 14.8; DB 1; Length 531;
Best Local Similarity 88.9%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTACGGTCTCGCT 18
Db 377 TATAGTGGCGGTCTCGCT 394

RESULT 7
US-08-652-127C-6
Sequence 6, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6

Query Match 82.2%; Score 14.8; DB 1; Length 581;
Best Local Similarity 88.9%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTACGGTCTCGCT 18
Db 427 TATAGTGGCGGTCTCGCT 444

RESULT 8
US-09-252-991A-2042
Sequence 2042, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,768
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2042
LENGTH: 1629
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2042

Query Match 80.0%; Score 14.4; DB 4; Length 1629;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAGTGACGGTCTCGCT 18
Db 440 TACTGACGGTCTCGCT 455

RESULT 9
US-09-252-991A-1914/c
Sequence 1914, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,768
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1914
LENGTH: 1908
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1914

Query Match 80.0%; Score 14.4; DB 4; Length 1908;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAGTGACGGTCTCGCT 18
Db 1286 TACTGACGGTCTCGCT 1271

```
RESULT 10
US-08-471-119A-1
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Letner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoerendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kasenoff, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
; US-08-471-119A-1

Query Match      80.0%; Score 14.4; DB 1; Length 46899;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTAGTACGGTCTCGC 17
Db      15595 CTGTGACGGTCTCGC 15610

RESULT 11
US-08-737-129A-1/c
; Sequence 1, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
```

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; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-737-129A-1
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Query Match      77.8%; Score 14; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GTGACGGTCTCGCT 18
Db      566 GTGACGGTCTCGCT 553
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RESULT 12
US-09-170-769A-1/c
; Sequence 1, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(639)
; US-09-170-769A-1
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```
Query Match      77.8%; Score 14; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GTGACGGTCTCGCT 18
|||||
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Db 590 GTGACGGTCTCGCT 577

RESULT 13

US-09-170-769A-5/c
Sequence 5, Application US/09170769A
Patent No. 6444206
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: LETURCO, Didier
APPLICANT: MORIATRY, Ann
APPLICANT: ULAVITCH, Richard
APPLICANT: TOBIAS, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
FILE REFERENCE: SCRIPI140-3
CURRENT APPLICATION NUMBER: US/09/170,769A
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/070,160
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 645
TYPE: DNA
ORGANISM: Murine
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(645)
OTHER INFORMATION: CDR1=Nucleic acids 85-99; CDR2=Nucleic acids 142-189; CDR3=Nuclei
US-09-170-769A-5

Query Match 77.8%; Score 14; DB 4; Length 645;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGACGGTCTCGCT 18

Db 596 GTGACGGTCTCGCT 583

RESULT 14

US-08-737-129A-5/c
Sequence 5, Application US/08737129A
Patent No. 5885816
GENERAL INFORMATION:
APPLICANT: IKUO FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,129A
FILING DATE: No. 5885816ember 15, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 666 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-737-129A-5

Qy 5 GTGACGGTCTCGCT 18

Db 596 GTGACGGTCTCGCT 583

RESULT 15

PCT-US94-14106-58/c
Sequence 58, Application PC/TUS9414106
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Process for Generating Specific Antibodies
NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..717
PCT-US94-14106-58

Query Match 77.8%; Score 14; DB 5; Length 717;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGACGGTCTCGCT 18

Db 653 GTGACGGTCTCGCT 640

Search completed: October 1, 2004, 08:05:42

Job time : 7.93182 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 73.304 Seconds
(without alignments)
1244.847 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcagcgtctgcgt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues 6681306

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-10-046-955-49	Sequence 49, Appl
2	16.4	91.1	310	US-10-046-955-7	Sequence 7, Appl1
3	16.4	91.1	534	US-09-961-755A-7	Sequence 33508, A
4	15	83.3	386	US-09-918-995-33508	Sequence 34287, A
5	15	83.3	449	US-09-918-995-34287	Sequence 1024, Ap
6	15	82.2	473	US-10-424-599-44516	Sequence 74582, A
7	14.8	82.2	558	US-10-437-963-215234	Sequence 215235, A
8	14.8	82.2	599	US-10-027-632-215234	Sequence 215235, A
9	14.8	82.2	599	US-10-027-632-215235	Sequence 215235, A
10	14.8	82.2	599	US-10-027-632-215235	Sequence 215235, A
11	14.8	82.2	599	US-10-027-632-215235	Sequence 215235, A
12	14.8	82.2	675	US-10-767-701-8208	Sequence 8208, Ap
13	14.8	82.2	675	US-10-767-701-8208	Sequence 82321, A
14	14.8	82.2	3461	US-10-437-963-82321	Sequence 82321, A

15	14.8	82.2	28573	17	US-10-741-601-5769	Sequence 5769, Ap
16	14.8	82.2	60500	13	US-10-087-192-1024	Sequence 1024, Ap
17	14.8	82.2	75839	13	US-10-087-192-1024	Sequence 156, App
18	14.8	82.2	198285	9	US-09-880-107-3814	Sequence 3814, App
19	14.8	82.2	198285	17	US-10-775-169-338	Sequence 338, App
20	14	77.8	479	9	US-09-864-761-25477	Sequence 25477, A
21	14	77.8	489	13	US-10-276-774-270	Sequence 270, App
22	14	77.8	550	9	US-09-864-761-8809	Sequence 8809, Ap
23	14	77.8	613	17	US-10-767-701-24494	Sequence 24494, A
24	14	77.8	662	17	US-10-679-620-81	Sequence 81, Appl
25	14	77.8	676	16	US-10-410-907A-35	Sequence 35, Appl
26	14	77.8	736	14	US-10-006-773-12	Sequence 12, Appl
27	14	77.8	741	16	US-10-251-215-48	Sequence 48, Appl
28	14	77.8	798	16	US-10-273-973-99	Sequence 99, Appl
29	14	77.8	830	16	US-10-273-973-115	Sequence 115, App
30	14	77.8	1056	17	US-10-134-188-30	Sequence 30, Appl
31	14	77.8	1314	9	US-09-903-327A-5	Sequence 5, Appl1
32	14	77.8	1353	17	US-10-679-620-77	Sequence 77, Appl
33	14	77.8	1371	17	US-10-719-642-82	Sequence 82, Appl
34	14	77.8	1383	17	US-10-719-642-95	Sequence 95, Appl
35	14	77.8	1383	17	US-10-719-642-96	Sequence 96, Appl
36	14	77.8	1386	15	US-10-281-479A-21	Sequence 21, Appl
37	14	77.8	1386	15	US-10-286-132A-21	Sequence 21, Appl
38	14	77.8	1398	15	US-10-275-180A-21	Sequence 21, Appl
39	14	77.8	1445	17	US-10-679-620-71	Sequence 71, Appl
40	14	77.8	1446	9	US-09-910-059-130	Sequence 130, App
41	14	77.8	1516	9	US-09-903-327A-1	Sequence 1, Appl1
42	14	77.8	1636	17	US-10-767-701-13810	Sequence 13810, A
43	14	77.8	1671	17	US-10-679-620-85	Sequence 85, Appl
44	14	77.8	1701	9	US-09-815-837-62	Sequence 62, Appl
45	14	77.8	1707	9	US-09-815-837-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-10-046-955-49
Sequence 49, Application US/10046955
Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-49
Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0

1 TCTAGTCAGCAGTCGCT 18
|||||

Db 1 TCTAGTACGCTCTCGCT 18

RESULT 2

US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030128600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Liliانا
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match 91.1%; Score 16.4; DB 15; Length 310;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCTCTCGCT 18
|||||
Db 174 TCTAGTACGCTCTCGCT 191

RESULT 3

US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match 91.1%; Score 16.4; DB 10; Length 534;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCTCTCGCT 18
|||||
Db 402 TCTAGTACGCTCTCGCT 419

RESULT 4

US-09-918-995-33508/C
; Sequence 33508, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33508
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33508

Query Match 83.3%; Score 15; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTGACGCTCTCGCT 18
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Db 208 AGTGACGCTCTCGCT 194

RESULT 5

US-09-918-995-34287/C
; Sequence 34287, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34287
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-34287

Query Match 83.3%; Score 15; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTGACGCTCTCGCT 18
|||||
Db 253 AGTGACGCTCTCGCT 239

RESULT 6

US-09-918-995-1024/C
; Sequence 1024, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995

;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: US/09/235,076
;; PRIOR FILING DATE: 1999-01-20
;; NUMBER OF SEQ ID NOS: 38054
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 1024
;; LENGTH: 473
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(473)
;; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1024

Query Match 83.3%; Score 15; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AGTGACGCTCTCGCT 18
DB 230 AGTGACGCTCTCGCT 216

RESULT 7
US-10-424-599-44516
; Sequence 44516, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 44516
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140197C.1
US-10-424-599-44516

Query Match 82.2%; Score 14.8; DB 13; Length 388;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGCTCTCGCT 18
DB 319 TTTACTGACGCTCTCGCT 336

RESULT 8
US-10-437-963-74582/C
; Sequence 74582, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barabazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 74582
;; LENGTH: 558
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_74754C.1
US-10-437-963-74582

Query Match 82.2%; Score 14.8; DB 17; Length 558;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGCTCTCGCT 18
DB 504 TCTAGACGCTCTCGCT 487

RESULT 9
US-10-027-632-215234
; Sequence 215234, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 215234
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215234

Query Match 82.2%; Score 14.8; DB 13; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGCTCTCGCT 18
DB 206 TCTAGACGCTCTCGCT 223

RESULT 10
US-10-027-632-215235
; Sequence 215235, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215235
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215235
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Query Match      82.2%; Score 14.8; DB 13; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
DB      206 TCTAGAGACGCGTCTGCGCT 223
```

```

RESULT 11
US-10-027-632-215234
; Sequence 215234, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215234
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215234
```

```
Query Match      82.2%; Score 14.8; DB 16; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
DB      206 TCTAGAGACGCGTCTGCGCT 223
```

RESULT 12

```

US-10-027-632-215235
; Sequence 215235, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215235
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215235
```

```
Query Match      82.2%; Score 14.8; DB 16; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
DB      206 TCTAGAGACGCGTCTGCGCT 223
```

```

RESULT 13
US-10-767-701-8208
; Sequence 8208, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; PRIOR FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8208
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS29720_1
US-10-767-701-8208
```

```
Query Match      82.2%; Score 14.8; DB 17; Length 675;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
DB      361 TCTGTGACGCGTCTGCTACT 378
```

RESULT 14

US-10-437-963-82321
 ; Sequence 82321, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Mu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 82321
 ; LENGTH: 3461
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81762C.1
 US-10-437-963-82321

Query Match 82.2%; Score 14.8; DB 17; Length 3461;
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCTAGTGACGGTCTCGCT 18
 |||||
 Db 2359 TCTAGTGATGCTTCTGCT 2376

RESULT 15
 US-10-741-601-5769
 ; Sequence 5769, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO001500
 ; CURRENT APPLICATION NUMBER: US/10/741,601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5769
 ; LENGTH: 28573
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-601-5769

Query Match 82.2%; Score 14.8; DB 17; Length 28573;
 Best Local Similarity 88.9%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCTAGTGACGGTCTCGCT 18
 |||||
 Db 27720 TCTGAGACGGTCTCGCT 27737

Search completed: October 1, 2004, 08:53:45
 Job time : 75.304 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 252 Seconds

(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcagcgtctcgt 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
5: em_estba:*
6: em_estba:*
7: em_estba:*
8: em_estba:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: gb_est7:*
16: em_estom:*
17: em_estom:*
18: em_estom:*
19: em_estom:*
20: em_estom:*
21: em_estom:*
22: em_estom:*
23: em_estom:*
24: em_estom:*
25: em_estom:*
26: em_estom:*
27: em_estom:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	621	14	CF947869
2	16.4	91.1	855	29	CG856355 ZMMBC026
3	16.4	91.1	870	29	CG856546 ZMMBC026
4	16.4	91.1	936	29	CNS03M43

5	16	88.9	714	29	CC623601	CC623601	OGVA230TH
6	16	88.9	784	29	CG416849	CG416849	ZMMBC002
7	16	88.9	817	29	CC623607	CC623607	OGVA230TH
8	16	88.9	955	28	B2819718	B2819718	PUGCC66TD
9	16	88.9	986	28	B2819712	B2819712	PUGCC66TD
10	15.4	85.6	464	14	CA991730	CA991730	HC0455 GI
11	15.4	85.6	481	28	BH625357	BH625357	1007106HO
12	15.4	85.6	486	10	BE784335	BE784335	601473488
13	15.4	85.6	571	14	CD317267	CD317267	SEFPU621.
14	15.4	85.6	626	12	BJ150132	BJ150132	BJ147480
15	15.4	85.6	629	12	BJ147480	BJ147480	BJ147480
16	15.4	85.6	665	29	CG740356	CG740356	ZMMBC019
17	15.4	85.6	670	29	CG807448	CG807448	111808380
18	15.4	85.6	680	29	CC640679	CC640679	OCMCL34TH
19	15.4	85.6	703	9	AU004847	AU004847	AU004847
20	15.4	85.6	710	29	CC640688	CC640688	OCMCL34TV
21	15.4	85.6	718	9	AV398645	AV398645	AV398645
22	15.4	85.6	738	29	CC623422	CC623422	OGJAK42TV
23	15.4	85.6	809	29	CG231200	CG231200	OCMHB17TV
24	15.4	85.6	811	14	CK240384	CK240384	AGENCOURT
25	15.4	85.6	821	28	B2647230	B2647230	OGM020TM
26	15.4	85.6	858	29	CG335667	CG335667	OC0CY21TH
27	15.4	85.6	868	29	CC621659	CC621659	OGUBX24TH
28	15.4	85.6	882	28	B2706123	B2706123	PUBMI90TD
29	15.4	85.6	883	28	CC348570	CC348570	OC0BVB7TV
30	15.4	85.6	930	29	CG186978	CG186978	PUPORX25TB
31	15.4	85.6	1005	12	BG760845	BG760845	602717012
32	15.4	85.6	1311	12	BG757034	BG757034	602710452
33	15	83.3	112	9	AV940706	AV940706	AV940706
34	15	83.3	168	9	AV922948	AV922948	AV922948
35	15	83.3	241	9	AA324668	AA324668	EST7818
36	15	83.3	256	9	AA367189	AA367189	EST78236
37	15	83.3	276	9	AA339193	AA339193	EST74299
38	15	83.3	292	12	BM709519	BM709519	UI-E-CQ1-
39	15	83.3	329	10	AW351943	AW351943	IL5-H7000
40	15	83.3	360	9	AJ464008	AJ464008	AJ464008
41	15	83.3	360	9	AJ464010	AJ464010	AJ464010
42	15	83.3	360	9	AJ467366	AJ467366	AJ467366
43	15	83.3	360	9	AJ468366	AJ468366	AJ468366
44	15	83.3	360	29	TA301E06P	TA301E06P	N49663
45	15	83.3	362	14	N49663	N49663	yv26d12.r1

ALIGNMENTS

RESULT 1
CF947869/c
LOCUS
DEFINITION
UI-D-GC1-aag-p-10-0-UI.81 UI-D-GC1 Alexandrium tamarense cDNA clone
CF947869
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

CF947869 621 bp mRNA linear EST 19-NOV-2003
UI-D-GC1-aag-p-10-0-UI.81 UI-D-GC1 Alexandrium tamarense cDNA clone
CF947869
CF947869.1 GI:38452687
EST.
Alexandrium tamarense
Alexandrium tamarense
Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Gonyaulacaceae;
Alexandrium.
1 (bases 1 to 621)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
Contact: Soares, MB
8889548
97044477
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Provasoli-Guillard National Center for Culture

of Marine Phytoplankton (CCMP)
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Cloning Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/dinoflagellate.html>
 Seq primer: M13 FORWARD
 PolyA=yes

FEATURES

source

Location/Qualifiers
 1. 621
 /organism="Alexandrium tamarense"
 /mol_type="mRNA"
 /strain="CCMP 1598"
 /db_xref="taxon:2926"
 /clone="UI-D-GC1-aag-p-10-0-UI"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_1lb="UI-D-GC1"
 /note="Vector: pT73-Pac (Pharmacia) with a modified
 polylinker. Site 1: EcoR I; Site 2: Not I; UI-D-GC1 is a
 normalized library derived from UI-D-GC0. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TACCTCGAGA. Tissue was obtained from the
 Provasoli-Guillard National Center for Culture of Marine
 Phytoplankton (CCMP).
 TAG TISSUE=Alexandrium tamarense
 TAG LIB=UI-D-GC1
 TAG_SEQ=TACCTCGAGA"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 621;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCTCTCGCT 18
 |||||
 Db 134 TCTTGTACGCTCTCGCT 117

RESULT 2
 CG856355 855 bp DNA linear GSS 19-NOV-2003
 LOCUS ZMMBSC0260G14r ZMMBSC (EcoRI) Zea mays subsp. mays genomic clone

DEFINITION ZMMBSC0260G14 3', genomic survey sequence.
 ACCESSION CG856355
 VERSION CG856355.1 GI:38429068

KEYWORDS
 SOURCE Zea mays subsp. mays (maize)
 ORGANISM Zea mays subsp. mays

REFERENCE
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 1 (bases 1 to 855)
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 Sequencing of the maize genome at PGR (2003c)
 Unpublished (2003)

TITLE
 JOURNAL
 COMMENT Contact: Bharti,A.K.
 Dr. Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6

Class: BAC ends
 High quality sequence start: 527.
 Location/Qualifiers

FEATURES

source

1. 855
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"
 /clone="ZMMBSC0260G14"
 /lab_host="E. coli DH10B"
 /clone_1lb="ZMMBSC (EcoRI)"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 855;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCTCTCGCT 18
 |||||
 Db 803 TCTAGTACGCTCTCGCT 820

RESULT 3
 CG856546 870 bp DNA linear GSS 19-NOV-2003
 LOCUS ZMMBSC0260N11r ZMMBSC (EcoRI) Zea mays subsp. mays genomic clone

DEFINITION ZMMBSC0260N11 3', genomic survey sequence.
 ACCESSION CG856546
 VERSION CG856546.1 GI:38429259

KEYWORDS
 SOURCE Zea mays subsp. mays (maize)
 ORGANISM Zea mays subsp. mays

REFERENCE
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 1 (bases 1 to 870)
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 Sequencing of the maize genome at PGR (2003c)
 Unpublished (2003)

TITLE
 JOURNAL
 COMMENT Contact: Bharti,A.K.
 Dr. Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6

Class: BAC ends
 High quality sequence start: 424.
 Location/Qualifiers

FEATURES

source

1. 870
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"
 /clone="ZMMBSC0260N11"
 /lab_host="E. coli DH10B"
 /clone_1lb="ZMMBSC (EcoRI)"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 870;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGCTCTCGCT 18
 |||||
 Db 788 TCTAGTACGCTCTCGCT 805

RESULT 4
CNS03M43
LOCUS
DEFINITION
Tetracodon nigroviridis genome survey sequence T7 end of clone 03103 of library G from Tetracodon nigroviridis, genomic survey sequence.
936 bp DNA linear GSS 01-SEP-2000

ACCESSION
AL250284.1
VERSION
AL250284.1
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetracodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetracodon.

REFERENCE
AUTHORS
1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fzames,C., Wincker,P., Brotier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE
Estimate of human gene number provided by genome-wide analysis using Tetracodon nigroviridis DNA sequence
JOURNAL
MEDLINE
20296633
PUBMED
10835645

REFERENCE
AUTHORS
2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C., Fzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracodon nigroviridis
JOURNAL
MEDLINE
20359837
PUBMED
10899143

REFERENCE
AUTHORS
3 (bases 1 to 936)
TITLE
Genoscope.
JOURNAL
MEDLINE
20359837
PUBMED
10899143

REFERENCE
AUTHORS
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
TITLE
This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetracodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetracodon.
JOURNAL
MEDLINE
20359837
PUBMED
10899143

FEATURES
source
1..936
/organism="Tetracodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="03103"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG037AE02LPI-end : T7"

ORIGIN
Query Match 91.1%; Score 16.4; DB 29; Length 936;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 TCTAGTGCAGCTCTCGCT 18
|||
168 TCCAGTACGCTCTCGCT 185

RESULT 5
CC623601
LOCUS
DEFINITION
CGVAZ30TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0493E12,
genomic survey sequence.
714 bp DNA linear GSS 19-JUN-2003

ACCESSION
CC623601
VERSION
CC623601.1
KEYWORDS
GSS.
Ze mays
SOURCE
Zea mays

ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 714)
WhiteLAW,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGVZ30TV
Contact: Cathy WhiteLAW
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..714
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0493E12"
/clone_1lb="ZM_0.7_1.5_KB"
/note="Vector: pBCKR-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN
Query Match 88.9%; Score 16; DB 29; Length 714;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
3 TAGTACGCTCTCGCT 18
|||
447 TAGTACGCTCTCGCT 462

RESULT 6
CG416849
LOCUS
DEFINITION
ZMMBMA0026J18f ZMMBc (EcORI) Zea mays subsp. mays genomic clone
ZMMBc0026J18 5', genomic survey sequence.
784 bp DNA linear GSS 22-SEP-2003

ACCESSION
CG416849
VERSION
CG416849.1
KEYWORDS
GSS.
Ze mays subsp. mays (maize)
Ze mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 784)
Bharti,A.K., Young,S., Kavchok,S., Keiser,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PeIR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 407.
Location/Qualifiers
1..784
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"

FEATURES
source

	Query Match	88.9%; Score 16; DB 29; Length 784;
	Best Local Similarity	100.0%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
	Matches 16; Conservative 0; Mismatches 0;	
OY	3 TAGTGACGGTCTCGCT 18 	/cultivar="B73" /sub_species="mays" /db_xref="taxon:4578" /clone="ZMMBBC0026U18" /_lab_host="E. coli DH10B" /_clone_lib="ZMMBBC (ECORI)" /note="Vector: pTRABAC2.1; Site_1: EcoRI; Site_2: EcoRI"
Db	586 TAGTGACGGTCTCGCT 601	
RESULT 7		
LOCUS	CC623607/c	817 bp DNA linear GSS 19-JUN-2003
DEFINITION	OGVAZ30TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0493E12,	
ACCESSION	CC623607	
VERSION	CC623607.1 GI:31990379	
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 817) Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Reitenek,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)	
TITLE	Other_GSSs: OGVAZ30TH	
JOURNAL	Contact: Cathy Whiteley	
COMMENT	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelewc@igr.org Seq primer: TP Class: sheared ends. Location/Qualifiers 1..817 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /_clone="ZMMBMA0493E12" /_clone_lib="ZM 0.7 1.5 KB" /note="Vector: pBOSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	
FEATURES		
source		
ORIGIN		
	Query Match	88.9%; Score 16; DB 29; Length 817;
	Best Local Similarity	100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
	Matches 16; Conservative 0; Mismatches 0;	
OY	3 TAGTGACGGTCTCGCT 18 	
Db	302 TAGTGACGGTCTCGCT 287	
RESULT 8		
LOCUS	BZ819718	955 bp DNA linear GSS 18-MAR-2003
DEFINITION	PUCGCC6TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBT8334L11,	
ACCESSION	BZ819718	
	Genomic survey sequence.	

VERSION	BZ819718.1	GI:29034540
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 955)	
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Rennick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneetzen,J.	
TITLE	Maize Genomics Consortium	
JOURNAL	Unpublished (2003)	
COMMENT	Other GSSs: PUGCC66TB Contact: Cathy Whitelaw	
TIGR	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends.	
FEATURES	location/Qualifiers	
SOURCE	1..955	
	/organism="Zea mays"	
	/mol_type="genomic DNA"	
	/strain="B73"	
	/db_xref="taxon:4577"	
	/clone="ZMMBTA334L11"	
	/clone_1b="ZM 0.6 1.0 KB"	
	/note="Vector: PCR4-T0B0; Site_1: EcoRI; 0.6-1.0 kb high cot selected genomic DNA library"	
ORIGIN		
Query Match	88.9%;	Score 16; DB 28; Length 955;
Best Local Similarity	100.0%;	Pred. No. 2.6e+03;
Matches	16;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	3	TAGTGACGCTCTCGCT 18
Db	658	TAGTGACGCTCTCGCT 673
RESULT 9		
BZ819712/c		
LOCUS	BZ819712	986 bp DNA linear GSS 18-MAR-2003
DEFINITION	PUGCC66TB ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTA334L11,	
ACCSSION	genomic survey sequence.	
VERSION	BZ819712	
KEYWORDS	BZ819712.1	GI:29034534
SOURCE	GSS.	
ORGANISM	Zea mays	
	Zea mays	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 986)	
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Rennick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneetzen,J.	
TITLE	Maize Genomics Consortium	
JOURNAL	Unpublished (2003)	
COMMENT	Other GSSs: PUGCC66TD Contact: Cathy Whitelaw	
TIGR	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TR Class: sheared ends.	
FEATURES	location/Qualifiers	
SOURCE	1..986	

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM0334111"
/clone_1lb="ZM 0.6_1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cor selected genomic DNA library"

ORIGIN

Query Match 88.9%; Score 16; DB 28; Length 986;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TAGTACGGCTCGCT 18
|||||
Db 349 TAGTACGGCTCGCT 334

RESULT 10
LOCUS CA991730 464 bp mRNA linear EST 10-OCT-2003
DEFINITION HC0455 GIBCOBRL CAT. NO. 19643-014 Brassica rapa subsp. pekinensis
CDNA, mRNA sequence.
ACCESSION CA991730
VERSION CA991730.1 GI:37621025
KEYWORDS EST.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 464)
Gao, R.J., Dai, D.P. and Ma, R.C.
Expressed sequence tags of heading leaf during the heading process
of Chinese cabbage
Unpublished (2003)
Contact: Rongcai Ma
Plant Functional Genomics
Beijing Agrobiotechnology Research Center
Haidian District, Ban-jing Rd., Beijing 100089, China
Tel: 86 10 5150 3831
Fax: 86 10 5150 3980
Email: rcma1@yahoo.com
Seq primer: 17
High quality sequence stop: 464
POLYA=No.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

SOURCE

1..464
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="mRNA"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/tissue_type="heading leaf"
/dev_stage="folding stage"
/lab_host="E.coli DH10B(ZIP)"
/clone_1lb="GIBCOBRL CAT. NO. 19643-014"
/note="Vector: pZL1; Site 1: NotI; Site 2: SalI; cDNA
library was constructed by SUPERScriptTM lambda system for
cDNA synthesis and cloning (GIBCOBRL, CAT. NO. 19643-014)."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 464;
Best Local Similarity 94.1%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CTAGTACGGCTCGCT 18
|||||
Db 140 CTAGTACGGCTCGCT 124

RESULT 11
BH625357/c

LOCUS BH625357 481 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007106H02.y1.1007 - Rescuemu Grid H Zea mays genomic, genomic
survey sequence.
ACCESSION BH625357
VERSION BH625357.1 GI:18438608
KEYWORDS GSS.
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 481)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot, V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2237
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1007106 Column: 29
Class: transposon-tagged.

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

SOURCE

1..481
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="1007 - Rescuemu Grid H"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
Rescuemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuemu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'Rescuemu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CTAGTACGGCTCGCT 18
|||||
Db 410 CTAGTACGGCTCGCT 394

RESULT 12
LOCUS BE784335/c 486 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473488F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:387672.6 5',
mRNA sequence.
ACCESSION BE784335
VERSION BE784335.1 GI:10205533
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 486)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE

AUTHORS

TITLE

JOURNAL

	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@biomail.nih.gov Tissue Procurement: DCTD/DTP/gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
	FEATURES	plate: LLM9637 row: 0 column: 21 High quality sequence stop: 180.
	SOURCE	Location/Qualifiers 1..486 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3876716" /tissue_type="large cell carcinoma" /lab_host="DH10B (phage-resistant)" /clone_id="NH_MCC_68" /note="Organ: lung; Vector: pCMV-SPORT6, Site_1: NotI, Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."
OY		2 CTAGGACGGTCGCCT 18
Db		 232 CAAGTACGGTCGCCT 216
RESULT 13		
LOCUS		CDJ17267 571 bp mRNA linear EST 17-SEP-2003
DEFINITION		StrPu621.001629 Sea urchin unfertilised egg cDNA library MPWGP621
ACCESSION		Strongylocentrotus purpuratus cDNA clone
VERSION		MPWGP621G2116/MPI_621_16G21 5', mRNA sequence.
KEYWORDS		CDJ17267
SOURCE		CDJ17267.1 GI:34789328
ORGANISM		EST.
		Strongylocentrotus purpuratus
		Strongylocentrotus purpuratus
		Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
		Echinoidea; Euechinoidea; Echnasea; Echinoidea;
		Strongylocentrotidae; Strongylocentrotus.
REFERENCE		1 (bases 1 to 571)
AUTHORS		Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
TITLE		Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters
JOURNAL		Genome Res. 13 (12), 2736-2746 (2003)
COMMENT		Contact: Poustka AU Laboratory 145, dept. Lehrach Max-Planck-Institut fuer Molekulare Genetik Innesstr.63-73, D-14195 Berlin, Germany Tel: +49 30 8413 1235 Fax: +49 30 8413 1128 Email: poustka@molgen.mpg.de The library was characterised by oligonucleotide fingerprinting (ONP) to reduce sequencing redundancy. According to the ONF procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag-seaurchin/ . cDNA clones and filters are distributed via the Resource Center/Primary

```

Database of the German Human Genome Project (http://www.rzpd.de)
PCR primers
FORWARD: 5' CCCAGCGCTTACCTTTATGCTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACCGCTACTGCGCAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCGGAAATTCCTCCGGGT-3' pSPORT3/86
High quality sequence stop: 571.
Location/Qualifiers
1. 571
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="MPMGp621G2116;MPI 621 16G21"
/tissue_type="whole unfertilised eggs"
/dev_stage="embryonic ohr"
/lab_host="E.coli, XL1 blue"
/clone_id="Sea urchin unfertilised egg cdna library
MPMGp621"
/name="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; Random
primed and directionally cloned in pSPORT1 vector using a
NotI (5'-TGACTGATTCATGATCGGACGGCGCC (T)15-3' and a
SalI 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."

FEATURES
source
ORIGIN
Query Match
Best Local Similarity 94.1%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY
1 TCTAGTACGGCTCTGCG 17
|||||
|||||
|||||
|||||
|||||
Db
507 TCTGTGACGGTCTCGC 491

RESULT 14
BU130132 626 bp mRNA linear EST 23-JAN-2002
LOCUS
DEFINITION
Caenorhabditis elegans cDNA clone YK1039d08 3', mRNA sequence.
ACCESSION
BU130132
VERSION
BU130132.1 GI:18290289
KEYWORDS
EST.
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderae; Caenorhabditis.
REFERENCE
1 (bases 1 to 626)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the C.elegans genome
Unpublished (2002)
TITLE
Unpublished (2002)
JOURNAL
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp.
COMMENT
Location/Qualifiers
1. 626
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="YK1039d08"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_id="unpublished oligo-capped cdna library, C.
elegans L1 stage"

FEATURES
source
ORIGIN
Query Match
Best Local Similarity 88.9%; Score 15.4; DB 14; Length 626;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```


Oy 1 TCTAGTACGGCTCGCT 18
 |||||
 Db 455 TCNAGTACGGGCTCGCT 472

RESULT 15

LOCUS BJI47480

DEFINITION BJI47480 unpublished oligo-capped cDNA library, C. elegans L1 stage

Caenorhabditis elegans cDNA clone yk1251f07 3', mRNA sequence.

ACCESSION BJI47480

VERSION BJI47480.1 GI:18315465

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Search completed: October 1, 2004, 08:01:43
 Job time : 259.333 secs

Oy 1 TCTAGTACGGCTCGCT 18
 |||||
 Db 456 TCNAGTACGGGCTCGCT 473

Query Match 85.6%; Score 15.4; DB 12; Length 629;
 Best Local Similarity 88.9%; Pred. No. 4.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES

SOURCE

REFERENCE

AUTHORS

REFERENCE

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XX Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.

XX Sequence 18 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGCTTCTGAATGTTG 18
1 CCCAAGCTTCTGAATGTTG 18

Db 1 CCCAAGCTTCTGAATGTTG 18

RESULT 2
AAV70851 standard; DNA; 310 BP.

XX AAV70851;
XX 17-OCT-2003 (revised)
DT 26-FEB-1999 (first entry)
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

DE Internal transcribed spacer 2 (ITS2) probe; *Aspergillus flavus*; *A. niger*; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*; *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*; *M. circinilloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*; *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*; *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

XX *Gibberella fujikuroi*.
XX WO9850584-A2.
XX 12-NOV-1998.
XX 01-MAY-1998; 98WO-US008926.
XX 02-MAY-1997; 97US-0045400P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;
PI WPI; 1999-034737/03.
XX New nucleic acid probes for filamentous fungi - for detecting e.g. *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*, *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix* species.
XX Claim 1; Page 12; 45bp; English.

XX The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.

CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.
(Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;

QY 1 CCCAAGCTTCTGAATGTTG 18
1 CCCAAGCTTCTGAATGTTG 18

Db 258 CCCAAGCTTCTGAATGTTG 275

RESULT 3
AAV70850 standard; DNA; 319 BP.

XX AAV70850;
XX 26-FEB-1999 (first entry)
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

DE Internal transcribed spacer 2 (ITS2) probe; *Aspergillus flavus*; *A. niger*; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*; *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*; *M. circinilloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*; *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*; *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

XX *Fusarium solani*.
XX WO9850584-A2.
XX 12-NOV-1998.
XX 01-MAY-1998; 98WO-US008926.
XX 02-MAY-1997; 97US-0045400P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;
PI WPI; 1999-034737/03.
XX New nucleic acid probes for filamentous fungi - for detecting e.g. *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*, *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix* species.
XX Claim 1; Page 12; 45bp; English.

XX The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi.

XX Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCGAATGTTG 18
 |||||
 Db 267 CCCAACTTCGAATGTTG 284

RESULT 4
 ID AAA61893 standard; DNA; 502 BP.
 XX AAA61893;

DT 15-SEP-2003 (revised)
 DT 14-NOV-2000 (first entry)

DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.

KM Ribosomal DNA, rDNA ITS region; internal transcribed spacer; ATCC 74469;
 KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
 KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
 KM symptomatic infection; asymptomatic infection; potential HIV exposure;
 KM combination therapy; de.

OS Fusarium sp; MF6381.

PN WO200036132-A1.

PD 22-JUN-2000.

PF 09-DEC-1999; 99WO-US029356.

PR 14-DEC-1998; 98US-0112168P.

PA (MERI) MERCK & CO INC.

PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
 PI Dombrowski AW;

DR WPI; 2000-431606/37.

PT New steroid compounds are HIV integrase inhibitors used for treating HIV
 PT infection and AIDS.

PS Disclosure; Page 14; 113pp; English.

XX The invention relates to novel steroid compounds derived from the African
 CC soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of
 CC HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381.
 CC The invention also relates to a composition comprising a compound of the
 CC invention in combination with an AIDS antiviral agent, an immunomodulator
 CC and an antineoplastic agent. The compounds of the invention may be used in
 CC the inhibition of HIV integrase and in the prevention and treatment of
 CC HIV infection. A wide range of state of HIV infection may be treated;
 CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
 CC both symptomatic and asymptomatic HIV infection; and actual or potential
 CC exposure to HIV. The compounds may be used to isolate HIV integrase
 CC mutants which are potentially useful as screening tools for antiviral
 CC compounds. The compounds may also be used to establish or determine the
 CC site at which other antivirals bind to HIV integrase (e.g., by
 CC competitive inhibition). The present sequence represents the ribosomal
 CC DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp.
 CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
 CC to standardise OS field)

SO Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 502;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCGAATGTTG 18
 |||||
 Db 455 CCCAACTTCGAATGTTG 472

RESULT 5
 ID AAT05401 standard; DNA; 503 BP.
 XX AAT05401;

DT 16-OCT-2003 (revised)
 DT 04-JUN-1996 (first entry)

DE *Fusarium* graminearum internal transcribed spacer sequence.

KM Plant pathogen; fungus; *Septoria nodorum*; *Septoria tritici*; *Fusarium*;
 KM *Pseudocercospora* *hepaticicola*; *Mycosphaerella* *fijiensis*; PCR;
 KM *Mycosphaerella* *musicola*; amplification; primer; ribosomal RNA gene;
 KM internal transcribed region; strain; capture; colourimetric assay;
 KM isolate; development; population; random amplified polymorphic DNA; ss.
 OS *Gibberella* *zeae*.

PN WO9529260-A2.

PD 02-NOV-1995.

PF 19-APR-1995; 95WO-US004712.

PR 25-APR-1994; 94US-00233608.

PA (CIBA) CIBA GEIGY AG.

PI Ligon JM, Beck JJ;

DR WPI; 1995-383005/49.

PT DNA encoding intervening transcribed sequence - used for detection of
 PT plant fungal pathogens.

PS Claim 1; Page 55; 65pp; English.

XX A novel method for the detection of plant pathogenic strains of fungi
 CC e.g. *Septoria nodorum*, *S. tritici*, *Pseudocercospora* *hepaticicola*,
 CC *Mycosphaerella* *fijiensis*, *M. musicola* or *Fusarium* spp. involves the PCR
 CC amplification of sequences found in the internal transcribed region (ITS)
 CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAO94359-93
 CC and AAT05357-72. These primers are derived from the ITS sequences of
 CC these fungi (AAT05394-T05404 and AAO94398) and are strain specific. The
 CC amplification products of the reactions using these primers can be used
 CC with the capture primers AAT05378-93 in colourimetric assays. The primers
 CC and ITS DNAs can be used for the detection of specific fungal pathogen
 CC isolates and in monitoring disease development in plant populations.
 CC (Updated on 16-OCT-2003 to standardise OS field)

SO Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;

Query Match 100.0%; Score 18; DB 2; Length 503;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCGAATGTTG 18
 |||||
 Db 451 CCCAACTTCGAATGTTG 468

RESULT 6
 ID AAV62592 standard; DNA; 503 BP.
 XX AAV62592;
 AC AAV62592;

```

XX 17-OCT-2003 (revised)
DT 17-DEC-1998 (first entry)
XX
DE Fusarium graminearum PCR amplified ITS region consensus DNA sequence.
XX
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
OS Gibberella zeae.
XX
FH Key Location/Qualifiers
FT misc_feature 1..9
FT /tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 10..155
FT /tag= b
FT /note= "ITS 1"
FT misc_feature 156..312
FT /tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 313..466
FT /tag= d
FT /note= "ITS 2"
FT misc_feature 467..503
FT /tag= e
FT /note= "5' end of large subunit rRNA gene"
XX
XX US5814453-A.
XX
XX 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-00887480.
XX
XX 19-APR-1995; 95WO-US004712.
XX 15-OCT-1996; 96US-00722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
XX sequence - used for detecting fungal pathogens in plant tissue.
XX
XX Claim 2; Fig 3; 56pp; English.
XX
XX This represents the consensus DNA sequence of the internal transcribed
XX spacer (ITS) region that was PCR amplified from Fusarium graminearum
XX isolates, R-8417, R-8422 and R-8546. The invention provides a DNA
XX molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX pathogen, where the DNA molecule consists of an ITS sequence selected
XX from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX moniliforme, Septoria avenae or Microdochium nivale. A method for
XX detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX avenaceum and M. nivale isolates is also provided. The method comprises
XX isolating DNA from a plant leaf infected with at least one of the above
XX pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX PCR using specific primers from within these sequences. The pathogen(s)
XX are detected by visualising the amplified part of the ITS sequence.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;
XX
Query Match 100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACTTCTGAATGTTG 18
|||||

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DB 451 CCCACTTCTGAATGTTG 468
RESULT 7
AAVS9029
ID AAVS9029 standard; DNA; 503 BP.
XX
XX AAVS9029;
XX
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
XX F. graminearum internal transcribed spacer.
XX
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX fungal pathogen identification; infection identification; ss.
XX
XX Gibberella zeae.
XX
FH Key Location/Qualifiers
FT misc_feature 10..155
FT /tag= a
FT /note= "ITS1"
FT misc_feature 313..466
FT /tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-593995/50.
XX
XX wheat pathogen internal transcribed spacer sequences - used as a basis
XX for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.
XX
XX Disclosure; Col 23-24; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing
XX the infection allows early, and more specific fungicidal treatment.
XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;
XX
Query Match 100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACTTCTGAATGTTG 18
|||||
DB 451 CCCACTTCTGAATGTTG 468
RESULT 8
AAT05400
ID AAT05400 standard; DNA; 504 BP.

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XX AC AAT05400;
XX XX
XX DT 04-JUN-1996 (first entry)
XX DE Fusarium culmorum internal transcribed spacer sequence.
XX KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
XX KW Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
XX KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
XX KW internal transcribed region; strain; capture; colourimetric assay;
XX KW isolate; development; population; random amplified polymorphic DNA; ss.
XX OS Fusarium culmorum.
XX PN MO9529260-A2.
XX PD 02-NOV-1995.
XX PF 19-APR-1995; 95MO-US004712.
XX PR 25-APR-1994; 94US-00233608.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Ligon JM, Beck JI;
XX DR WPI; 1995-383005/49.
XX PT DNA encoding intervening transcribed sequence - used for detection of
XX PT plant fungal pathogens.
XX PS Claim 1; Page 54-55; 65pp; English.
XX CC A novel method for the detection of plant pathogenic strains of fungi
XX CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,
XX CC Mycosphaerella fijiensis, M. musicola or Fusarium spp. involves the PCR
XX CC amplification of sequences found in the internal transcribed region (ITS)
XX CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AA094359-93
XX CC and AA05357-72. These primers are derived from the ITS sequences of
XX CC these fungi (AAT05394-105404 and AA094398) and are strain specific. The
XX CC amplification products of the reactions using these primers can be used
XX CC with the capture primers AAT05378-93 in colourimetric assays. The primers
XX CC and ITS DNAs can be used for the detection of specific fungal pathogen
XX CC isolates and in monitoring disease development in plant populations
XX SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGATGTTG 18
Db 457 CCCAACTTCTGATGTTG 474

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XX FH Key Location/Qualifiers
XX FT misc_feature 1..12
XX FT /tag= a
XX FT /note= "3' end of small subunit rRNA gene"
XX FT 13..161
XX FT /tag= b
XX FT /note= "ITS 1"
XX FT 162..318
XX FT /tag= c
XX FT /note= "5.8S rRNA gene"
XX FT 319..472
XX FT /tag= d
XX FT /note= "ITS 2"
XX FT 473..504
XX FT /tag= e
XX FT /note= "5' end of large subunit rRNA gene"
XX PN US5814453-A.
XX PD 29-SEP-1998.
XX PF 02-JUL-1997; 97US-00887480.
XX PR 19-APR-1995; 95MO-US004712.
XX PR 15-OCT-1996; 96US-00722187.
XX PA (NOVUS ) NOVARTIS FINANCE CORP.
XX PI Beck JI;
XX DR WPI; 1998-541745/46.
XX PT DNA isolated from fungal RNA, and its internal transcribed spacer
XX PT sequence - used for detecting fungal pathogens in plant tissue.
XX PS Claim 2; Fig 3; 56pp; English.
XX CC This represents the consensus DNA sequence of the internal transcribed
XX CC spacer (ITS) region that was PCR amplified from Fusarium culmorum
XX CC isolates, R-5106, R-5126 and R-5146. The invention provides a DNA
XX CC molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX CC pathogen, where the DNA molecule consists of an ITS sequence selected
XX CC from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX CC moniliforme, Septoria avenae or Microdochium nivale. A method for
XX CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX CC avenaceum and M. nivale isolates is also provided. The method comprises
XX CC isolating DNA from a plant leaf infected with at least one of the above
XX CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX CC PCR using specific primers from within these sequences. The pathogen(s)
XX CC are detected by visualising the amplified part of the ITS sequence
XX SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGATGTTG 18
Db 457 CCCAACTTCTGATGTTG 474

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RESULT 9
ID AAV62591 standard; DNA; 504 BP.
XX AC AAV62591;
XX DT 17-DEC-1998 (first entry)
XX DE Fusarium culmorum PCR amplified ITS region consensus DNA sequence.
XX KW Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX KW Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX KW PCR; nucleic acid detection; ss.
XX OS Fusarium culmorum.

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RESULT 10
ID AAV59028 standard; DNA; 504 BP.
XX AC AAV59028;
XX DT 25-MAR-2003 (revised)
XX DT 06-JAN-1999 (first entry)
XX DE F. culmorum internal transcribed spacer.

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XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.
XX
XX Fusarium culmorum.
XX
XX Key Location/Qualifiers
XX misc_feature 13..161
XX /tag= a
XX /note= "ITS1"
XX 319..472
XX /tag= b
XX /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ;
XX
XX WPI; 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a basis
XX for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.
XX
XX Disclosure; Col 21-22; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing
XX the infection allows early, and more specific fungicidal treatment.
XX (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
XX Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCCAACTTCTGATGTTG 18
XX ||||||||||||||||
XX 457 CCCAACTTCTGATGTTG 474
XX
XX RESULT 11
XX AAS08426
XX ID AAS08426 standard; DNA; 504 BP.
XX
XX AAS08426;
XX
XX 26-SEP-2001 (first entry)
XX
XX Internal transcribed spacer, ITS, region #16.
XX
XX Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;
XX Sharp eyespot; fungal pathotype identification; isolate 62215.
XX
XX Fusarium culmorum.
XX
XX WO200151653-A1.
XX

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PD 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-EP000172.
XX
XX 11-JAN-2000; 2000US-00481293.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JJ, Barnett CJ;
XX
XX WPI; 2001-442154/47.
XX
XX New internal transcribed spacer DNA sequences, useful for identifying
XX fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring
XX disease development in plant population.
XX
XX Disclosure; Page 31; 35pp; English.
XX
XX The sequence is an internal transcribed spacer (ITS) region from Fusarium
XX culmorum, isolate 62215. The ITS DNA sequences are useful for detecting
XX Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot.
XX for monitoring disease development in plant population, and for providing
XX detailed information on the development and spread of specific pathogen
XX races over extended geographical areas. The DNA sequences are
XX specifically used as primers in PCR-based analysis for the identification
XX of fungal pathotypes
XX
XX Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;
XX
XX Query Match 100.0%; Score 18; DB 4; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCCAACTTCTGATGTTG 18
XX ||||||||||||||||
XX 459 CCCAACTTCTGATGTTG 476
XX
XX RESULT 12
XX ACC50000
XX ID ACC50000 standard; DNA; 521 BP.
XX
XX ACC50000;
XX
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #2.
XX
XX Mitochondria; fungal pathogen; ds.
XX
XX Gibberella zeae.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JJ, Barnett CJ;
XX
XX WPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
XX comprises subjecting the DNA to PCR amplification using at least one
XX primer having sequence identity with at least 10 contiguous nucleotides
XX of Fusarium spp.
XX
XX Claim 5; Page 38; 44pp; English.
XX

```


CC This invention relates to the detection of a fungal pathogen comprising
 CC isolating DNA from a plant leaf infected with a pathogen. The methods and
 CC primers are useful for identifying fungal isolates of fungal pathogens
 CC and monitoring of disease development in plant populations. The present
 CC sequence represents an internal transcribed spacer RNA encoding sequence
 XX
 SQ Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 521;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
 |||||
 DB 473 CCCAACTTCTGAATGTTG 490

RESULT 13
 ACC4999
 ID ACC49999 standard; DNA; 522 BP.
 XX
 AC ACC49999;

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence.

XX Mitochondria; fungal pathogen; ds.

OS Fusarium subglutinans.

PN WO2003027635-A2.

PD 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Beck JI, Barnett CJ;

DR WPI; 2003-363229/34.

XX
 PT Detecting a fungal pathogen, useful for monitoring disease development,
 PT comprises subjecting the DNA to PCR amplification using at least one
 PT primer having sequence identity with at least 10 contiguous nucleotides
 of Fusarium spp.

PS Claim 5; Page 38; 44pp; English.

CC This invention relates to the detection of a fungal pathogen comprising
 CC isolating DNA from a plant leaf infected with a pathogen. The methods and
 CC primers are useful for identifying fungal isolates of fungal pathogens
 CC and monitoring of disease development in plant populations. The present
 CC sequence represents an internal transcribed spacer RNA encoding sequence
 XX
 SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 522;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
 |||||
 DB 474 CCCAACTTCTGAATGTTG 491

RESULT 14
 ACC50002
 ID ACC50002 standard; DNA; 522 BP.
 XX

AC ACC50002;

XX 27-OCT-2003 (revised)

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #4.

XX Mitochondria; fungal pathogen; ds.

OS Gibberella moniliformis.

PN WO2003027635-A2.

PD 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Beck JI, Barnett CJ;

DR WPI; 2003-363229/34.

XX
 PT Detecting a fungal pathogen, useful for monitoring disease development,
 PT comprises subjecting the DNA to PCR amplification using at least one
 PT primer having sequence identity with at least 10 contiguous nucleotides
 of Fusarium spp.

PS Claim 5; Page 39; 44pp; English.

CC This invention relates to the detection of a fungal pathogen comprising
 CC isolating DNA from a plant leaf infected with a pathogen. The methods and
 CC primers are useful for identifying fungal isolates of fungal pathogens
 CC and monitoring of disease development in plant populations. The present
 CC sequence represents an internal transcribed spacer RNA encoding sequence.
 (Updated on 27-OCT-2003 to standardise OS field)

XX SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 522;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
 |||||
 DB 474 CCCAACTTCTGAATGTTG 491

RESULT 15
 ACC50001

ID ACC50001 standard; DNA; 534 BP.

AC ACC50001;

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #3.

XX Mitochondria; fungal pathogen; ds.

OS Fusarium proliferatum.

PN WO2003027635-A2.

PD 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Beck JJ, Barnett CJ;
PI WPI; 2003-363229/34.
XX
DR
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of *Fusarium* spp.
XX
XX
PS Claim 5; Page 38-39; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
SQ Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 534;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCAAGTTCTGATGTTG 18
|||||
Db 486 CCCAAGTTCTGATGTTG 503

Search completed: October 1, 2004, 03:41:25
Job time : 35.9347 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 146.608 Seconds
(without alignments)
5321.503 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18

Sequence: 1 cccactctcgatgctg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vt:*

15: gb_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vt:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_hngo_hum:*

40: em_hngo_mus:*

41: em_hngo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	18 100.0	18 6	AR206453	AR206453 Sequence
2	18 100.0	18 6	BD083644	BD083644 Nucleic a
3	18 100.0	298 8	AY226096	AY226096 Nectria h
4	18 100.0	310 6	AR206401	AR206401 Sequence
5	18 100.0	310 6	BD083592	BD083592 Nucleic a
6	18 100.0	310 8	AF117922	AF117922 Gibberella
7	18 100.0	319 6	AR206400	AR206400 Sequence
8	18 100.0	319 6	BD083591	BD083591 Nucleic a
9	18 100.0	319 8	AF117921	AF117921 Nectria h
10	18 100.0	332 8	AF162901	AF162901 Fusarium
11	18 100.0	334 8	AF162902	AF162902 Fusarium
12	18 100.0	335 8	AF162898	AF162898 Fusarium
13	18 100.0	335 8	AF162899	AF162899 Fusarium
14	18 100.0	336 8	AF162900	AF162900 Fusarium
15	18 100.0	338 8	AF339418	AF339418 Fusarium
16	18 100.0	338 8	AY074751	AY074751 Theobroma
17	18 100.0	338 8	AY074752	AY074752 Theobroma
18	18 100.0	338 8	AY074753	AY074753 Theobroma
19	18 100.0	349 8	AF162897	AF162897 Fusarium
20	18 100.0	351 8	AF162903	AF162903 Fusarium
21	18 100.0	432 8	AY273305	AY273305 Unculture
22	18 100.0	434 8	AY243055	AY243055 Ascomycet
23	18 100.0	447 8	AY387701	AY387701 Fusarium
24	18 100.0	449 8	AY143084	AY143084 Fusarium
25	18 100.0	451 8	AF502788	AF502788 Leaf lict
26	18 100.0	471 8	AF161222	AF161222 Fusarium
27	18 100.0	472 8	AY210325	AY210325 Fusarium
28	18 100.0	472 8	AY210328	AY210328 Fusarium
29	18 100.0	473 8	AY210333	AY210333 Fusarium
30	18 100.0	475 8	SCAJ2875	AY002875 Fungul is
31	18 100.0	477 8	AY210330	AY210330 Fusarium
32	18 100.0	480 8	AY210331	AY210331 Fusarium
33	18 100.0	480 8	AY210332	AY210332 Fusarium
34	18 100.0	481 8	AY210327	AY210327 Nectria s
35	18 100.0	482 8	AF111057	AF111057 Fusarium
c	36 18 100.0	483 8	AY043477	AY043477 Nectria h
37	18 100.0	483 8	AY273333	AY273333 Unculture
38	18 100.0	486 8	SCAJ2876	AY002876 Fungul is
39	18 100.0	487 8	AF165875	AF165875 Fusarium
40	18 100.0	489 8	AF502862	AF502862 Leaf lict
41	18 100.0	489 8	AY160207	AY160207 Fusarium
42	18 100.0	489 8	AY160209	AY160209 Fusarium
43	18 100.0	490 8	AF502792	AF502792 Leaf lict
44	18 100.0	492 8	AF111053	AF111053 Fusarium
45	18 100.0	492 8	AF111059	AF111059 Fusarium

ALIGNMENTS

RESULT 1

AR206453

LOCUS AR206453 18 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 59 from patent US 6372430.

ACCESSION AR206453

VERSION AR206453.1 GI:21505059

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.

Nucleic acids for detecting Aspergillus species and other filamentous fungi

PATENT: US 6372430-A 59 16-APR-2002;

JOURNAL

FEATURES	Location/Qualifiers
source	1..18 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 42;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCAACTTCTGAATGTTG 18
DB	1 CCCAACTTCTGAATGTTG 18
RESULT 2	
BD083644	BD083644 18 bp DNA linear PAT 27-AUG-2002
LOCUS	
DEFINITION	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi.
ACCESSION	BD083644
VERSION	BD083644.1 GI:22629254
KEYWORDS	JP 2001525665-A/59.
SOURCE	<i>Rhizopus microsporus</i>
ORGANISM	<i>Rhizopus microsporus</i> <i>Eukaryota</i> ; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae; <i>Rhizopus</i> .
REFERENCE	1 (bases 1 to 18) Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
AUTHORS	
TITLE	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi
JOURNAL	Patent: JP 2001525665-A 59 11-DEC-2001; THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
COMMENT	PN JP 2001525665-A/59 PD 11-DEC-2001 PF 01-MAY-1998 JP 1998548275 PR 02-MAY-1997 US 60/045400 PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO PI CHOI
PC	CI2QI/68
CC	Strandedness: Single;
CC	Topology: Linear;
FH	Key Location/Qualifiers.
FEATURES	
source	1..18 Location/Qualifiers /organism="Rhizopus microsporus" /mol_type="genomic DNA" /db_xref="taxon:58291"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 42;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCAACTTCTGAATGTTG 18
DB	1 CCCAACTTCTGAATGTTG 18
RESULT 3	
AY226096	AY226096 298 bp DNA linear PLN 27-MAR-2003
LOCUS	
DEFINITION	<i>Nectria haematococca</i> 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AY226096
VERSION	AY226096.1 GI:29293692
KEYWORDS	
SOURCE	<i>Nectria haematococca</i>

ORGANISM	Nectria haematococca
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
AUTHORS	1 (bases 1 to 298)
TITLE	Millar,B.C., Xu,J. and Moore,J.E.
JOURNAL	Direct Submission
FEATURES	Submitted (28-JUN-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
source	location/Qualifiers 1..298 /organism="Nectria haematococca" /mol_type="genomic DNA" /strain="260499/24" /db_xref="taxon:140110" <1..132 /product="r5.8S ribosomal RNA" 133..245 /product="internal transcribed spacer 2" 246..>298 /product="28S ribosomal RNA"
rRNA	
misc_RNA	
Query Match	100.0%; Score 18; DB 8; Length 298;
Best Local Similarity	100.0%; Pred. No. 44;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CCCAAGCTTCGAATGTTG 18
Db	240 CCCAAGCTTCGAATGTTG 257
RESULT 4	
LOCUS	AR206401 310 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 7 from patent US 6372430.
ACCESSION	AR206401
VERSION	AR206401.1 GI:21504992
KEYWORDS	.
SOURCE	Unknown. Unknwn.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 310)
AUTHORS	Morrison,C.V., Reis,E., Aldrevich,L. and Choi,V.Soo.
TITLE	Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL	Patent: US 6372430-A 7 16-Apr-2002;
FEATURES	location/Qualifiers 1..310 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 310;
Best Local Similarity	100.0%; Pred. No. 44;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 CCCAACTTCGAATGTG 18
Db	258 CCCAACTTCGAATGTG 275
RESULT 5	
LOCUS	BD083592 310 bp DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION	BD083592
VERSION	BD083592.1 GI:22629202
KEYWORDS	JP 2001525665-A/7.
SOURCE	Gibberella fujikuroi
ORGANISM	Gibberella fujikuroi
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hydrocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujiikuroi complex.
1 (bases 1 to 310)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other filamentous fungi.
Patent: JP 2001525665-A 7 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
OS Fusarium moniliforme
PN JP 2001525665-A/7
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
PC C1201/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Source 1. .310
/organism="Gibberella fujiikuroi"
/mol_type="genomic DNA"
/db_xref="taxon:5127"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 CCCAAGTTCTGAATGTTG 18
|||||
258 CCCAAGTTCTGAATGTTG 275
RESULT 6
AF117922 310 bp DNA linear PLN 17-JUN-2000
LOCUS Gibberella fujiikuroi ATCC 38519 5.8S ribosomal RNA gene, partial
DEFINITION sequence: internal transcribed spacer 2, complete sequence; and 26S
ribosomal RNA gene, partial sequence.
ACCESSION AF117922 GI:8570108
VERSION AF117922.1 GI:8570108
KEYWORDS
ORGANISM Gibberella fujiikuroi
Gibberella fujiikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujiikuroi complex.
1 (bases 1 to 310)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
Rapid differentiation of filamentous fungi using species-specific DNA probes
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
2 (bases 1 to 310)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Direct Submission
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA
FEATURES
Source Location/Qualifiers
1. .310
/organism="Gibberella fujiikuroi"
/mol_type="genomic DNA"
/strain="ATCC 38519"
/db_xref="ATCC:38519"
/db_xref="taxon:5127"
rRNA
/product="5.8S ribosomal RNA"
159. .272
misc_RNA

/product="internal transcribed spacer 2"
/note="ITS2"
273. .310
/product="28S ribosomal RNA"
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Query Match 100.0%; Score 18; DB 8; Length 310;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 CCCAAGTTCTGAATGTTG 18
|||||
258 CCCAAGTTCTGAATGTTG 275
RESULT 7
AR206400 319 bp DNA linear PAT 20-JUN-2002
LOCUS AR206400
DEFINITION Sequence 6 from patent US 6372430.
ACCESSION AR206400
VERSION AR206400.1 GI:21504990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 319)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.
Nucleic acids for detecting Aspergillus species and other filamentous fungi
Patent: US 6372430-A 6 16-APR-2002;
FEATURES
Source 1. .319
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 CCCAAGTTCTGAATGTTG 18
|||||
267 CCCAAGTTCTGAATGTTG 284
RESULT 8
BD083591 319 bp DNA linear PAT 27-AUG-2002
LOCUS BD083591
DEFINITION Nucleic acids for detecting Aspergillus species and other
filamentous fungi.
ACCESSION BD083591
VERSION BD083591.1 GI:22629201
KEYWORDS JP 2001525665-A/6.
SOURCE Fusarium solani
ORGANISM Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 319)
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
Nucleic acids for detecting Aspergillus species and other filamentous fungi
Patent: JP 2001525665-A 6 11-DEC-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
OS Fusarium solani
PN JP 2001525665-A/6
PD 11-DEC-2001
PF 01-MAY-1998 JP 1998548275
PR 02-MAY-1997 US 60/045400
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO

[illegible]

ACCESSION	RNA gene, partial sequence.									
VERSION	AF162901									
KEYWORDS	AF162901.1 GI:5690390									
SOURCE	Fusarium equiseti									
ORGANISM	Fusarium equiseti									
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.									
AUTHORS	1 (bases 1 to 332)									
TITLE	Min,B.R.									
JOURNAL	Direct Submission									
FEATURES	Submitted (28-JUN-1999) BIOLOGY, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea									
SOURCE	Location/Qualifiers									
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	/strain="MAFF 236724"									
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	<1..128									
	/product="5.8S ribosomal RNA"									
	129..274									
	/product="internal transcribed spacer 2"									
	275..>332									
	/product="28S ribosomal RNA"									
ORIGIN										
Query Match	100.0%; Score 18; DB 8; Length 332;									
Best Local Similarity	100.0%; Pred. No. 44;									
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1 CCCAACTTCGAATGTTG 18									
Db	260 CCCAACTTCGAATGTTG 277									
RESULT 11										
AF162902	334 bp DNA linear PLN 04-AUG-1999									
LOCUS	Fusarium pallidoreum 5.8S ribosomal RNA gene, partial sequence;									
DEFINITION	internal transcribed spacer 2, complete sequence; and 28S ribosomal									
	RNA gene, partial sequence.									
ACCESSION	AF162902									
VERSION	AF162902.1 GI:5690391									
KEYWORDS	Fusarium pallidoreum									
SOURCE	Fusarium pallidoreum									
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.									
REFERENCE	1 (bases 1 to 334)									
AUTHORS	Min,B.R.									
TITLE	Direct Submission									
JOURNAL	Submitted (28-JUN-1999) BIOLOGY, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea									
FEATURES	Location/Qualifiers									
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	129..276									
	/product="internal transcribed spacer 2"									
	277..>334									
	/product="28S ribosomal RNA"									
ORIGIN										
Query Match	100.0%; Score 18; DB 8; Length 334;									
Best Local Similarity	100.0%; Pred. No. 44;									
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1 CCCAACTTCGAATGTTG 18									

Db 262 CCNACTTCTGAATGTTG 279

RESULT 12
AF162898 335 bp DNA linear PLN 15-NOV-2001
LOCUS AF162898
DEFINITION Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF162898.1 GI:5690387
VERSION AF162898
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. conglutinans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 335)
Min,B.R.
REFERENCE Direct Submission
AUTHORS Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
TITLE Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL Location/Qualifiers
FEATURES
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1..335
/organism="Fusarium oxysporum f. sp. conglutinans"
/mol_type="genomic DNA"
/strain="MAF 744001"
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/product="5.8S ribosomal RNA"
129..277
/product="internal transcribed spacer 2"
278..335
/product="28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNACTTCTGAATGTTG 18
|||||
263 CCNACTTCTGAATGTTG 280

RESULT 13
AF162899 335 bp DNA linear PLN 04-AUG-1999
LOCUS AF162899
DEFINITION Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF162899.1 GI:5690388
VERSION AF162899
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 335)
Min,B.R.
REFERENCE Direct Submission
AUTHORS Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
TITLE Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL Location/Qualifiers
FEATURES
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/organism="Fusarium oxysporum f. sp. fragariae"
/mol_type="genomic DNA"
/strain="MAF 744009"
/db_xref="taxon:100903"

RNA
/note="forma specialis: fragariae"
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<1..128
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129..277
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ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNACTTCTGAATGTTG 18
|||||
263 CCNACTTCTGAATGTTG 280

RESULT 14
AF162900 336 bp DNA linear PLN 04-AUG-1999
LOCUS AF162900
DEFINITION Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF162900.1 GI:5690389
VERSION AF162900
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
1 (bases 1 to 336)
Min,B.R.
REFERENCE Direct Submission
AUTHORS Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
TITLE Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL Location/Qualifiers
FEATURES
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<1..128
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129..274
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275..336
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Query Match 100.0%; Score 18; DB 8; Length 336;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNACTTCTGAATGTTG 18
|||||
264 CCNACTTCTGAATGTTG 281

RESULT 15
AF339418 338 bp DNA linear PLN 25-OCT-2002
LOCUS AF339418
DEFINITION Fusarium oxysporum strain FS-1 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF339418.1 GI:24369714
VERSION AF339418
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum
Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 338)
AUTHORS Tooley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M.
TITLE Use of ligase chain reaction for detection of Phytophthora
infestans in potatoes

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 338)
AUTHORS Tooley,P.W., Hatziloukas,E., Scott,D.L. Jr. and Carras,M.M.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2001) Agricultural Research Service, U.S.
Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD
21702-5023, USA

FEATURES
source location/Qualifiers
1..338
/organism="Fusarium oxysporum"
/mol_type="genomic DNA"
/strain="PS-1"
/db_xref="taxon:5507"
misc_RNA
/note="contains 5.8S ribosomal RNA, internal transcribed
spacer 2, and 28S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 338;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGCTTCGAATGTTG 18
|||
Db 265 CCCAAGCTTCGAATGTTG 282

Search completed: October 1, 2004, 05:17:04
Job time : 148.108 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds
(without alignments)
1693.989 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18

Sequence: 1 cccactctcgatgttg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	18	100.0	18	US-09-423-233-59
2	18	100.0	310	US-09-423-233-7
3	18	100.0	319	US-09-423-233-6
4	18	100.0	503	US-08-887-480-83
5	18	100.0	503	US-08-905-314A-20
6	18	100.0	503	US-08-722-187-83
7	18	100.0	503	PCT-US95-04712-83
8	18	100.0	504	US-08-887-480-82
9	18	100.0	504	US-08-905-314A-19
10	18	100.0	504	US-08-722-187-82
11	18	100.0	504	US-09-481-293-32
12	18	100.0	504	PCT-US95-04712-82
13	18	100.0	545	US-08-887-480-84
14	18	100.0	545	US-08-905-314A-21
15	18	100.0	546	US-08-887-480-96
16	18	100.0	546	US-08-905-314A-22
17	18	100.0	561	US-08-905-314A-24
18	18	100.0	2293	US-09-645-073-1
19	18	94.4	1258	US-08-335-518-1
20	17	94.4	1258	US-08-988-054-1
21	15.4	85.6	583	US-08-652-127C-8
22	15.4	85.6	611	US-08-986-727-4
23	15	83.3	1309	US-08-933-750C-63
24	15	83.3	1309	US-09-234-613-63
25	15	83.3	1426	US-09-121-425-4
26	15	83.3	1426	US-09-634-483A-4
27	15	83.3	2513	US-09-016-434-1166

ALIGNMENTS

28	15	83.3	39982	4	US-09-820-924-3	Sequence 3, Appli
29	14.8	82.2	894	4	US-09-107-532A-1065	Sequence 1065, Ap
30	14.8	82.2	1536	4	US-09-489-039A-511	Sequence 511, App
31	14.8	82.2	4079	4	US-09-016-434-1219	Sequence 1219, Ap
32	14.8	82.2	4910	3	US-09-023-655-1125	Sequence 1125, Ap
33	14.8	82.2	11703	3	US-09-101-886B-3	Sequence 3, Appli
34	14.8	82.2	246240	2	US-08-724-394A-20	Sequence 20, Appl
35	14.8	82.2	246240	2	US-08-724-394A-21	Sequence 21, Appl
36	14.8	82.2	246240	2	US-08-724-394A-22	Sequence 22, Appl
37	14.4	80.0	163	3	US-08-986-727-13	Sequence 13, Appl
38	14.4	80.0	284	4	US-09-313-294A-1021	Sequence 1021, Ap
39	14.4	80.0	415	3	US-08-905-223-166	Sequence 166, App
40	14.4	80.0	1053	3	US-09-148-545-91	Sequence 91, Appl
41	14.4	80.0	1075	4	US-09-148-545-92	Sequence 92, Appl
42	14.4	80.0	1105	4	US-09-148-545-26	Sequence 26, Appl
43	14.4	80.0	1317	4	US-09-350-756-5	Sequence 5, Appli
44	14.4	80.0	2088	1	US-08-331-194-1	Sequence 1, Appli
45	14.4	80.0	2088	1	US-08-250-858-1	Sequence 1, Appli

RESULT 1
US-09-423-233-59
Sequence 59, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT FILING DATE: US/09/423.233
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium sp.
US-09-423-233-59

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCCAATTCTGAATGTTG 18
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RESULT 2
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT FILING DATE: US/09/423.233
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match 100.0%; Score 18; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
Db 258 CCCACTTCTGAATGTTG 275

RESULT 3
US-09-423-233-6
; Sequence 6, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
; US-09-423-233-6

Query Match 100.0%; Score 18; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
Db 267 CCCACTTCTGAATGTTG 284

RESULT 4
US-08-887-480-83
; Sequence 83, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium graminearum
INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..9
OTHER INFORMATION: /note="3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10..155
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 156..312
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 313..466
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 467..503
OTHER INFORMATION: /note="5' end of large subunit
OTHER INFORMATION: rRNA gene"
; US-08-887-480-83

Query Match 100.0%; Score 18; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
Db 451 CCCACTTCTGAATGTTG 468

RESULT 5
US-08-905-314A-20
; Sequence 20, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 20:

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SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium graminearum
INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..9
OTHER INFORMATION: /note="3' end of small subunit"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10..155
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 156..312
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 313..466
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 467..503
OTHER INFORMATION: /note="5' end of large subunit"
OTHER INFORMATION: RNA gene"
US-08-905-314A-20
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Query Match 100.0%; Score 18; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCAAGCTTCGAAGTTG 18
Db 451 CCCAAGCTTCGAAGTTG 468
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RESULT 6
US-08-722-187-83
Sequence 83, Application US/08722187
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722.187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
```

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NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..503
OTHER INFORMATION: /note="DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium graminearum"
US-08-722-187-83
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Query Match 100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCAAGCTTCGAAGTTG 18
Db 451 CCCAAGCTTCGAAGTTG 468
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RESULT 7
PCT-US95-04712-83
Sequence 83, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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; HYPOTHETICAL: NO
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..503
; OTHER INFORMATION: /note= "DNA sequence for the
; OTHER INFORMATION: internal transcribed spacer region of Fusarium graminearum
; OTHER INFORMATION: (fgam.con)"
; PCT-US95-04712-83

Query Match      100.0%; Score 18; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCCAATTCTGATGTTG 18
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Db      451 CCCAATTCTGATGTTG 468

RESULT 8
US-08-887-480-82
; Sequence 82, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; NAME/KEY: misc feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 319..472
; OTHER INFORMATION: /note= "ITS 2"
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 473..504
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
; US-08-887-480-82

Query Match      100.0%; Score 18; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCCAATTCTGATGTTG 18
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Db      457 CCCAATTCTGATGTTG 474

RESULT 9
US-08-905-314A-19
; Sequence 19, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
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/ NAME/KEY: misc_feature
/ LOCATION: 13..161
/ OTHER INFORMATION: /note="ITS 1"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 162..318
/ OTHER INFORMATION: /note="5.8S rRNA gene"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 319..472
/ OTHER INFORMATION: /note="ITS 2"
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/ OTHER INFORMATION: /note="5' end of large subunit"
/ OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match      100.0%; Score 18; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCAAGTTCTGAATGTTG 18
Db      457 CCCAAGTTCTGAATGTTG 474

RESULT 10
US-08-722-187-82
/ Sequence 82, Application US/08722187
/ Patent No. 5955274
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M
/ TITLE OF INVENTION: Detection of Fungal Pathogens Using the
/ TITLE OF INVENTION: Polymerase Chain Reaction
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ciba-Geigy Corporation
/ STREET: 7 Skyline Drive
/ CITY: Hawthorne
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10532
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/722.187
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/233,608
/ FILING DATE: 04-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Walsh, Andrea C.
/ REGISTRATION NUMBER: 34,988
/ REFERENCE/DOCKET NUMBER: CGC 1739
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8666
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 82:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 504 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ FEATURE:
/ NAME/KEY: misc_feature
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/ LOCATION: 1..504
/ OTHER INFORMATION: /note="DNA sequence for the
/ OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
/ OTHER INFORMATION: (fcultm.con)"
US-08-722-187-82

Query Match      100.0%; Score 18; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCAAGTTCTGAATGTTG 18
Db      457 CCCAAGTTCTGAATGTTG 474

RESULT 11
US-09-481-293-32
/ Sequence 32, Application US/09481293
/ Patent No. 6485907
/ GENERAL INFORMATION:
/ APPLICANT: Beck, James
/ APPLICANT: Barnett, Jason
/ TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
/ FILE REFERENCE: PB/5-31135PI
/ CURRENT APPLICATION NUMBER: US/09/481,293
/ CURRENT FILING DATE: 2000-01-11
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 504
/ TYPE: DNA
/ ORGANISM: Fusarium culmorum
US-09-481-293-32

Query Match      100.0%; Score 18; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CCCAAGTTCTGAATGTTG 18
Db      459 CCCAAGTTCTGAATGTTG 476

RESULT 12
PCT-US95-04712-82
/ Sequence 82, Application PC/TUS9504712
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M
/ APPLICANT: Beck, James J
/ TITLE OF INVENTION: Detection of Fungal Pathogens Using the
/ TITLE OF INVENTION: Polymerase Chain Reaction
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ciba-Geigy Corporation
/ STREET: 7 Skyline Drive
/ CITY: Hawthorne
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10532
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04712
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/233,608
/ FILING DATE: 04-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Walsh, Andrea C.
```

REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fcu1m.con)"
PCT-US95-04712-82

Query Match 100.0%; Score 18; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTCTGATGTTG 18
Db 457 CCCACTCTGATGTTG 474

RESULT 13
US-08-887-480-84
; Sequence 84, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8687
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: PCRMON1
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-887-480-84

Query Match 100.0%; Score 18; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTCTGATGTTG 18
Db 473 CCCACTCTGATGTTG 490

RESULT 14
US-08-905-314A-21
; Sequence 21, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium moniliforme
INDIVIDUAL ISOLATE: 4551
IMMEDIATE SOURCE:
CLONE: PCRPMON1
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..178
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-21

Query Match 100.0%; Score 18; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCAAGTTCTGATGTTG 18
Db 473 CCCAAGTTCTGATGTTG 490

RESULT 15
US-08-887-480-96
Sequence 96, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: PCRpoaeT427(1-2), PCRpoaeT534(2-2), and
CLONE: PCRpoaeT756(3-1)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-887-480-96

Query Match 100.0%; Score 18; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCAAGTTCTGATGTTG 18
Db 474 CCCAAGTTCTGATGTTG 491

Search completed: October 1, 2004, 08:06:06
Job time : 7.93182 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 : Search time 73.304 Seconds
(without alignments)
1244.847 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18
Sequence: 1 cccaacttcgactgttg 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	100.0	18	15	US-10-046-955-59
2	18	100.0	310	15	US-10-046-955-7
3	18	100.0	319	15	US-10-046-955-6
4	18	100.0	521	10	US-09-961-755A-6
5	18	100.0	522	10	US-09-961-755A-5
6	18	100.0	522	10	US-09-961-755A-8
7	18	100.0	534	10	US-09-961-755A-7
8	17	94.4	666	13	US-10-027-632-229494
9	17	94.4	666	16	US-10-027-632-229494
10	16.4	91.1	382	13	US-10-424-599-66950
11	16.4	91.1	879	17	US-10-767-701-4881
12	16.4	91.1	906	17	US-10-437-963-82909
13	16.4	91.1	1566	17	US-10-437-963-82910
14	16.4	91.1	13444	9	US-09-764-877-3660

15	16.4	91.1	13444	16	US-10-242-515-3660	Sequence 3660, Ap
16	16.4	91.1	67672	17	US-10-316-242-11	Sequence 11, Appl
17	15.4	85.6	332	13	US-10-424-599-19065	Sequence 19065, A
18	15.4	85.6	340	13	US-10-198-846-11981	Sequence 11981, A
19	15.4	85.6	385	13	US-10-424-599-120953	Sequence 120953, A
20	15.4	85.6	476	13	US-10-424-599-70014	Sequence 70014, A
21	15.4	85.6	579	13	US-10-424-599-57294	Sequence 57294, A
22	15.4	85.6	617	13	US-10-027-632-94609	Sequence 94609, A
23	15.4	85.6	617	13	US-10-027-632-305503	Sequence 305503, A
24	15.4	85.6	617	16	US-10-027-632-94609	Sequence 94609, A
25	15.4	85.6	617	16	US-10-027-632-305503	Sequence 305503, A
26	15.4	85.6	660	17	US-10-767-701-24598	Sequence 24598, A
27	15.4	85.6	739	15	US-10-198-846-3876	Sequence 3876, Ap
28	15.4	85.6	828	13	US-10-424-599-4529	Sequence 4529, Ap
29	15.4	85.6	1500	16	US-10-369-493-27922	Sequence 27922, A
30	15.4	85.6	1582	13	US-10-424-599-114901	Sequence 114901, A
31	15.4	85.6	1599	13	US-10-282-122A-12302	Sequence 12302, A
32	15.4	85.6	3607	13	US-10-424-599-19067	Sequence 19067, A
33	15.4	85.6	23640	13	US-10-087-192-12439	Sequence 1249, Ap
34	15.4	85.6	46030	17	US-10-367-094-1	Sequence 1, Appl
35	15.4	85.6	55155	9	US-09-735-933-1	Sequence 3, Appl
36	15.4	85.6	89213	17	US-10-322-281-843	Sequence 843, App
37	15.4	85.6	90100	12	US-09-397-722-295	Sequence 295, App
38	15.4	85.6	188794	17	US-10-322-696-112	Sequence 112, App
39	15	83.3	211	13	US-10-085-783A-33208	Sequence 33208, A
40	15	83.3	211	16	US-10-242-535A-33208	Sequence 33208, A
41	15	83.3	309	13	US-10-085-783A-55973	Sequence 55973, A
42	15	83.3	309	16	US-10-242-535A-55973	Sequence 55973, A
43	15	83.3	350	13	US-10-085-783A-9757	Sequence 9757, Ap
44	15	83.3	350	16	US-10-242-535A-9757	Sequence 9757, Ap
45	15	83.3	575	13	US-10-424-599-47112	Sequence 47112, A

ALIGNMENTS

RESULT 1

US-10-046-955-59
Sequence 59, Application US/10046955
Publication No. US20030129600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
Secretary of the Department of Health and Human Services, Centers for Dis
eases Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Amdorovich, Liliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium sp.
US-10-046-955-59

Query Match 100.0%, Score 18, DB 15, Length 18,
Best Local Similarity 100.0%, Pred. No. 12,
Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
1 CCAACTTCGACTGTG 18
|||||

Db 1 CCCAACTTCTGAATGTTG 18

RESULT 2

US-10-046-955-7
; Sequence 7, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliانا
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match 100.0%; Score 18; DB 15; Length 310;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18

Db 258 CCCAACTTCTGAATGTTG 275

RESULT 3

US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Liliانا
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6

Query Match 100.0%; Score 18; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
Db 267 CCCAACTTCTGAATGTTG 284

RESULT 4

US-09-961-755A-6
; Sequence 6, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6

Query Match 100.0%; Score 18; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
Db 473 CCCAACTTCTGAATGTTG 490

Db 473 CCCAACTTCTGAATGTTG 490

RESULT 5
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

Query Match 100.0%; Score 18; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18
Db 474 CCCAACTTCTGAATGTTG 491

RESULT 6
US-09-961-755A-8
; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:

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; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match          100.0%; Score 18; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCAACTTCTGAATGTTG 18
Db      474 CCAACTTCTGAATGTTG 491

RESULT 7
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match          100.0%; Score 18; DB 10; Length 534;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCAACTTCTGAATGTTG 18
Db      486 CCAACTTCTGAATGTTG 503

RESULT 8
US-10-027-632-229494/c
; Sequence 229494, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 229494
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (666)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-229494

Query Match          94.4%; Score 17; DB 13; Length 666;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CCAACTTCTGAATGTTG 18
Db      434 CCAACTTCTGAATGTTG 418

RESULT 9
US-10-027-632-229494/c
; Sequence 229494, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 229494
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (666)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-229494

Query Match          94.4%; Score 17; DB 16; Length 666;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CCAACTTCTGAATGTTG 18
Db      434 CCAACTTCTGAATGTTG 418

RESULT 10
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US-10-424-599-66950/C
; Sequence 66950, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 66950
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31471C.1
US-10-424-599-66950
Query Match          91.1%; Score 16.4; DB 13; Length 382;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  CCCAATTCTGATGTTG 18
        |||||
Db      72  CCCAATTATGATGTTG 55

RESULT 11
US-10-767-701-4881
; Sequence 4881, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4881
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MA103-CLUS91898_1
US-10-767-701-4881
Query Match          91.1%; Score 16.4; DB 17; Length 879;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  CCCAATTCTGATGTTG 18
        |||||
Db      809  CTCACCTTCTGATGTTG 826

RESULT 12
US-10-437-963-82909/C
; Sequence 82909, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82909
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(906)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_82292C.1
US-10-437-963-82909
Query Match          91.1%; Score 16.4; DB 17; Length 906;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  CCCAATTCTGATGTTG 18
        |||||
Db      539  CCCAATTCTGATGTTG 522

RESULT 13
US-10-437-963-82910/C
; Sequence 82910, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82910
; LENGTH: 1566
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_82293C.1
US-10-437-963-82910
Query Match          91.1%; Score 16.4; DB 17; Length 1566;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  CCCAATTCTGATGTTG 18
        |||||
Db      879  CCCAATTCTGATGTTG 862

RESULT 14
US-09-764-877-3660
; Sequence 3660, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
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; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3660
; LENGTH: 13444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3660
```

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Query Match          91.1% Score 16.4; DB 9; Length 13444;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 CCCAACTTCTGATGTTG 18
        |||||
Db      299 CCCAACTTATGATGTTG 316
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```
RESULT 15
US-10-242-515-3660
; Sequence 3660, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OR INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3660
; LENGTH: 13444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3660
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Query Match          91.1% Score 16.4; DB 16; Length 13444;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 CCCAACTTCTGATGTTG 18
        |||||
Db      299 CCCAACTTATGATGTTG 316
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Job time : 75.304 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 252 Seconds
(without alignments)
2133.013 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18
Sequence: 1 cccacactcgaatgctg 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estcl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_rum:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gsscl:*
29: gb_gsscl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	379	9	AA112191
2	16.4	91.1	403	14	AA112191 zn60e02.r
3	16.4	91.1	473	10	W19631 w19631
4	16.4	91.1	523	13	BU713295 BU713295

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
AA112191	zn60e02.r1	Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562586 5' similar to WP:FO8C.3 CE02592 ;, mRNA sequence.	AA112191	1	GI:1664478	EST.	Homo sapiens (human)	1 (bases 1 to 379)	Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gibb, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, N., Marling, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M.	Generation and analysis of 280,000 human expressed sequence tags	Genome Res. 6 (9), 807-828 (1996)	8889549	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	

ALIGNMENTS

C	5	16.4	91.1	524	14	CD885707	CD885707 G118..100C
C	6	16.4	91.1	548	12	BJ108367	BJ108367
C	7	16.4	91.1	555	28	CE323958	CE323958 t19r-g88-
C	8	16.4	91.1	579	28	AQ665757	AQ665757 HS_5354_B
C	9	16.4	91.1	584	13	CA032813	CA032813 HX14E13r
C	10	16.4	91.1	587	12	BJ126336	BJ126336
C	11	16.4	91.1	604	14	CD910198	CD910198 G468..114K
C	12	16.4	91.1	606	10	AM857324	AM857324 CM1-CT030
C	13	16.4	91.1	616	14	CA220452	CA220452 SC8BR401
C	14	16.4	91.1	631	12	BI111174	BI111174 602899366
C	15	16.4	91.1	632	10	AM857329	AM857329 CM1-CT030
C	16	16.4	91.1	641	29	CE070578	CE070578 t19r-g88-
C	17	16.4	91.1	642	10	AM857322	AM857322 CM1-CT030
C	18	16.4	91.1	647	13	BY726648	BY726648
C	19	16.4	91.1	661	10	AM861372	AM861372 CM1-CT030
C	20	16.4	91.1	704	14	CA188988	CA188988 SCCCL4C0
C	21	16.4	91.1	712	13	CB657614	CB657614 OSJNEC13B
C	22	16.4	91.1	719	13	BY739516	BY739516
C	23	16.4	91.1	749	9	AV382703	AV382703 AV382703
C	24	16.4	91.1	794	14	CB657615	CB657615 OSJNEC13B
C	25	16.4	91.1	798	28	BZ995379	BZ995379 PURID06TB
C	26	16.4	91.1	802	10	BF62787	BF62787 HVSMB000
C	27	16.4	91.1	802	29	CG037213	CG037213 PUJAW96TD
C	28	16.4	91.1	808	13	BU417573	BU417573 60323292
C	29	16.4	91.1	891	28	CC382957	CC382957 PUNHGR8TD
C	30	16.4	91.1	905	28	CG165155	CG165155 PUJEL74TB
C	31	16.4	91.1	943	28	BZ169939	BZ169939 CH230..463
C	32	16.4	91.1	947	29	CG313931	CG313931 OGWH424TV
C	33	16.4	91.1	1016	12	BM919869	BM919869 AGENCOURT
C	34	16.4	91.1	284	9	AV214144	AV214144 AV214144
C	35	16.4	91.1	317	9	AV109406	AV109406 AV109406
C	36	16.4	91.1	518	28	AQ204622	AQ204622 HS_3229_B
C	37	16.4	91.1	533	12	BU590239	BU590239 BU590239
C	38	16.4	91.1	547	12	BI396526	BI396526 t054411.Y
C	39	16.4	91.1	599	29	CC843236	CC843236 NDL..112C2
C	40	16.4	91.1	610	14	CB824672	CB824672 t429E02.Y
C	41	16.4	91.1	650	14	CB378989	CB378989 t416406.Y
C	42	16.4	91.1	651	14	CB279388	CB279388 t444b02.Y
C	43	16.4	91.1	701	13	BX469546	BX469546
C	44	16.4	91.1	925	14	CB564460	CB564460 AGENCOURT
C	45	16.4	91.1	963	29	CG122910	CG122910 PUFU677B

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 768 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amerisham
 High quality sequence stop: 287.
 Location/Qualifiers

FEATURES

source

1. 379
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:4595876"
 /db_xref="taxon:9606"
 /clone="IMAGE:562586"
 /tissue_type="muscle"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene muscle 937209"
 /note="Organ: skeletal muscle; Vector: pBluescript SK-;
 Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
 Primer: Oligo dT. Skeletal muscle from patient with
 malignant hyperthermia. Average insert size: 1.0 kb;
 Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GATTGGGACGAG
 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 379;
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTTCGATGTTG 18
 |||||
 Db 361 CCCAAGTTTCGATGTTG 378

RESULT 2

W19631 403 bp mRNA linear EST 03-MAY-1996
 LOCUS zb55d09.r1 Soares_Parathyroid_tumor_NbHRA Homo sapiens cDNA clone
 DEFINITION IMAGE:305585 5', mRNA sequence.
 W19631
 W19631.1 GI:1295540

EST.
 Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 403)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P.,
 Trevaethick, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

TITLE The Mashu-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: mob.NEAG+ET
 High quality sequence stop: 264.
 Location/Qualifiers

FEATURES

source

1. 403
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1248995"
 /db_xref="taxon:9606"
 /clone="IMAGE:305585"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 403;
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTTCGATGTTG 18
 |||||
 Db 94 CCCAAGTTTCGATGTTG 77

RESULT 3

BE592535 473 bp mRNA linear EST 18-AUG-2000
 LOCUS WS1_94.C12.bl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
 DEFINITION mRNA sequence.
 BE592535
 BE592535.1 GI:9847608

EST.
 Sorghum bicolor (sorghum)
 SOURCE Sorghum bicolor
 ORGANISM Sorghum bicolor

REFERENCE
 AUTHORS
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 473)
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
 Pratt, L.H.

AN EST database from Sorghum: water-stressed plants
 Unpublished (2000)
 CONTACT: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

Email: amprat@uga.edu
 Sequences have been trimmed to exclude polyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: JEN REV
 High quality sequence stop: 464
 PolyA=No.

FEATURES

source

1. 473
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /db_xref="taxon:4558"
 /clone_lib="Water-stressed 1 (WS1)"
 /note="Organ: Mix of 5-week old plants on days 7 & 8 after
 water was withheld; Vector: Lambda Zap; Site 1: XhoI;
 Site 2: EcoRI; The library was made from poly-A RNA in the
 cloning vector lambda Zap II. Clones to be sequenced were
 prepared by mass excision."

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 473;
 Best Local Similarity 94.4%; Pred. No. 2.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCAAGTTTGAAATGTTG 18
 |||||
 Db 403 CTCACATTCGAAATGTTG 420

RESULT 4
 BU713295 523 bp mRNA linear EST 23-OCT-2003
 LOCUS SJAABOB11 Adult SJC 7/94 Schistosoma japonicum cDNA, mRNA sequence.
 DEFINITION BU713295
 ACCESSION BU713295.1 GI:28320657
 VERSION EST.
 KEYWORDS Schistosoma japonicum
 SOURCE Schistosoma japonicum
 ORGANISM Schistosoma japonicum
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 523)
 Hu, W., Yan, Q., Shen, D. K., Liu, F., Zhu, Z. D., Song, H. D., Xu, X. R.,
 Wang, Z. J., Rong, Y. P., Zeng, L. C., Wu, J., Zhang, X., Wang, J. J.,
 Xu, X. N., Wang, S. Y., Fu, G., Zhang, X. L., Wang, Z. Q., Brindley, P. J.,
 McManus, D. P., Xue, C. L., Feng, Z., Chen, Z., and Han, Z. G.
 Evolutionary and biomedical implications of a Schistosoma japonicum
 complementary DNA resource
 Nat. Genet. 35 (2), 139-147 (2003)
 22879925
 JOURNAL Contact: Zeguang Han
 MEDLINE Chinese National Human Genome Center at Shanghai
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn.
 Location/Qualifiers
 1..523
 /organism="Schistosoma japonicum"
 /mol_type="mRNA"
 /strain="Chinese (Anhui) strain"
 /db_xref="taxon:6182"
 /sex="Male and female"
 /tissue_type="Whole body"
 /dev_stage="Adult worms"
 /lab_host="Mouse and rabbit"
 /clone_id="Adult SJC 7/94"
 /note="Vector: Lambda ZAP-11 XR; Site 1: EcoR I; Site 2:
 XhoI I; Several hundred adult Schistosoma japonicum
 (Anhui, P. R. China, strain), of mixed sex, were perfused
 from the mesenteries of experimentally infected mice and
 rabbits at the Queensland Institute of Medical Research,
 Brisbane, Australia (QIMR), and stored for several months
 in liquid nitrogen. Subsequently, mRNA was isolated at the
 QIMR from lysates of these worms by oligo dt
 chromatography, using a kit from Pharmacia. The mRNA was
 then shipped to Clontech, Palo Alto, CA, USA, who
 constructed a cDNA library. First strand synthesis was
 primed with an oligo-dt-XhoI-primer and synthesized using
 M-MuLV reverse transcriptase. Second strand synthesis was
 accomplished with RNase H and T4 DNA polymerase. The
 double stranded cDNA was ligated to EcoRI linkers,
 digested with EcoRI and XhoI, and ligated into the
 phagemid vector lambda ZAP 11 XR. After construction of
 this directional library by Clontech, it was returned to
 the QIMR. During analysis of the library at the QIMR, we
 have found that a small percentage, 2% to 3%, of the
 clones contain inserts that appear to be highly homologous
 to sequences from salmonid fishes, as determined by
 homology comparisons using BLAST and by Southern
 hybridization analysis to genomic DNA from salmon (Sigma
 Chemical Co., St. Louis, MO) under stringent washing
 conditions. The remainder of the clones appear to contain

ORIGIN S. japonicum sequences."

Query Match 91.1%; Score 16.4; DB 13; Length 523;
 Best Local Similarity 94.4%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCAAGTTTGAAATGTTG 18
 |||||
 Db 489 CACACATTCGAAATGTTG 506

RESULT 5
 CD885707 524 bp mRNA linear EST 14-JUL-2003
 LOCUS G118.100C21F010423 G118 Triticum aestivum cDNA clone G118100C21,
 DEFINITION mRNA sequence.
 ACCESSION CD885707
 VERSION CD885707.1 GI:32651023
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 524)
 Genoplane.
 Genoplane, a major partnership french program in plant genomics
 Unpublished (2003)
 COMMENT Contact: Genoplane
 Genoplane
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplane' (<http://www.genoplane.com>
 and <http://genoplane-info.infobiogen.fr>).
 Location/Qualifiers
 1..524
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="rectal"
 /db_xref="taxon:4565"
 /clone="G118100C21"
 /tissue_type="grain (118 degrees per day after
 pollination)"
 /clone_id="G118"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 524;
 Best Local Similarity 94.4%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCAAGTTTGAAATGTTG 18
 |||||
 Db 226 CCCAAGTTTGAAATGTTG 209

RESULT 6
 BJ108367 548 bp mRNA linear EST 30-MAY-2003
 LOCUS BJ108367/c
 DEFINITION BJ108367 unpublished oligo-capped cDNA library, C. elegans L1 stage
 Caenorhabditis elegans cDNA clone YK1107a11 5', mRNA sequence.
 ACCESSION BJ108367
 VERSION BJ108367.2 GI:31243821
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 548)
 Kohara, Y., Shih, I. T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
 and Sugano, S.

TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT On Jan 23, 2002 this sequence version replaced gi:18268395.
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
source
1. .548
Location/Qualifiers

/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="YK107a11"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_id="unpublished oligo-capped cDNA library, C.
elegans L1 stage"

ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 548;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18
152 CCCAACTTCTGAATGTTG 135

RESULT 7
CE323958 555 bp DNA linear GSS 26-SEP-2003
LOCUS tigr-gss-dog-17000360306070 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE323958
VERSION CE323958.1 GI:36133381
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 555)
Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL MEDLINE
PUBMED 22875432
14512627

COMMENT Contact: Kirkness EF

The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: Shotgun.

FEATURES
source
Location/Qualifiers

1. .555
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_id="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 555;

Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18
Db 188 CCCAACTTCTGAATGTTG 171

RESULT 8
A0665757 579 bp DNA linear GSS 23-JUN-1999
LOCUS HS 5354 B2 E01 T7A RPCI-11 Human Male BAC library Homo sapiens
DEFINITION genomic clone Plate=930 Col=2 Row=J, genomic survey sequence.
ACCESSION A0665757
VERSION A0665757.1 GI:5173525
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end web server:
http://www.htsc.washington.edu
Plate: 930 row: J column: 2
Seq primer: T7
Class: BAC ends
High quality sequence stop: 579.
Location/Qualifiers

FEATURES
source
1. .579
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=930 Col=2 Row=J"
/sex="male"
/clone_id="RPCI-11 Human Male BAC Library"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

ORIGIN

Query Match 91.1%; Score 16.4; DB 28; Length 579;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18
Db 426 CCCAACTTCTGAATGTTG 443

RESULT 9
CA032813/c 584 bp mRNA linear EST 24-OCT-2002
LOCUS CA032813

DEFINITION HX14E13r HX Hordeum vulgare subsp. vulgare cDNA clone HX14E13
5-PRIME, mRNA sequence.
ACCESSION CA032813
VERSION
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 584)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 584 Std Error: 0.00
Plate: 14 row: E column: 13
Seq primer: M3rev.
Location/Qualifiers
1..584
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:273489"
/db_xref="taxon:112509"
/clone="HX14E13"
/tissue_type="apex"
/dev_stage="apex (3-5 mm in size)"
/lab_host="XL10-Gold"
/clone_1lb="HX"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN
Query Match 91.1%; Score 16.4; DB 13; Length 584;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGATGTTG 18
|||||
Db 396 CCCAGCTTCGATGTTG 379

RESULT 10
BU126336 587 bp mRNA linear EST 23-JAN-2002
LOCUS BU126336 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1333h08 5', mRNA sequence.
ACCESSION BU126336
VERSION BU126336.1 GI:18286488
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 587)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
TITLE A complementary view of the C. elegans genome
JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@gene.nig.ac.jp.
Location/Qualifiers
1..587
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1333h08"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_1lb="unpublished oligo-capped cDNA library, C. elegans L1 stage"

ORIGIN
Query Match 91.1%; Score 16.4; DB 12; Length 587;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGATGTTG 18
|||||
Db 401 CCCAAGCTTCGATGTTG 384

RESULT 11
CD910198/c 604 bp mRNA linear EST 14-JUL-2003
LOCUS CD910198 G468.114K19F010821 G468 Triticum aestivum cDNA clone G468114K19,
DEFINITION mRNA sequence.
ACCESSION CD910198
VERSION CD910198.1 GI:32684522
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 604)
Genoplane.
AUTHORS Genoplane.
TITLE Genoplane, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplane
Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>
and <http://genoplane-info.infobiogen.fr>).
Location/Qualifiers
1..604
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="rectal"
/db_xref="taxon:4565"
/clone="G468114K19"
/tissue_type="grain (468 degrees per day after
pollination)"
/clone_1lb="G468"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 604;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGATGTTG 18
|||||

Db 343 CCCAGCTTCTGAATGTTG 326

RESULT 12
LOCUS AW857324/c 606 bp mRNA linear EST 19-MAY-2000
DEFINITION CM1-CT0309-071399-057-b10 CT0309 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW857324
VERSION AW857324.1 GI:7953017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jorgensen,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202863
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ct2-cm1-CT0309-071399-057-b10&ct3=1999-12-07&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 606.
Location/Qualifiers
1..606
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0309"
/note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 606;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 361 CCCACTTCTGAATGTTG 344

RESULT 13
LOCUS CA220452 616 bp mRNA linear EST 25-SEP-2003
DEFINITION SCSBFL4014F10.g FL4 Saccharum officinarum cDNA clone SCSBFL4014F10
ACCESSION CA220452
VERSION CA220452.1 GI:35273771
KEYWORDS EST.

SOURCE
ORGANISM Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: patricia@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 014 row: F column: 10
Seq primer: 17 Promoter Primer.
Location/Qualifiers
1..616
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSBFL4014F10"
/lab_host="DH10B"
/clone_lib="FL4"
/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSPORT1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a Sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 616;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 330 CTCACCTTCTGAATGTTG 347

RESULT 14
LOCUS B111174/c 631 bp mRNA linear EST 26-JUN-2001
DEFINITION 60289366F1 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:5029192 5', mRNA sequence.
ACCESSION B111174
VERSION B111174.1 GI:14562075
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lnl.gov
Plate: LMAN1082 row: C column: 17
High quality sequence stop: 620.

FEATURES

source

```

1..631
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5029192"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

```

ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 631;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCAAGCTTCGATGTTG 18
|||||
Db 458 CCCAAGCTTCGATGTTG 441

RESULT 15

AW857329/c 632 bp mRNA linear EST 19-MAY-2000
LOCUS CML-CT0309-071299-057-g11 CT0309 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW857329
ACCESSION AW857329
VERSION AW857329.1 GI:7953022

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 632)
AUTHORS Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripte/gethtml2.pl?l=ct2-cml-CT0309-071299-057-g11&t3=1999-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 630.

FEATURES

source

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/mol_type="mRNA"

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ORIGIN

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Best Local Similarity 94.4%; Pred. No. 2.4e+03;
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QY 1 CCCAAGCTTCGATGTTG 18
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Db 361 CCCAAGCTTCGATGTTG 344

Search completed: October 1, 2004, 08:02:06
Job time : 259.333 secs

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